OM protein - protein search, using sw model
Run on: November 21, 2006, 20:10:39 ; Search time 259.113 Seconds
(without alignments)
404.080 Million cell updates/sec
Title: US-10-063-553-48
Perfect score: 1215
Sequence: 1 MTCCEGWTSCNGFSLLVLLL.....IVIGFLGCLCGVSKRRSQIV 229
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2589679 seqs, 457216429 residues
Total number of hits satisfying chosen parameters: 2589679
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries
Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
SUMMARIES
No. Score Match Length DB ID Description
RESULT 1
ID AAY66703 standard; protein; 229 AA.
DE Membrane-bound protein PRO994.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 2
ID AAU29122 standard; protein; 229 AA.
DE Human PRO polypeptide sequence #99.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 4; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 3
ID AAB87549 standard; protein; 229 AA.
DE Human PRO994.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 4; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 4
ID AAB65226 standard; protein; 229 AA.
DE Human PRO994 (UNQ518) protein sequence SEQ ID NO:258.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 4; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 5
ID ABG95874 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 5; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 6
ID ABU58498 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 7
ID ABU88046 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 8
ID ABU84361 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 9
ID ABR66235 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 10
ID ABR65625 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 11
ID ABU99565 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 12
ID ABU58041 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 13
ID ABU59119 standard; protein; 229 AA.
DE Novel human secreted or transmembrane protein PRO994.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 14
ID ABU82631 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 15
ID ABU82804 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 16
ID ABU89925 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036147-A1.
PD 20-FEB-2003.

Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 17
ID ABR68174 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 18
ID ABU60550 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, #103.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 19
ID ABU96227 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 20
ID ABU92658 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 21
ID ABO08735 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 22
ID ABO02787 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 23
ID ABR74941 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 24
ID ABR94703 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 25
ID ABU13932 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 26
ID ABU85676 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 27
ID ABU98836 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 28
ID ABU98051 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 29
ID ABU91757 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 30
ID ABU89450 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 31
ID ABU86291 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 32
ID ABU67504 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 33
ID ABU80532 standard; protein; 229 AA.
DE Human PRO protein #99.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 34
ID ABU72517 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 35
ID ABU90899 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 36
ID ABO33958 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.

PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 37
ID ABR99450 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 38
ID ABR98840 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 39
ID ABO16363 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 40
ID ABR92263 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 41
ID ABO18904 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 42
ID ABR78325 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 43
ID ABU71975 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 44
ID ABU85061 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 45
ID ABO00200 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 46
ID ABO11532 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 47
ID ABO02177 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 48
ID ABU88751 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 49
ID ABU83446 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 50
ID ABO06247 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 51
ID ABR59283 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 52
ID ABO09345 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 53
ID ABO19209 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 54
ID ABO11227 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 55
ID ABR66845 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 56
ID ABO16058 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040060-A1.
PD 27-FEB-2003.

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  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 57
ID   ABO13764 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003044916-A1.
PD   06-MAR-2003.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 58
ID   ABU71529 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994.
PN   US2003013855-A1.
PD   16-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 59
ID   ABU65667 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein, SEQ ID 198.
PN   US2003036156-A1.
PD   20-FEB-2003.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 60
ID   ABO07515 standard; protein; 229 AA.
DE   Human PRO polypeptide #99.
PN   US2003032117-A1.
PD   13-FEB-2003.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 61
ID   ABO03702 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003036128-A1.
PD   20-FEB-2003.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 62
ID   ABR67150 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003027266-A1.
PD   06-FEB-2003.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 63
ID   ABO15753 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003054483-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 64
ID   ABU56034 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein, PRO994.
PN   US2003022298-A1.
PD   30-JAN-2003.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 65
ID   ABU72310 standard; protein; 229 AA.
DE   Human PRO polypeptide #24.
PN   US2002182638-A1.
PD   05-DEC-2002.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 66
ID   ABU65362 standard; protein; 229 AA.
DE   Human PRO polypeptide #99.
PN   US2003032102-A1.
PD   13-FEB-2003.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 67
ID   ABU95307 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003036117-A1.
PD   20-FEB-2003.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 68
ID   ABU71210 standard; protein; 229 AA.
DE   Human PRO994 protein.
PN   US2003036143-A1.
PD   20-FEB-2003.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 69
ID   ABO07820 standard; protein; 229 AA.
DE   Human PRO polypeptide #99.
PN   US2003032130-A1.
PD   13-FEB-2003.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 70
ID   ABR70061 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003032138-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 71
ID   ABR69394 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003036132-A1.
PD   20-FEB-2003.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 72
ID   ABO01535 standard; protein; 229 AA.
DE   Human PRO polypeptide #99.
PN   US2003008353-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 73
ID   ABU81337 standard; protein; 229 AA.
DE   Human PRO polypeptide #99.
PN   US2003017542-A1.
PD   23-JAN-2003.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 74
ID   ABR60134 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003032137-A1.
PD   13-FEB-2003.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 75
ID   ABU90983 standard; protein; 229 AA.
DE   Human PRO polypeptide #24.
PN   US2003018168-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 76
ID   ABR67869 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003027269-A1.
PD   06-FEB-2003.
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Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 77
ID ABR65257 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 78
ID ABR68479 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 79
ID ABR71891 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 80
ID ABU59266 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, #103.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 81
ID ABU85371 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 82
ID ABU89061 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 83
ID ABU83141 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 84
ID ABU94997 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 85
ID ABU90545 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 86
ID ABU84056 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 87
ID ABU93707 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 88
ID ABO25963 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 89
ID ABR64952 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 90
ID ABO27304 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO994.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 91
ID ABR68784 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 92
ID ABO06600 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 93
ID ABR99145 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 94
ID ABU57029 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 95
ID ABU85981 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 96
ID ABU82268 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;

RESULT 97
ID ABU87279 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 98
ID ABU83751 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 99
ID ABO08125 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 100
ID ABU92499 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 101
ID ABU81836 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 102
ID ABU66000 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 103
ID ABU81169 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 104
ID ABR59829 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 105
ID ABU94017 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 106
ID ABU99870 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 107
ID ABR66540 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 108
ID ABR90958 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 109
ID ABO53284 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 110
ID ABU58972 standard; protein; 229 AA.
DE Human sectreted/transmembrane protein, #103.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 111
ID ABU94385 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 112
ID ABU79267 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 113
ID ABU86596 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 114
ID ABU86901 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 115
ID ABU94690 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 116
ID ABO04617 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 117

ID ABR70366 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 118
ID ABU92350 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 119
ID ABU98531 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 120
ID ABR65930 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 121
ID ABR64647 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 122
ID ABU59415 standard; protein; 229 AA.
DE Novel human secreted or transmembrane protein PRO812.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 123
ID ABU79572 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 124
ID ABU92963 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 125
ID ABU95922 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 126
ID ABU91142 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 127
ID ABU90235 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 128
ID ABO09650 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 129
ID ABO10922 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 130
ID ABR70976 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 131
ID ABU98286 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 132
ID ABU87584 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 133
ID ABU91452 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 134
ID ABU89291 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 135
ID ABU84666 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 136
ID ABR69756 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 137
ID ABU80133 standard; protein; 229 AA.
DE Human PRO protein #99.
PN US2003036139-A1.

PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 138
ID ABU82498 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 139
ID ABU92181 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 140
ID ABU93402 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 141
ID ABO09955 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 142
ID ABO09040 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 143
ID ABU96462 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 144
ID ABU10887 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 145
ID ABU10608 standard; protein; 229 AA.
DE Human secreted/transmembrane protein #99.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 146
ID ABU81639 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 147
ID ABU72132 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 148
ID ABU95617 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 149
ID ABU96826 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 150
ID ABR70671 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 151
ID ABO05022 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 152
ID ABO08430 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 153
ID ABU88578 standard; protein; 229 AA.
DE Human secreted and transmembrane polypeptide PRO994.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 154
ID ABO34092 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 155
ID ABO05637 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 156
ID ABR74026 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 157

ID ABR95618 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 158
ID ABR80915 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 159
ID ABR81220 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 160
ID ABM00916 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 161
ID ABR88518 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 162
ID ABM77339 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 163
ID ABO28823 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 164
ID ABO31568 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 165
ID ABM07985 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 166
ID ABO40465 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 167
ID ABO35890 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 168
ID ABO44029 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 169
ID ADA77950 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 170
ID ABM24824 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 171
ID ABO03092 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 172
ID ABR90348 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 173
ID ABM17262 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 174
ID ABR95008 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 175
ID ABR95313 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;

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  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 176
ID   ADB17105 standard; protein; 229 AA.
DE   Human transmembrane PRO polypeptide (SeqID 48).
PN   US2003050462-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 177
ID   ABO21551 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003054471-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 178
ID   ABR97815 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003064452-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 179
ID   ABR87603 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068705-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 180
ID   ABM77644 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003054473-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 181
ID   ABM27874 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003064440-A1.
PD   03-APR-2003.
  Query Match           100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 182
ID   ABM06155 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068704-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 183
ID   ABM03661 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068722-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 184
ID   ABM35112 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003073183-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 185
ID   ABM26349 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003104549-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 186
ID   ABO48131 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003049749-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 187
ID   ABR92873 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003064462-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 188
ID   ABO24634 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003065159-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 189
ID   ADA37769 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein PRO994.
PN   US2003008297-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 190
ID   ABM11645 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003064447-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 191
ID   ABM02746 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003073184-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 192
ID   ABM16042 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003064463-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 193
ID   ABO27603 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003064451-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 194
ID   ABM29094 standard; protein; 229 AA.
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DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 195
ID ABM07070 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 196
ID ABM21164 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 197
ID ABM09510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 198
ID ABO41380 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 199
ID ABO36195 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 200
ID ABO43724 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 201
ID ABM76424 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 202
ID ABM76120 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 203
ID ABM25739 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 204
ID ABM26044 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 205
ID ADA21455 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO994.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 206
ID ABO03397 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 207
ID ABO02482 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 208
ID ABO44262 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO 994.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 209
ID ABR90653 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 210
ID ABR73721 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 211
ID ABO16973 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 212
ID ABR94398 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 213
ID ABR75905 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044929-A1.

PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 214
ID ABR71281 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 215
ID ABR93178 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 216
ID ABR93483 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 217
ID ADA10242 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, PRO994.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 218
ID ABR87908 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 219
ID ABO27908 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 220
ID ABO30043 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 221
ID ABO33252 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 222
ID ABM04940 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 223
ID ABM08900 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 224
ID ABO36500 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 225
ID ABO35585 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 226
ID ABO39550 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 227
ID ABM10425 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 228
ID ABM11950 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 229
ID ABO52096 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 230
ID ABO52401 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 231
ID ADA19910 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;

RESULT 232
ID ABO23719 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 233
ID ADB17293 standard; protein; 229 AA.
DE Human transmembrane PRO polypeptide (SeqID 48).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 234
ID ADA17786 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 235
ID ABR97205 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 236
ID ABR86993 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 237
ID ABM11035 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 238
ID ABM28179 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 239
ID ABO32178 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 240
ID ABM15305 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 241
ID ABM06460 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 242
ID ABM04271 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 243
ID ABM22384 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 244
ID ABM07680 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 245
ID ABO40770 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 246
ID ABM35417 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 247
ID ABM33180 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 248
ID ABO52706 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 249
ID ABO50266 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 250
ID ABU99260 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040055-A1.
PD 27-FEB-2003.

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  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 251
ID   ABO04312 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003036164-A1.
PD   20-FEB-2003.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 252
ID   ABO05942 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003040074-A1.
PD   27-FEB-2003.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 253
ID   ABM18482 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003054480-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 254
ID   ADA27894 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein PRO994.
PN   US2003054359-A1.
PD   20-MAR-2003.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 255
ID   ABR97510 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003059885-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 256
ID   ABR80610 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003049740-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 257
ID   ABM01221 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003049770-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 258
ID   ABR88823 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003073169-A1.
PD   17-APR-2003.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 259
ID   ABM13475 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003064457-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 260
ID   ABM20859 standard; protein; 229 AA.
DR   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068711-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 261
ID   ABO41990 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003049745-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 262
ID   ABO42600 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003049751-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 263
ID   ABM10120 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003067478-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 264
ID   ABO38635 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003068773-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 265
ID   ABM32875 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003073185-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 266
ID   ABM22689 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003087373-A1.
PD   08-MAY-2003.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 267
ID   ABM74900 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003096353-A1.
PD   22-MAY-2003.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 268
ID   ADA79742 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003073173-A1.
PD   17-APR-2003.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 269
ID   ABR96290 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003054458-A1.
PD   20-MAR-2003.
  Query Match            100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
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RESULT 270
ID ABM02441 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 271
ID ABR86383 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 272
ID ABR86688 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 273
ID ABM16652 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 274
ID ABM29704 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 275
ID ABO29128 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 276
ID ABM23909 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 277
ID ABM23299 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 278
ID ABM22079 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 279
ID ABO37720 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 280
ID ABM28484 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 281
ID ABM28789 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 282
ID ABM66433 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 283
ID ABM75815 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 284
ID ABM34095 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 285
ID ABM34400 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 286
ID ABO20331 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 287
ID ABO21246 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 288
ID ABO22161 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 289
ID ADA20082 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 290
ID ABO34190 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO 994.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 291
ID ABR96595 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 292
ID ADA94474 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 293
ID ABR85773 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 294
ID ABR99755 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 295
ID ABM00306 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 296
ID ABM00611 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 297
ID ABO29738 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 298
ID ABM23604 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 299
ID ABM29399 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 300
ID ABO38330 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 301
ID ABO45630 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 302
ID ABM20554 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 303
ID ADA81469 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 304
ID ABO16668 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 305
ID ABO18294 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 306
ID ABO22721 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 307
ID ABO23026 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

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  Query Match             100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 308
ID   ABR92568 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003064446-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 309
ID   ABR81525 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003049744-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 310
ID   ABM77949 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003049783-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 311
ID   ABR89738 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003073171-A1.
PD   17-APR-2003.
  Query Match             100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 312
ID   ABM26654 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003032121-A1.
PD   13-FEB-2003.
  Query Match             100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 313
ID   ABM13780 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003064458-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 314
ID   ABO28518 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003064460-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 315
ID   ABO30348 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003064464-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 316
ID   ABM07375 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068702-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 317
ID   ABM03966 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068734-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 318
ID   ABO37110 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003068719-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 319
ID   ABO41685 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003068729-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 320
ID   ABO35280 standard; protein; 229 AA.
DE   Human PRO polypeptide #99.
PN   US2003068738-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 321
ID   ABM25129 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003104540-A1.
PD   05-JUN-2003.
  Query Match             100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 322
ID   ABO47521 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003049742-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 323
ID   ABO47826 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003049747-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 324
ID   ABO48436 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003049750-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 325
ID   ABO51486 standard; protein; 229 AA.
DE   Human PRO polypeptide #99.
PN   US2003049766-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 326
ID   ABO51791 standard; protein; 229 AA.
DE   Human PRO polypeptide #99.
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PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 327
ID ABO50571 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 328
ID ABR79695 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 329
ID ABM16957 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 330
ID ABO17989 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 331
ID ABO20941 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 332
ID ABR96900 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 333
ID ADA38699 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 334
ID ABM12255 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 335
ID ABM16347 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 336
ID ABM24214 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 337
ID ABM14695 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 338
ID ABM04576 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 339
ID ABM06765 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 340
ID ABM09205 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 341
ID ABO39245 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 342
ID ABM75510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 343
ID ABM25434 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 344
ID ABM19944 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 345
ID ABO46850 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049762-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 346
ID ABO47155 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 347
ID ADA83267 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 348
ID ABR71586 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 349
ID ABR72196 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 350
ID ABR98535 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 351
ID ABO06905 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 352
ID ABR84858 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 353
ID ABR73416 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 354
ID ABR76510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 355
ID ABR73111 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 356
ID ABM18177 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 357
ID ABO20636 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 358
ID ABO25379 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 359
ID ABO25684 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 360
ID ABR94093 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 361
ID ADA92820 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 362
ID ABR80000 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 363
ID ABM11340 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 364
ID ABO32947 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;

RESULT 365
ID ABO30653 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 366
ID ABO30958 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 367
ID ABM27264 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 368
ID ABM30009 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 369
ID ABM05545 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 370
ID ABM15610 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 371
ID ABM08595 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 372
ID ABO42295 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 373
ID ABO38025 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 374
ID ABO45935 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 375
ID ABM66738 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 376
ID ADB20310 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 377
ID ABM19639 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 378
ID ABO49351 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 379
ID ABO49656 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 380
ID ADA78562 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 381
ID ABR88213 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 382
ID ADA00379 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO 994.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 383
ID ABM26959 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.

PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 384
ID ABM03356 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 385
ID ABO39855 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 386
ID ABO49961 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 387
ID ABO50876 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 388
ID ABO05332 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 389
ID ABR74636 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 390
ID ABR77115 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 391
ID ABM17872 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 392
ID ABR95923 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 393
ID ABO21856 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 394
ID ABO20026 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 395
ID ABO24329 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 396
ID ABR86078 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 397
ID ABM10730 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 398
ID ABM76729 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 399
ID ABR89433 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 400
ID ABM12560 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 401
ID ABM05850 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 402
ID ABO34975 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068728-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 403
ID ABM03051 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 404
ID ABM19029 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 405
ID ABM19334 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 406
ID ABO46545 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 407
ID ABO49046 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 408
ID ABR69089 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 409
ID ABR89128 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 410
ID ABR72501 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 411
ID ABR74331 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;

RESULT 412
ID ABO18599 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 413
ID ABR80305 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 414
ID ABM01526 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 415
ID ABM02136 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 416
ID ABR87298 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 417
ID ABM12865 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 418
ID ABM30619 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 419
ID ABM24519 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 420
ID ABO29433 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 421
ID ABO31263 standard; protein; 229 AA.

DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 422
ID ABM14390 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 423
ID ABM09815 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 424
ID ABO38940 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 425
ID ABM34705 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 426
ID ABO51181 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 427
ID ABO04007 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 428
ID ABO10477 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 429
ID ABO53178 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 430
ID ABR77720 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 431
ID ABR78930 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 432
ID ABO24024 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 433
ID ABR93788 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 434
ID ABM01831 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 435
ID ABM78254 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 436
ID ABR90043 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 437
ID ADA22381 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO994.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 438
ID ABM27569 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 439
ID ABM13170 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 440
ID ABO31873 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.

PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 441
ID ABM14085 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 442
ID ABM08290 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 443
ID ABO40160 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 444
ID ABM74595 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 445
ID ABM33790 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 446
ID ABM20249 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 447
ID ABO48741 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 448
ID ABO22548 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 449
ID ABR72806 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 450
ID ABO15448 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 451
ID ABR85163 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 452
ID ABO15143 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 453
ID ABO17278 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 454
ID ABM17567 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 455
ID ADA06547 standard; protein; 229 AA.
DE Human secreted/transmembrane PRO polypeptide #73.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 456
ID ADA39240 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 457
ID ABR85468 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 458
ID ABM77034 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 459
ID ABO28213 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;

Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 460
ID ABM22994 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 461
ID ABM30314 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 462
ID ABM21774 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 463
ID ABM21469 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 464
ID ABM15000 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 465
ID ABO41075 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 466
ID ABO36805 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 467
ID ABO37415 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 468
ID ABM75205 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 469
ID ABM33485 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 470
ID ABO46240 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 471
ID ADA82633 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 472
ID ADB85621 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 473
ID ADB96266 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 474
ID ABM31839 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 475
ID ABM31229 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 476
ID ADB85941 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 477
ID ABM32144 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 478
ID ABM32449 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.

PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 479
ID ADB68300 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 480
ID ADB68107 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 481
ID ABM31534 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 482
ID ABM30924 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 483
ID ADB90924 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 484
ID ADC57738 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 485
ID ADC55102 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 486
ID ADC11969 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 487
ID ADC07004 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 488
ID ADC56391 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 489
ID ADC17183 standard; protein; 229 AA.
DE Mammalian PRO polypeptide (SeqID 48).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 490
ID ADC07446 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 491
ID ADC11436 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 492
ID ADC14881 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 493
ID ADC52376 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 494
ID ADC14558 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 495
ID ADD08090 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 496
ID ADC81915 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 497
ID ADD07557 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.

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  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 498
ID   ADC82448 standard; protein; 229 AA.
DE   Human PRO polypeptide #73.
PN   US2003059833-A1.
PD   27-MAR-2003.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 499
ID   ADD05671 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003087376-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 500
ID   ADD08628 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003073090-A1.
PD   17-APR-2003.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 501
ID   ADD06877 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2002193300-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 502
ID   ADC83124 standard; protein; 229 AA.
DE   Human PRO polypeptide #73.
PN   US2003059783-A1.
PD   27-MAR-2003.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 503
ID   ADD55231 standard; protein; 229 AA.
DE   Human PRO polypeptide #73.
PN   US2003077593-A1.
PD   24-APR-2003.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 504
ID   ADD36052 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003105298-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 505
ID   ADD56189 standard; protein; 229 AA.
DE   Human PRO polypeptide #73.
PN   US2003077594-A1.
PD   24-APR-2003.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 506
ID   ADD54627 standard; protein; 229 AA.
DE   Human PRO polypeptide #73.
PN   US2002132253-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 507
ID   ADE26781 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003087304-A1.
PD   08-MAY-2003.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 508
ID   ADE26248 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003087305-A1.
PD   08-MAY-2003.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 509
ID   ADF67185 standard; protein; 229 AA.
DE   Human PRO994 amino acid sequence SEQ ID NO:258.
PN   US2002198148-A1.
PD   26-DEC-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 510
ID   ADG01053 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003078387-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 511
ID   ADG08606 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003180793-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 512
ID   ADG02666 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003207397-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 513
ID   ADG01373 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003207399-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 514
ID   ADF95548 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003207398-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 515
ID   ADF95227 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003180795-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 516
ID   ADG12363 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003207392-A1.
PD   06-NOV-2003.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
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RESULT 517
ID ADH24080 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 518
ID ADH34106 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 519
ID ADH29939 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 520
ID ADH23910 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 521
ID ADH09023 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 522
ID ADG85314 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 523
ID ADH24590 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 524
ID ADH37446 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 525
ID ADH02035 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 526
ID ADH37616 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 527
ID ADG85654 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 528
ID ADH24250 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 529
ID ADH38544 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 530
ID ADG83665 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 531
ID ADH29473 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 532
ID ADH27589 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 533
ID ADH37786 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 534
ID ADH37963 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 535
ID ADH57383 standard; protein; 229 AA.

DE Novel human secreted and transmembrane protein PRO994.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 536
ID ADH53525 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 537
ID ADH53695 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 538
ID ADH52031 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 539
ID ADH49886 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 540
ID ADI25396 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 541
ID ADH90189 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 542
ID ADI25566 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 543
ID ADH97740 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 544
ID ADI35439 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 545
ID ADI03588 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 546
ID ADI11945 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 547
ID ADH90019 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 548
ID ADH99931 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 549
ID ADH98420 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 550
ID ADI11095 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 551
ID ADI11605 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 552
ID ADH98250 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 553
ID ADH98590 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

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  Query Match            100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 554
ID   ADH98080 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181673-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 555
ID   ADI05068 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003180848-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 556
ID   ADI03418 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181654-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 557
ID   ADI04813 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181657-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 558
ID   ADH78267 standard; protein; 229 AA.
DE   Human PRO polypeptide #24.
PN   US2003181668-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 559
ID   ADI19611 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181676-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 560
ID   ADH90359 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181699-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 561
ID   ADI03078 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181653-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 562
ID   ADH77927 standard; protein; 229 AA.
DE   Human PRO polypeptide #24.
PN   US2003181666-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 563
ID   ADH97910 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181674-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 564
ID   ADI01295 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003190669-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 565
ID   ADI01990 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181652-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 566
ID   ADI03248 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181655-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 567
ID   ADI11435 standard; protein; 229 AA.
DE   Human PRO polypeptide #24.
PN   US2003181681-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 568
ID   ADI02337 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181650-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 569
ID   ADI11775 standard; protein; 229 AA.
DE   Human PRO polypeptide #24.
PN   US2003181685-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 570
ID   ADI05412 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003190716-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
RESULT 571
ID   ADH79484 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003191290-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-132;
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RESULT 572
ID   ADI19441 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181675-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 573
ID   ADI05242 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181677-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 574
ID   ADH79654 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003191288-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 575
ID   ADI01480 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181678-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 576
ID   ADI01650 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181679-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 577
ID   ADI01820 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181680-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 578
ID   ADH79824 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003191289-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 579
ID   ADI04642 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003171550-A1.
PD   11-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 580
ID   ADI02778 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181651-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 581
ID   ADH78097 standard; protein; 229 AA.
DE   Human PRO polypeptide #24.
PN   US2003181667-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 582
ID   ADI25736 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181670-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 583
ID   ADI25906 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181671-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 584
ID   ADK65418 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003073821-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 585
ID   ADH98760 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003191284-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 586
ID   ADH80001 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003191287-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 587
ID   ADL32804 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003207396-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 588
ID   ADM30338 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003073813-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 589
ID   ADL93732 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003040013-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1215;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-132;
RESULT 590
ID   ADC52186 standard; protein; 229 AA.
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DE Novel human secreted and transmembrane protein PRO994.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 591
ID ADE74335 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 592
ID ADE74947 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 593
ID ADF35384 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 594
ID ADG11634 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 595
ID ADF96160 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 596
ID ADG04431 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 597
ID ADG00591 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 598
ID ADH06618 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 599
ID ADH06448 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 600
ID ADG68869 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 601
ID ADH27759 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 602
ID ADH25100 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 603
ID ADH33732 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 604
ID ADG82847 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 605
ID ADH02375 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 606
ID ADH07982 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 607
ID ADG69379 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 608
ID ADH39200 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;

RESULT 609
ID ADH26128 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 610
ID ADG83940 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 611
ID ADH19504 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 612
ID ADG85484 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 613
ID ADH06278 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 614
ID ADH30108 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 615
ID ADH24420 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 616
ID ADH33097 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 617
ID ADG69549 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 618
ID ADH07812 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 619
ID ADG85824 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 620
ID ADH39370 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 621
ID ADH33562 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 622
ID ADH33902 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 623
ID ADH01112 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 624
ID ADG69719 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 625
ID ADH20997 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 626
ID ADH02205 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 627
ID ADG69209 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.

PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 628
ID ADG85994 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 629
ID ADH24930 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 630
ID ADH39547 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 631
ID ADH20037 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 632
ID ADH02545 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 633
ID ADG69039 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 634
ID ADH07642 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 635
ID ADG86164 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 636
ID ADH24760 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 637
ID ADH25808 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 638
ID ADH38374 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 639
ID ADH57213 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 640
ID ADH52201 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 641
ID ADH49567 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 642
ID ADH90529 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 643
ID ADI11265 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 644
ID ADH98930 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 645
ID ADI02160 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003190699-A1.
PD 09-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 646
ID ADH90699 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 647
ID ADJ54836 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 648
ID ADJ98574 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 649
ID ADJ98744 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 650
ID ADH78903 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 651
ID ADJ99137 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 652
ID ADJ99307 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 653
ID ADJ98925 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 654
ID ADH79073 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 655
ID ADK00933 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 656
ID ADK14454 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 657
ID ADJ64607 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 658
ID ADM31503 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 659
ID ADM36550 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 660
ID ADM40355 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 661
ID ADM80903 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 662
ID ADN37963 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 663
ID ADY77743 standard; protein; 229 AA.
DE Neoplastic disease detection protein PRO994.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.

PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1215; DB 9; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 664
ID AEA38511 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, #141.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 9; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 665
ID AED50193 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2005163766-A1.
PD 28-JUL-2005.
Query Match 100.0%; Score 1215; DB 9; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 666
ID AEF12574 standard; protein; 229 AA.
DE Human PRO994 protein SEQ ID NO:48.
PN US2006008901-A1.
PD 12-JAN-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1215; DB 10; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 667
ID AEF74263 standard; protein; 229 AA.
DE Human PRO994 protein SEQ ID NO:48.
PN US2005260647-A1.
PD 24-NOV-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W L.
Query Match 100.0%; Score 1215; DB 10; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.4e-132;
RESULT 668
ID ABM85217 standard; protein; 229 AA.
DE Human protein sequence hCP1734062.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 99.5%; Score 1209; DB 7; Length 229;
Best Local Similarity 99.6%; Pred. No. 2.2e-131;
RESULT 669
ID ADR14507 standard; protein; 229 AA.
DE Human NF-kappaB pathway-associated protein SeqID508.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 99.2%; Score 1205; DB 8; Length 229;
Best Local Similarity 99.1%; Pred. No. 6.4e-131;
RESULT 670
ID ABM85216 standard; protein; 230 AA.
DE Mouse protein sequence mCP5099.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 76.1%; Score 924.5; DB 7; Length 230;
Best Local Similarity 74.2%; Pred. No. 2.5e-98;
RESULT 671
ID ABP41230 standard; protein; 205 AA.
DE Human ovarian antigen HSPSI74, SEQ ID NO:2362.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 14.3%; Score 173.5; DB 5; Length 205;
Best Local Similarity 27.7%; Pred. No. 3.8e-11;
RESULT 672
ID ADR66063 standard; protein; 205 AA.
DE Human prostatic carcinoma derived protein SEQ ID 259 #1.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 14.3%; Score 173.5; DB 8; Length 205;
Best Local Similarity 27.7%; Pred. No. 3.8e-11;
RESULT 673
ID ADR66405 standard; protein; 205 AA.
DE Human prostatic carcinoma derived protein SEQ ID 259 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 14.3%; Score 173.5; DB 8; Length 205;
Best Local Similarity 27.7%; Pred. No. 3.8e-11;
RESULT 674
ID ADX97549 standard; protein; 205 AA.
DE Pancreatic cancer associated human protein, SEQ ID 97.
PN EP1471075-A2.
PD 27-OCT-2004.
PA (HINZ/) HINZMANN B.
PA (ROSE/) ROSENTHAL A.
PA (PILA/) PILARSKY C.
PA (DAHL/) DAHL E.
PA (SPEC/) SPECHT T.
PA (LICH/) LICHTNER R.
Query Match 14.3%; Score 173.5; DB 8; Length 205;
Best Local Similarity 27.7%; Pred. No. 3.8e-11;
RESULT 675
ID AED74140 standard; protein; 205 AA.
DE Human placental protein SEQ ID NO:968.
PN US2005255114-A1.
PD 17-NOV-2005.
PA (NUVE-) NUVELO INC.
Query Match 14.3%; Score 173.5; DB 9; Length 205;
Best Local Similarity 27.7%; Pred. No. 3.8e-11;
RESULT 676
ID AAW61625 standard; protein; 197 AA.
DE Clone HGBGV89 of TM4SF superfamily.
PN WO9831799-A2.
PD 23-JUL-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 14.0%; Score 170; DB 2; Length 197;
Best Local Similarity 26.5%; Pred. No. 9.2e-11;
RESULT 677
ID AAW88494 standard; protein; 197 AA.
DE Human stomach cancer clone HP01440-encoded transmembrane protein.
PN WO9855508-A2.
PD 10-DEC-1998.
PA (SAGA) SAGAMI CHEM RES CENTRE.
PA (PROT-) PROTEGENE INC.
Query Match 14.0%; Score 170; DB 2; Length 197;
Best Local Similarity 26.5%; Pred. No. 9.2e-11;
RESULT 678
ID AAW84273 standard; protein; 197 AA.
DE A tumour associated antigen designated TUAN.
PN WO9851706-A1.

PD 19-NOV-1998.
PA (INCY-) INCYTE PHARM INC.
Query Match 14.0%; Score 170; DB 2; Length 197;
Best Local Similarity 26.5%; Pred. No. 9.2e-11;
RESULT 679
ID ADD10280 standard; protein; 197 AA.
DE Human tumour-associated antigen, TUAN.
PN US6632617-B1.
PD 14-OCT-2003.
PA (INCY-) INCYTE CORP.
Query Match 14.0%; Score 170; DB 7; Length 197;
Best Local Similarity 26.5%; Pred. No. 9.2e-11;
RESULT 680
ID ABW01507 standard; protein; 197 AA.
DE Human receptor protein from clone HGBGV89.
PN US2003129696-A1.
PD 10-JUL-2003.
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (GENT/) GENTZ R.
Query Match 14.0%; Score 170; DB 7; Length 197;
Best Local Similarity 26.5%; Pred. No. 9.2e-11;
RESULT 681
ID ADN41032 standard; protein; 197 AA.
DE Novel human secreted protein seqid 154.
PN US2004044191-A1.
PD 04-MAR-2004.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAW/) KYAW H.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAFL/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (OLSE/) OLSEN H.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Query Match 14.0%; Score 170; DB 8; Length 197;
Best Local Similarity 26.5%; Pred. No. 9.2e-11;
RESULT 682
ID AEB98438 standard; protein; 197 AA.
DE Human HGBV89 cDNA clone encoded protein SEQ ID NO:27.
PN US2005176044-A1.
PD 11-AUG-2005.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 14.0%; Score 170; DB 9; Length 197;
Best Local Similarity 26.5%; Pred. No. 9.2e-11;
RESULT 683
ID AAY02732 standard; protein; 198 AA.
DE Human secreted protein encoded by gene 83 clone HGBGV89.
PN WO9902546-A1.
PD 21-JAN-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 14.0%; Score 170; DB 2; Length 198;
Best Local Similarity 26.5%; Pred. No. 9.3e-11;
RESULT 684
ID ADA07411 standard; protein; 198 AA.
DE Human secreted protein from gene 83.
PN US2003064412-A1.
PD 03-APR-2003.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAW/) KYAW H.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAFL/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (OLSE/) OLSEN H S.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
Query Match 14.0%; Score 170; DB 7; Length 198;
Best Local Similarity 26.5%; Pred. No. 9.3e-11;
RESULT 685
ID AAW14123 standard; protein; 202 AA.
DE Human tumour-associated L6 antigen.
PN US5597707-A.
PD 28-JAN-1997.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 14.0%; Score 170; DB 2; Length 202;
Best Local Similarity 27.4%; Pred. No. 9.5e-11;
RESULT 686
ID AAY92049 standard; protein; 202 AA.
DE HrPCa3 polypeptide from androgen-inducible gene clone.
PN WO200018961-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 14.0%; Score 170; DB 3; Length 202;
Best Local Similarity 27.4%; Pred. No. 9.5e-11;
RESULT 687
ID AAB34199 standard; protein; 202 AA.
DE Gene 36 human secreted protein homologous amino acid sequence #167.
PN WO200056755-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 14.0%; Score 170; DB 3; Length 202;
Best Local Similarity 27.4%; Pred. No. 9.5e-11;
RESULT 688
ID ABP68619 standard; protein; 202 AA.
DE Human pancreatic cancer expressed protein SEQ ID NO 168.
PN WO200260317-A2.
PD 08-AUG-2002.
PA (CORI-) CORIXA CORP.
Query Match 14.0%; Score 170; DB 5; Length 202;
Best Local Similarity 27.4%; Pred. No. 9.5e-11;
RESULT 689
ID ADD10288 standard; protein; 202 AA.
DE human tumour-associated L6antigen.
PN US6632617-B1.
PD 14-OCT-2003.
PA (INCY-) INCYTE CORP.
Query Match 14.0%; Score 170; DB 7; Length 202;
Best Local Similarity 27.4%; Pred. No. 9.5e-11;
RESULT 690
ID ABW01521 standard; protein; 202 AA.
DE Protein #9 used in the present invention.
PN US2003129696-A1.
PD 10-JUL-2003.
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (GENT/) GENTZ R.
Query Match 14.0%; Score 170; DB 7; Length 202;
Best Local Similarity 27.4%; Pred. No. 9.5e-11;
RESULT 691
ID ADF61842 standard; protein; 202 AA.
DE Human transmembrane 4 superfamily member 1 protein.
PN WO2003088910-A2.
PD 30-OCT-2003.
PA (RIGE-) RIGEL PHARM INC.
Query Match 14.0%; Score 170; DB 7; Length 202;
Best Local Similarity 27.4%; Pred. No. 9.5e-11;
RESULT 692
ID ADK98674 standard; protein; 202 AA.
DE Human prostate cancer associated protein HRPCa 3.
PN US2003138865-A1.
PD 24-JUL-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 14.0%; Score 170; DB 7; Length 202;
Best Local Similarity 27.4%; Pred. No. 9.5e-11;
RESULT 693
ID ADN40006 standard; protein; 202 AA.

DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C376.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 14.0%; Score 170; DB 7; Length 202;
Best Local Similarity 27.4%; Pred. No. 9.5e-11;
RESULT 694
ID ADR46681 standard; protein; 202 AA.
DE Cancer-associated protein, SEQ ID 94.
PN WO2004073657-A2.
PD 02-SEP-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 14.0%; Score 170; DB 8; Length 202;
Best Local Similarity 27.4%; Pred. No. 9.5e-11;
RESULT 695
ID ADU06510 standard; protein; 202 AA.
DE Novel bronchial cancer-associated human protein SeqID734.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 14.0%; Score 170; DB 8; Length 202;
Best Local Similarity 27.4%; Pred. No. 9.5e-11;
RESULT 696
ID AEB98452 standard; protein; 202 AA.
DE Human tumor-associated antigen protein L6 SEQ ID NO:41.
PN US2005176044-A1.
PD 11-AUG-2005.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 14.0%; Score 170; DB 9; Length 202;
Best Local Similarity 27.4%; Pred. No. 9.5e-11;
RESULT 697
ID ABP68635 standard; protein; 202 AA.
DE Human pancreatic cancer expressed protein SEQ ID NO 4558.
PN WO200260317-A2.
PD 08-AUG-2002.
PA (CORI-) CORIXA CORP.
Query Match 13.7%; Score 166.5; DB 5; Length 202;
Best Local Similarity 26.7%; Pred. No. 2.4e-10;
RESULT 698
ID ADN39985 standard; protein; 202 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C355.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 13.7%; Score 166.5; DB 7; Length 202;
Best Local Similarity 26.7%; Pred. No. 2.4e-10;
RESULT 699
ID ADQ14681 standard; protein; 202 AA.
DE Human liver regeneration-associated protein hLRTM4 SEQ ID NO:2.
PN WO2004060914-A1.
PD 22-JUL-2004.
PA (SHAN-) SHANGHAI INST BIOLOGICAL SCI.
Query Match 13.7%; Score 166.5; DB 8; Length 202;
Best Local Similarity 26.7%; Pred. No. 2.4e-10;
RESULT 700
ID ADR46671 standard; protein; 202 AA.
DE Cancer-associated protein, SEQ ID 84.
PN WO2004073657-A2.
PD 02-SEP-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 13.7%; Score 166.5; DB 8; Length 202;
Best Local Similarity 26.7%; Pred. No. 2.4e-10;
RESULT 701
ID AEC64816 standard; protein; 202 AA.
DE Deregulated, liver cancer-associated protein, SEQ ID NO:131.
PN WO2005085861-A2.
PD 15-SEP-2005.
PA (ORID-) ORIDIS BIOMED FORSCHUNGS & ENTWICKLUNGS.
Query Match 13.7%; Score 166.5; DB 9; Length 202;
Best Local Similarity 26.7%; Pred. No. 2.4e-10;
RESULT 702
ID ADI21569 standard; protein; 209 AA.
DE Novel human polypeptide #48.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 13.7%; Score 166.5; DB 7; Length 209;
Best Local Similarity 26.7%; Pred. No. 2.5e-10;
RESULT 703
ID ABW01520 standard; protein; 197 AA.
DE Protein #8 used in the present invention.
PN US2003129696-A1.
PD 10-JUL-2003.
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (GENT/) GENTZ R.
Query Match 13.7%; Score 166; DB 7; Length 197;
Best Local Similarity 26.1%; Pred. No. 2.7e-10;
RESULT 704
ID AEB98451 standard; protein; 197 AA.
DE Human transmembrane protein L6H SEQ ID NO:40.
PN US2005176044-A1.
PD 11-AUG-2005.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.7%; Score 166; DB 9; Length 197;
Best Local Similarity 26.1%; Pred. No. 2.7e-10;
RESULT 705
ID ABR61633 standard; protein; 202 AA.
DE LRTM4 protein #SEQ ID 2.
PN CN1367179-A.
PD 04-SEP-2002.
PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.
Query Match 13.2%; Score 160.5; DB 6; Length 202;
Best Local Similarity 21.6%; Pred. No. 1.2e-09;
RESULT 706
ID ADD10289 standard; protein; 202 AA.
DE Mouse tumour-associated L6antigen.
PN US6632617-B1.
PD 14-OCT-2003.
PA (INCY-) INCYTE CORP.
Query Match 13.2%; Score 160; DB 7; Length 202;
Best Local Similarity 23.6%; Pred. No. 1.4e-09;
RESULT 707
ID AAO30178 standard; protein; 132 AA.
DE Human transmembrane 4 super family member 5 splice variant (TM4SF5).
PN WO2003046180-A2.
PD 05-JUN-2003.
PA (GEST) GENSET SA.
Query Match 12.6%; Score 153; DB 6; Length 132;
Best Local Similarity 34.5%; Pred. No. 4.9e-09;
RESULT 708
ID ADI21083 standard; protein; 184 AA.
DE Novel human protein #58.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 12.1%; Score 147.5; DB 7; Length 184;
Best Local Similarity 25.2%; Pred. No. 3.4e-08;
RESULT 709
ID AAB44087 standard; protein; 153 AA.
DE Human cancer associated protein sequence SEQ ID NO:1532.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.9%; Score 144; DB 3; Length 153;
Best Local Similarity 33.3%; Pred. No. 6.7e-08;
RESULT 710
ID AAB54023 standard; protein; 245 AA.
DE Human pancreatic cancer antigen protein sequence SEQ ID NO:475.
PN WO200055320-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.7%; Score 142; DB 3; Length 245;
Best Local Similarity 31.0%; Pred. No. 2.2e-07;

RESULT 711
ID ABB72399 standard; protein; 145 AA.
DE Human protein isolated from skin cells SEQ ID NO: 723.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 11.6%; Score 140.5; DB 5; Length 145;
Best Local Similarity 33.3%; Pred. No. 1.6e-07;
RESULT 712
ID ADD69578 standard; protein; 170 AA.
DE Human REMAP protein - SEQ ID 7.
PN WO2003048305-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.4%; Score 138.5; DB 7; Length 170;
Best Local Similarity 24.9%; Pred. No. 3.4e-07;
RESULT 713
ID AAW61626 standard; protein; 201 AA.
DE Clone HUVBB80 of TM4SF superfamily.
PN WO9831799-A2.
PD 23-JUL-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 126; DB 2; Length 201;
Best Local Similarity 21.8%; Pred. No. 1.2e-05;
RESULT 714
ID ABU03461 standard; protein; 201 AA.
DE Angiogenesis-associated human protein sequence #6.
PN WO200279492-A2.
PD 10-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 10.4%; Score 126; DB 6; Length 201;
Best Local Similarity 21.8%; Pred. No. 1.2e-05;
RESULT 715
ID ABW01508 standard; protein; 201 AA.
DE Human receptor protein from clone HUVBB80.
PN US2003129696-A1.
PD 10-JUL-2003.
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (GENT/) GENTZ R.
Query Match 10.4%; Score 126; DB 7; Length 201;
Best Local Similarity 21.8%; Pred. No. 1.2e-05;
RESULT 716
ID ADN38692 standard; protein; 201 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:10.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 10.4%; Score 126; DB 7; Length 201;
Best Local Similarity 21.8%; Pred. No. 1.2e-05;
RESULT 717
ID AEB98439 standard; protein; 201 AA.
DE Human HUVBB80 cDNA clone encoded protein SEQ ID NO:28.
PN US2005176044-A1.
PD 11-AUG-2005.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 126; DB 9; Length 201;
Best Local Similarity 21.8%; Pred. No. 1.2e-05;
RESULT 718
ID AAW80948 standard; protein; 205 AA.
DE Amino acid sequence of the human integral membrane protein-2.
PN WO9846752-A1.
PD 22-OCT-1998.
PA (INCY-) INCYTE PHARM INC.
Query Match 10.3%; Score 125; DB 2; Length 205;
Best Local Similarity 21.8%; Pred. No. 1.6e-05;
RESULT 719
ID AAB34200 standard; protein; 202 AA.
DE Human secreted protein sequence encoded by gene 36 SEQ ID NO:168.
PN WO200056755-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 122; DB 3; Length 202;
Best Local Similarity 23.2%; Pred. No. 3.6e-05;
RESULT 720
ID AAU30786 standard; protein; 226 AA.
DE Novel human secreted protein #1277.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.0%; Score 121; DB 4; Length 226;
Best Local Similarity 25.5%; Pred. No. 5.5e-05;
RESULT 721
ID AAY12177 standard; protein; 122 AA.
DE Human 5' EST secreted protein SEQ ID NO: 490.
PN WO9906554-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 9.9%; Score 120; DB 2; Length 122;
Best Local Similarity 28.8%; Pred. No. 3e-05;
RESULT 722
ID AAY12854 standard; protein; 136 AA.
DE Human 5' EST secreted protein SEQ ID NO:444.
PN WO9906549-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 9.9%; Score 120; DB 2; Length 136;
Best Local Similarity 28.8%; Pred. No. 3.5e-05;
RESULT 723
ID AAY12178 standard; protein; 150 AA.
DE Human 5' EST secreted protein SEQ ID NO: 491.
PN WO9906554-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 9.9%; Score 120; DB 2; Length 150;
Best Local Similarity 28.8%; Pred. No. 4e-05;
RESULT 724
ID AAB64612 standard; protein; 108 AA.
DE Human secreted protein BLAST search protein SEQ ID NO: 122.
PN WO200077197-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 9.8%; Score 119.5; DB 4; Length 108;
Best Local Similarity 33.7%; Pred. No. 2.9e-05;
RESULT 725
ID AAB64564 standard; protein; 180 AA.
DE Human secreted protein #16.
PN WO200077197-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 9.8%; Score 119.5; DB 4; Length 180;
Best Local Similarity 33.7%; Pred. No. 6e-05;
RESULT 726
ID ABP76262 standard; protein; 109 AA.
DE Human GENSET protein SEQ ID 812.
PN WO200283898-A1.
PD 24-OCT-2002.
PA (GEST) GENSET.
Query Match 9.4%; Score 114.5; DB 6; Length 109;
Best Local Similarity 33.3%; Pred. No. 0.00011;
RESULT 727
ID AAB64611 standard; protein; 108 AA.
DE Human secreted protein BLAST search protein SEQ ID NO: 121.
PN WO200077197-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 9.3%; Score 113.5; DB 4; Length 108;
Best Local Similarity 33.7%; Pred. No. 0.00014;
RESULT 728
ID AAW64540 standard; protein; 209 AA.
DE Human fibrosarcoma cell line HT-1080 clone HP10034 protein.
PN WO9821328-A2.
PD 22-MAY-1998.

PA (SAGA) SAGAMI CHEM RES CENTRE.
PA (PROT-) PROTEGENE INC.
Query Match 9.2%; Score 111.5; DB 2; Length 209;
Best Local Similarity 20.2%; Pred. No. 0.00063;
RESULT 729
ID AAM51208 standard; protein; 209 AA.
DE Human osteoclast expressed polypeptide SEQ ID NO 2.
PN JP2001231573-A.
PD 28-AUG-2001.
PA (SHIO) SHIONOGI & CO LTD.
Query Match 9.2%; Score 111.5; DB 4; Length 209;
Best Local Similarity 20.2%; Pred. No. 0.00063;
RESULT 730
ID AAU29953 standard; protein; 107 AA.
DE Novel human secreted protein #444.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.6%; Score 105; DB 4; Length 107;
Best Local Similarity 31.2%; Pred. No. 0.0014;
RESULT 731
ID ADP66649 standard; protein; 450 AA.
DE Mouse GHB receptor related polypeptide.
PN WO2004046315-A2.
PD 03-JUN-2004.
PA (SLOW-) SLOWAVE INC.
Query Match 8.3%; Score 101; DB 8; Length 450;
Best Local Similarity 23.0%; Pred. No. 0.031;
RESULT 732
ID AAY11655 standard; protein; 86 AA.
DE Human 5' EST secreted protein SEQ ID NO:307.
PN WO9906439-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 7.9%; Score 95.5; DB 2; Length 86;
Best Local Similarity 32.9%; Pred. No. 0.013;
RESULT 733
ID ADP66647 standard; protein; 450 AA.
DE Rat GHB receptor related polypeptide.
PN WO2004046315-A2.
PD 03-JUN-2004.
PA (SLOW-) SLOWAVE INC.
Query Match 7.7%; Score 93; DB 8; Length 450;
Best Local Similarity 23.7%; Pred. No. 0.26;
RESULT 734
ID ABG29044 standard; protein; 426 AA.
DE Novel human diagnostic protein #29035.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.4%; Score 90.5; DB 4; Length 426;
Best Local Similarity 30.8%; Pred. No. 0.47;
RESULT 735
ID ABG24776 standard; protein; 708 AA.
DE Novel human diagnostic protein #24767.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.4%; Score 90.5; DB 4; Length 708;
Best Local Similarity 30.8%; Pred. No. 0.97;
RESULT 736
ID ABG29047 standard; protein; 997 AA.
DE Novel human diagnostic protein #29038.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.4%; Score 90.5; DB 4; Length 997;
Best Local Similarity 30.8%; Pred. No. 1.6;
RESULT 737
ID ABG24324 standard; protein; 1118 AA.
DE Novel human diagnostic protein #24315.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.4%; Score 90.5; DB 4; Length 1118;
Best Local Similarity 30.8%; Pred. No. 1.9;
RESULT 738
ID ABU49046 standard; protein; 1036 AA.
DE Protein encoded by Prokaryotic essential gene #34573.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.2%; Score 88; DB 6; Length 1036;
Best Local Similarity 31.5%; Pred. No. 3.3;
RESULT 739
ID ADB65669 standard; protein; 117 AA.
DE Human protein encoded by clone TRACH20011540.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.2%; Score 87.5; DB 7; Length 117;
Best Local Similarity 23.0%; Pred. No. 0.17;
RESULT 740
ID AAU30827 standard; protein; 185 AA.
DE Novel human secreted protein #1318.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.2%; Score 87.5; DB 4; Length 185;
Best Local Similarity 28.1%; Pred. No. 0.32;
RESULT 741
ID ADJ48738 standard; protein; 1174 AA.
DE Oil-associated gene related protein #238.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 7.2%; Score 87; DB 8; Length 1174;
Best Local Similarity 20.8%; Pred. No. 5.1;
RESULT 742
ID ABU49666 standard; protein; 891 AA.
DE Protein encoded by Prokaryotic essential gene #35193.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.1%; Score 86.5; DB 6; Length 891;
Best Local Similarity 22.6%; Pred. No. 3.9;
RESULT 743
ID ABB48024 standard; protein; 283 AA.
DE Listeria monocytogenes protein #728.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 7.1%; Score 86; DB 5; Length 283;
Best Local Similarity 24.7%; Pred. No. 0.88;
RESULT 744
ID AAW98770 standard; protein; 449 AA.
DE H. pylori GHPO 1130 protein.
PN WO9843478-A1.
PD 08-OCT-1998.
PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.1%; Score 86; DB 2; Length 449;
Best Local Similarity 31.5%; Pred. No. 1.7;
RESULT 745
ID AAY59127 standard; protein; 271 AA.
DE Protein encoded by V. cholerae thyA gene 5' flanking region.
PN WO9961634-A1.
PD 02-DEC-1999.
PA (SBLV-) SBL VACCIN AB.
Query Match 7.0%; Score 85.5; DB 3; Length 271;
Best Local Similarity 23.1%; Pred. No. 0.95;

RESULT 746
ID AAW52812 standard; protein; 344 AA.
DE Human induced tumour protein.
PN WO9806846-A1.
PD 19-FEB-1998.
PA (INCY-) INCYTE PHARM INC.
Query Match 7.0%; Score 85.5; DB 2; Length 344;
Best Local Similarity 23.1%; Pred. No. 1.3;
RESULT 747
ID AAY07771 standard; protein; 356 AA.
DE Human secreted protein fragment encoded from gene 28.
PN WO9909155-A1.
PD 25-FEB-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.0%; Score 85.5; DB 2; Length 356;
Best Local Similarity 23.1%; Pred. No. 1.4;
RESULT 748
ID AAY95015 standard; protein; 453 AA.
DE Human secreted protein vc61_1, SEQ ID NO:70.
PN WO200011015-A1.
PD 02-MAR-2000.
PA (ALPH-) ALPHAGENE INC.
Query Match 7.0%; Score 85.5; DB 3; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 749
ID AAG65236 standard; protein; 453 AA.
DE Protein tyrosine kinase 50.
PN CN1298944-A.
PD 13-JUN-2001.
PA (BODA-) BODAO GENE TECHNOLOGY CO LTD SHANGHAI.
Query Match 7.0%; Score 85.5; DB 4; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 750
ID AAU29065 standard; protein; 453 AA.
DE Human PRO polypeptide sequence #42.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 4; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 751
ID AAM39489 standard; protein; 453 AA.
DE Human polypeptide SEQ ID NO 2634.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 85.5; DB 4; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 752
ID AAB65170 standard; protein; 453 AA.
DE Human PRO732 (UNQ396) protein sequence SEQ ID NO:73.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 4; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 753
ID ABB90299 standard; protein; 453 AA.
DE Human polypeptide SEQ ID NO 2675.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.0%; Score 85.5; DB 5; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 754
ID ABU58441 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 755
ID ABU87989 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 756
ID ABU84304 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 757
ID ABR66178 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 758
ID ABR65568 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 759
ID ABU99508 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 760
ID ABU57985 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 761
ID ABU59063 standard; protein; 453 AA.
DE Novel human secreted or transmembrane protein PRO732.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 762
ID ABU82575 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 763
ID ABU82747 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 764
ID ABU89868 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 765
ID ABR68117 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027264-A1.

PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 766
ID ABU60494 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, #24.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 767
ID ABU96170 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 768
ID ABU92601 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 769
ID ABO08678 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 770
ID ABO02730 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 771
ID ABR74884 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 772
ID ABR94646 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 773
ID ABU13876 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 774
ID ABU85619 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 775
ID ABU98779 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 776
ID ABU97994 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 777
ID ABU91700 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 778
ID ABU89393 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 779
ID ABU86234 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 780
ID ABU67447 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 781
ID ABU80475 standard; protein; 453 AA.
DE Human PRO protein #42.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 782
ID ABU72461 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 783
ID ABR99393 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 784
ID ABR98783 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 785
ID ABO16306 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.

PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 786
ID ABR92206 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 787
ID ABO18847 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 788
ID ABR78268 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 789
ID ABU85004 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 790
ID ABO00143 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 791
ID ABO11475 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 792
ID ABO02120 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 793
ID ABU88694 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 794
ID ABU83389 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 795
ID ABO06190 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 796
ID ABR59226 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 797
ID ABO09288 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 798
ID ABO19152 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 799
ID ABO11170 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 800
ID ABR66788 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 801
ID ABO16001 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 802
ID ABO13707 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 803
ID ABU65610 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, SEQ ID 84.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 804
ID ABO07458 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 805
ID ABO03645 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 806
ID ABR67093 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 807
ID ABO15696 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 808
ID ABU55977 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, PRO732.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 809
ID ABU65305 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 810
ID ABU95250 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 811
ID ABU71153 standard; protein; 453 AA.
DE Human PRO732 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 812
ID ABO07763 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 813
ID ABR70004 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 814
ID ABR69337 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 815
ID ABO01478 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 816
ID ABU81280 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 817
ID ABR60077 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 818
ID ABR67812 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 819
ID ABR65200 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 820
ID ABR68422 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 821
ID ABR71834 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 822
ID ABU59210 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, #24.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 823
ID ABU85314 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 824
ID ABU89004 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 825
ID ABU83084 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 826
ID ABU94940 standard; protein; 453 AA.

DE Novel human secreted and transmembrane protein PRO732.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 827
ID ABU90488 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 828
ID ABU83999 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 829
ID ABU93650 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 830
ID ABO25907 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 831
ID ABR64895 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 832
ID ABR68727 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 833
ID ABO06543 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 834
ID ABR99088 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 835
ID ABU56972 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 836
ID ABU85924 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 837
ID ABU82211 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 838
ID ABU87222 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 839
ID ABU83694 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 840
ID ABO08068 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 841
ID ABU81779 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 842
ID ABU65943 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 843
ID ABR59772 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 844
ID ABU93960 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 845
ID ABU99813 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 846
ID ABR66483 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 847
ID ABR90901 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 848
ID ABU58916 standard; protein; 453 AA.
DE Human sectreted/transmembrane protein, #24.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 849
ID ABU94328 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 850
ID ABU79210 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 851
ID ABU86539 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 852
ID ABU86844 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 853
ID ABU94633 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 854
ID ABO04560 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 855
ID ABR70309 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 856
ID ABU92294 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 857
ID ABU98474 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 858
ID ABR65873 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 859
ID ABR64590 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 860
ID ABU59359 standard; protein; 453 AA.
DE Novel human secreted or transmembrane protein PRO1120.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 861
ID ABU79515 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 862
ID ABU92906 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 863
ID ABU95865 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 864
ID ABU91085 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 865
ID ABU90178 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 866
ID ABO09593 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 867
ID ABO10865 standard; protein; 453 AA.

DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 868
ID ABR70919 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 869
ID ABU87527 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 870
ID ABU91395 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 871
ID ABU84609 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 872
ID ABR69699 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 873
ID ABU80076 standard; protein; 453 AA.
DE Human PRO protein #42.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 874
ID ABU92125 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 875
ID ABU93345 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 876
ID ABO09898 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 877
ID ABO08983 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 878
ID ABU10831 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 879
ID ABU10551 standard; protein; 453 AA.
DE Human secreted/transmembrane protein #42.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 880
ID ABU81583 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 881
ID ABU95560 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 882
ID ABU96769 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 883
ID ABR70614 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 884
ID ABO04965 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 885
ID ABO08373 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 886
ID ABU88522 standard; protein; 453 AA.
DE Human secreted and transmembrane polypeptide PRO732.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 887
ID ABO34036 standard; protein; 453 AA.

DE Human PRO732 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 888
ID ABO05580 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 889
ID ABR73969 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 890
ID ABR95561 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 891
ID ABR80858 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 892
ID ABR81163 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 893
ID ABM00859 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 894
ID ABR88461 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 895
ID ABM77282 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 896
ID ABO28766 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 897
ID ABO31511 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 898
ID ABM07928 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 899
ID ABO40408 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 900
ID ABO35833 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 901
ID ABO43972 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 902
ID ADA77836 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 903
ID ABM24767 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 904
ID ABO03035 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 905
ID ABR90291 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 906
ID ABM17205 standard; protein; 453 AA.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 907
ID ABR94951 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 908
ID ABR95256 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US200304.0071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 909
ID ABO21494 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 910
ID ABR97758 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 911
ID ABR87546 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 912
ID ABM77587 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 913
ID ABM27817 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 914
ID ABM06098 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 915
ID ABM03604 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 916
ID ABM35055 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 917
ID ABM26292 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 918
ID ABO48074 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 919
ID ABR92816 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 920
ID ABO24577 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 921
ID ADA37584 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 922
ID ABM11588 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 923
ID ABM02689 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 924
ID ABM15985 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 925
ID ABO27546 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 926
ID ABM29037 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 927
ID ABM07013 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 928
ID ABM21107 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 929
ID ABM09453 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 930
ID ABO41323 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 931
ID ABO36138 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 932
ID ABO43667 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 933
ID ABM76367 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 934
ID ABM76063 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 935
ID ABM25682 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 936
ID ABM25987 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 937
ID ADA21270 standard; protein; 453 AA.
DE Human secreted/transmembrane polypeptide PRO732.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 938
ID ABO03340 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 939
ID ABO02425 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 940
ID ABR90596 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 941
ID ABR73664 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 942
ID ABO16916 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 943
ID ABR94341 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 944
ID ABR75848 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 945
ID ABR71224 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 946
ID ABR93121 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 947
ID ABR93426 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 948
ID ADA10057 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, PRO732.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 949
ID ABR87851 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 950
ID ABO27851 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 951
ID ABO29986 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 952
ID ABO33195 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 953
ID ABM04883 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 954
ID ABM08843 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 955
ID ABO36443 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 956
ID ABO35528 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 957
ID ABO39493 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 958
ID ABM10368 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 959
ID ABM11893 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 960
ID ABO52039 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 961
ID ABO52344 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 962
ID ABO23662 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032134-A1.

PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 963
ID ADA17601 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 964
ID ABR97148 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 965
ID ABR86936 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 966
ID ABM10978 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 967
ID ABM28122 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 968
ID ABO32121 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 969
ID ABM15248 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 970
ID ABM06403 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 971
ID ABM04214 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 972
ID ABM22327 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 973
ID ABM07623 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 974
ID ABO40713 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 975
ID ABM35360 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 976
ID ABM33123 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 977
ID ABO52649 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 978
ID ABO50209 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 979
ID ABU99203 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 980
ID ABO04255 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 981
ID ABO05885 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.

PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 982
ID ABM18425 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 983
ID ADA27709 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 984
ID ABR97453 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 985
ID ABR80553 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 986
ID ABM01164 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 987
ID ABR88766 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 988
ID ABM13418 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 989
ID ABM20802 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 990
ID ABO41933 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 991
ID ABO42543 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 992
ID ABM10063 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 993
ID ABO38578 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 994
ID ABM32818 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 995
ID ABM22632 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 996
ID ABM74843 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 997
ID ADA79628 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 998
ID ABR96233 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 999
ID ABM02384 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1000
ID ABR86326 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049758-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1001
ID ABR86631 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1002
ID ABM16595 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1003
ID ABM29647 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1004
ID ABO29071 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1005
ID ABM23852 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1006
ID ABM23242 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1007
ID ABM22022 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1008
ID ABO37663 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1009
ID ABM28427 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1010
ID ABM28732 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1011
ID ABM66376 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1012
ID ABM75758 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1013
ID ABM34038 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1014
ID ABM34343 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1015
ID ABO20274 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1016
ID ABO21189 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1017
ID ABO22104 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1018
ID ABR96538 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1019
ID ADA94289 standard; protein; 453 AA.

DE Human secreted/transmembrane protein PRO732.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1020
ID ABR85716 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1021
ID ABR99698 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1022
ID ABM00554 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1023
ID ABM00249 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1024
ID ABO29681 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1025
ID ABM23547 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1026
ID ABM29342 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1027
ID ABO38273 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1028
ID ABO45573 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1029
ID ABM20497 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1030
ID ADA81355 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1031
ID ABO16611 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1032
ID ABO18237 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1033
ID ABO22664 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1034
ID ABO22969 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1035
ID ABR92511 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1036
ID ABR81468 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1037
ID ABM77892 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1038
ID ABR89681 standard; protein; 453 AA.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1039
ID ABM26597 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1040
ID ABM13723 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1041
ID ABO28461 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1042
ID ABO30291 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1043
ID ABM07318 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1044
ID ABM03909 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1045
ID ABO37053 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1046
ID ABO41628 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1047
ID ABO35223 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1048
ID ABM25072 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1049
ID ABO47464 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1050
ID ABO47769 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1051
ID ABO48379 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1052
ID ABO51429 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1053
ID ABO51734 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1054
ID ABO50514 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1055
ID ABR79638 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1056
ID ABM16900 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 1057
ID ABO17932 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1058
ID ABO20884 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1059
ID ABR96843 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1060
ID ADA38514 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1061
ID ABM12198 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1062
ID ABM16290 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1063
ID ABM24157 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1064
ID ABM14638 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1065
ID ABM04519 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1066
ID ABM06708 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1067
ID ABM09148 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1068
ID ABO39188 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1069
ID ABM75453 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1070
ID ABM25377 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1071
ID ABM19887 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1072
ID ABO46793 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1073
ID ABO47098 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1074
ID ADA83153 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1075
ID ABR71529 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1076

ID ABR72139 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1077
ID ABR98478 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1078
ID ABO06848 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1079
ID ABR84801 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1080
ID ABR73359 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1081
ID ABR76453 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1082
ID ABR73054 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1083
ID ABM18120 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1084
ID ABO20579 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1085
ID ABO25322 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1086
ID ABO25627 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1087
ID ABR94036 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1088
ID ADA92635 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1089
ID ABR79943 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1090
ID ABM11283 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1091
ID ABO32890 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1092
ID ABO30596 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1093
ID ABO30901 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1094
ID ABM27207 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1095
ID ABM29952 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068769-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1096
ID ABM05488 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1097
ID ABM15553 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1098
ID ABM08538 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1099
ID ABO42238 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1100
ID ABO37968 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1101
ID ABO45878 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1102
ID ABM66681 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1103
ID ADB20196 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1104
ID ABM19582 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1105
ID ABO49294 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1106
ID ABO49599 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1107
ID ADA78448 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1108
ID ABR88156 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1109
ID ABM26902 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1110
ID ABM03299 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1111
ID ABO39798 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1112
ID ABO49904 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1113
ID ABO50819 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;

Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1114
ID ABO05275 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1115
ID ABR74579 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1116
ID ABR77058 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1117
ID ABM17815 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1118
ID ABR95866 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1119
ID ABO21799 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1120
ID ABO19969 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1121
ID ABO24272 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1122
ID ABR86021 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1123
ID ABM10673 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1124
ID ABM76672 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1125
ID ABR89376 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1126
ID ABM12503 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1127
ID ABM05793 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1128
ID ABO34918 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1129
ID ABM02994 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1130
ID ABM18972 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1131
ID ABM19277 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1132
ID ABO46488 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 1133
ID ABO48989 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1134
ID ABR69032 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1135
ID ABR89071 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1136
ID ABR72444 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1137
ID ABR74274 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1138
ID ABO18542 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1139
ID ABR80248 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1140
ID ABM01469 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1141
ID ABM02079 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1142
ID ABR87241 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1143
ID ABM12808 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1144
ID ABM30562 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1145
ID ABM24462 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1146
ID ABO29376 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1147
ID ABO31206 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1148
ID ABM14333 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1149
ID ABM09758 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1150
ID ABO38883 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1151
ID ABM34648 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;

Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1152
ID ABO51124 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1153
ID ABO03950 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1154
ID ABO10420 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1155
ID ABO53122 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1156
ID ABR77663 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1157
ID ABR78873 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1158
ID ABO23967 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1159
ID ABR93731 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1160
ID ABM01774 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1161
ID ABM78197 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1162
ID ABR89986 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1163
ID ADA22196 standard; protein; 453 AA.
DE Human secreted/transmembrane polypeptide PRO732.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1164
ID ABM27512 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1165
ID ABM13113 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1166
ID ABO31816 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1167
ID ABM14028 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1168
ID ABM08233 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1169
ID ABO40103 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1170
ID ABM74538 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1171

ID ABM33733 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1172
ID ABM20192 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1173
ID ABO48684 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1174
ID ABO22492 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1175
ID ABR72749 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1176
ID ABO15391 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1177
ID ABR85106 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1178
ID ABO15086 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1179
ID ABO17221 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1180
ID ABM17510 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;

RESULT 1181
ID ADA06362 standard; protein; 453 AA.
DE Human secreted/transmembrane PRO polypeptide #17.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1182
ID ADA39055 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1183
ID ABR85411 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1184
ID ABM76977 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1185
ID ABO28156 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1186
ID ABM22937 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1187
ID ABM30257 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1188
ID ABM21717 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1189
ID ABM21412 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1190
ID ABM14943 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.

PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1191
ID ABO41018 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1192
ID ABO36748 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1193
ID ABO37358 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1194
ID ABM75148 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1195
ID ABM33428 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1196
ID ABO46183 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1197
ID ADA82519 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1198
ID ADB96081 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1199
ID ABM31782 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1200
ID ABM31172 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1201
ID ADB85827 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1202
ID ABM32087 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1203
ID ABM32392 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1204
ID ABM31477 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1205
ID ABM30867 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1206
ID ADC57553 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1207
ID ADC54917 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1208
ID ADC11784 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1209
ID ADC56206 standard; protein; 453 AA.

DE Human PRO polypeptide #17.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1210
ID ADC07261 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1211
ID ADC11251 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1212
ID ADC14373 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1213
ID ADD07905 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1214
ID ADC81730 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1215
ID ADD07372 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1216
ID ADC77580 standard; protein; 453 AA.
DE Human TMS2 amino acid sequence.
PN WO2003066829-A2.
PD 14-AUG-2003.
PA (DISC-) DISCOVERY GENOMICS INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1217
ID ADC82263 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1218
ID ADD05557 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1219
ID ADD08443 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1220
ID ADD06692 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1221
ID ADC82939 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1222
ID ADD55046 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1223
ID ADD56004 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1224
ID ADD54442 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1225
ID ADE26596 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1226
ID ADE26063 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1227
ID ADF67000 standard; protein; 453 AA.
DE Human PRO732 amino acid sequence SEQ ID NO:73.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1228
ID ADG02552 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1229

ID ADG01259 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1230
ID ADF95434 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1231
ID ADG12249 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1232
ID ADH08909 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1233
ID ADI35254 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1234
ID ADH99746 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1235
ID ADL32690 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1236
ID ADM30224 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1237
ID ADE74221 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 7.0%; Score 85.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1238
ID ADE74833 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 7.0%; Score 85.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1239
ID ADF35199 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 7.0%; Score 85.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1240
ID ADG11449 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1241
ID ADF96046 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 7.0%; Score 85.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1242
ID ADG04317 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1243
ID ADG00477 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1244
ID ADG82733 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1245
ID ADH26014 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1246
ID ADH19319 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1247
ID ADH32983 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1248
ID ADH20812 standard; protein; 453 AA.

DE Human secreted/transmembrane protein PRO732.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 7.0%; Score 85.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1249
ID ADH19852 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1250
ID ADJ54722 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1251
ID ADJ64493 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1252
ID ADM31389 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1253
ID ADM36436 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1254
ID ADM40241 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1255
ID ADN37849 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1256
ID ADR09184 standard; protein; 453 AA.
DE Human protein useful for treating neurological disease Seq 2690.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.0%; Score 85.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1257
ID ABM80816 standard; protein; 453 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81457, SEQ:2102.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1258
ID ADR99176 standard; protein; 453 AA.
DE KIAA1253, SEQ ID 182.
PN WO2004078035-A2.
PD 16-SEP-2004.
PA (FARB) BAYER PHARM CORP.
Query Match 7.0%; Score 85.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1259
ID ADV69528 standard; protein; 453 AA.
DE Human tyrosine kinase 50 amino acid sequence - SEQ ID 2.
PN CN1510134-A.
PD 07-JUL-2004.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 7.0%; Score 85.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1260
ID AEA38376 standard; protein; 453 AA.
DE Human secreted/transmembrane protein cDNA, #86.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 9; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1261
ID AED50079 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2005163766-A1.
PD 28-JUL-2005.
Query Match 7.0%; Score 85.5; DB 9; Length 453;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1262
ID AAY66647 standard; protein; 455 AA.
DE Membrane-bound protein PRO732.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 3; Length 455;
Best Local Similarity 23.1%; Pred. No. 2;
RESULT 1263
ID ADG10618 standard; protein; 472 AA.
DE Human STAT6-activating protein, SEQ ID NO:208.
PN WO200296943-A1.
PD 05-DEC-2002.
PA (ASAH) ASAHI KASEI KOGYO KK.
Query Match 7.0%; Score 85.5; DB 7; Length 472;
Best Local Similarity 23.1%; Pred. No. 2.1;
RESULT 1264
ID AAM41275 standard; protein; 477 AA.
DE Human polypeptide SEQ ID NO 6206.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 85.5; DB 4; Length 477;
Best Local Similarity 23.1%; Pred. No. 2.1;
RESULT 1265
ID AAG72466 standard; protein; 318 AA.
DE Human OR-like polypeptide query sequence, SEQ ID NO: 2147.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 7.0%; Score 85; DB 4; Length 318;
Best Local Similarity 19.5%; Pred. No. 1.4;
RESULT 1266
ID AAG71752 standard; protein; 318 AA.
DE Human olfactory receptor polypeptide, SEQ ID NO: 1433.
PN WO200127158-A2.
PD 19-APR-2001.

PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 7.0%; Score 85; DB 4; Length 318;
Best Local Similarity 19.5%; Pred. No. 1.4;
RESULT 1267
ID AAU31533 standard; protein; 450 AA.
DE Novel human secreted protein #2024.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 85; DB 4; Length 450;
Best Local Similarity 25.6%; Pred. No. 2.2;
RESULT 1268
ID AED85676 standard; protein; 557 AA.
DE Nitrogen responsive protein #127.
PN WO2005103270-A2.
PD 03-NOV-2005.
PA (CERE-) CERES INC.
Query Match 7.0%; Score 85; DB 9; Length 557;
Best Local Similarity 25.4%; Pred. No. 3;
RESULT 1269
ID AED85384 standard; protein; 557 AA.
DE Nitrogen responsive protein SEQ ID NO 103.
PN WO2005103270-A2.
PD 03-NOV-2005.
PA (CERE-) CERES INC.
Query Match 7.0%; Score 85; DB 9; Length 557;
Best Local Similarity 25.4%; Pred. No. 3;
RESULT 1270
ID AAY11065 standard; protein; 449 AA.
DE H. pylori ORF 09cp10713_36359687_c1_119 inner membrane protein.
PN WO9824475-A1.
PD 11-JUN-1998.
PA (ASTR) ASTRA AB.
Query Match 6.9%; Score 84; DB 2; Length 449;
Best Local Similarity 31.5%; Pred. No. 2.9;
RESULT 1271
ID ADR43499 standard; protein; 3056 AA.
DE CSA-binding malarial variant surface antigen.
PN WO2004067559-A1.
PD 12-AUG-2004.
PA (UYKO-) UNIV KOBENHAVNS.
Query Match 6.9%; Score 84; DB 8; Length 3056;
Best Local Similarity 25.0%; Pred. No. 44;
RESULT 1272
ID ADO78101 standard; protein; 261 AA.
DE Human Claudin-18A2.1.
PN DE10254601-A1.
PD 03-JUN-2004.
PA (GANY-) GANYMED PHARM AG.
Query Match 6.9%; Score 83.5; DB 8; Length 261;
Best Local Similarity 25.6%; Pred. No. 1.5;
RESULT 1273
ID AEE48637 standard; protein; 261 AA.
DE Human claudin 18A1 protein SEQ ID NO 16.
PN WO2005113587-A2.
PD 01-DEC-2005.
PA (GANY-) GANYMED PHARM AG.
Query Match 6.9%; Score 83.5; DB 10; Length 261;
Best Local Similarity 25.6%; Pred. No. 1.5;
RESULT 1274
ID ADL95659 standard; protein; 316 AA.
DE Human novel GPCR1c.
PN US2003165829-A1.
PD 04-SEP-2003.
PA (PADI/) PADIGARU M.
PA (MAJU/) MAJUMDER K.
PA (BURG/) BURGESS C E.
PA (VERN/) VERNET C A M.
PA (FERN/) FERNANDES E R.
PA (SHIM/) SHIMKETS R A.
PA (TCHE/) TCHERNEV V T.
PA (MISH/) MISHRA V.
PA (CASM/) CASMAN S.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
Query Match 6.9%; Score 83.5; DB 7; Length 316;
Best Local Similarity 22.1%; Pred. No. 2;
RESULT 1275
ID AAB90779 standard; protein; 180 AA.
DE Human shear stress-response protein SEQ ID NO: 58.
PN WO200125427-A1.
PD 12-APR-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
PA (NOJI/) NOJIMA H.
Query Match 6.8%; Score 82.5; DB 4; Length 180;
Best Local Similarity 27.4%; Pred. No. 1.2;
RESULT 1276
ID ADE83497 standard; protein; 180 AA.
DE Human Protein P53801, SEQ ID NO 11093.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.8%; Score 82.5; DB 7; Length 180;
Best Local Similarity 27.4%; Pred. No. 1.2;
RESULT 1277
ID ABM82306 standard; protein; 180 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO36872, SEQ:5922.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 6.8%; Score 82.5; DB 8; Length 180;
Best Local Similarity 27.4%; Pred. No. 1.2;
RESULT 1278
ID AAB58380 standard; protein; 185 AA.
DE Lung cancer associated polypeptide sequence SEQ ID 718.
PN WO200055180-A2.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 6.8%; Score 82.5; DB 3; Length 185;
Best Local Similarity 27.4%; Pred. No. 1.2;
RESULT 1279
ID AED74302 standard; protein; 185 AA.
DE Human placental protein SEQ ID NO:1130.
PN US2005255114-A1.
PD 17-NOV-2005.
PA (NUVE-) NUVELO INC.
Query Match 6.8%; Score 82.5; DB 9; Length 185;
Best Local Similarity 27.4%; Pred. No. 1.2;
RESULT 1280
ID AAE07073 standard; protein; 261 AA.
DE Human gene 1 encoded secreted protein HTPFX16, SEQ ID NO:90.
PN WO200154708-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.8%; Score 82.5; DB 4; Length 261;
Best Local Similarity 25.8%; Pred. No. 2;
RESULT 1281
ID ABG65079 standard; protein; 261 AA.
DE Human albumin fusion protein #1754.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.8%; Score 82.5; DB 5; Length 261;
Best Local Similarity 25.8%; Pred. No. 2;
RESULT 1282
ID ADL78346 standard; protein; 261 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1828.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 6.8%; Score 82.5; DB 8; Length 261;
Best Local Similarity 25.8%; Pred. No. 2;

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RESULT 1283
ID   AED85385 standard; protein; 572 AA.
DE   Nitrogen responsive protein SEQ ID NO 104.
PN   WO2005103270-A2.
PD   03-NOV-2005.
PA   (CERE-) CERES INC.
  Query Match             6.7%;  Score 82;  DB 9;  Length 572;
  Best Local Similarity   25.3%;  Pred. No. 7;
RESULT 1284
ID   AED85795 standard; protein; 572 AA.
DE   Nitrogen responsive protein #129.
PN   WO2005103270-A2.
PD   03-NOV-2005.
PA   (CERE-) CERES INC.
  Query Match             6.7%;  Score 82;  DB 9;  Length 572;
  Best Local Similarity   25.3%;  Pred. No. 7;
RESULT 1285
ID   ABM87647 standard; protein; 614 AA.
DE   Rice abiotic stress responsive polypeptide SEQ ID NO:5893.
PN   WO2003008540-A2.
PD   30-JAN-2003.
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
  Query Match             6.7%;  Score 82;  DB 7;  Length 614;
  Best Local Similarity   25.3%;  Pred. No. 7.7;
RESULT 1286
ID   AEF35386 standard; protein; 858 AA.
DE   NOV7 related protein, SEQ ID 135.
PN   US2006013813-A1.
PD   19-JAN-2006.
PA   (MEZE/) MEZES P S.
PA   (RAST/) RASTELLI L.
PA   (HERR/) HERRMANN J L.
PA   (MACD/) MACDOUGALL J R.
PA   (ZHON/) ZHONG H.
PA   (CASM/) CASMAN S J.
PA   (BOLD/) BOLDOG F L.
PA   (SHIM/) SHIMKETS R A.
PA   (GORM/) GORMAN L.
PA   (EISE/) EISEN A J.
PA   (SPAD/) SPADERNA S K.
PA   (VERN/) VERNET C A M.
PA   (BERG/) BERGHS C.
PA   (SPYT/) SPYTEK K A.
PA   (DIPI/) DIPIPPO V A.
PA   (ZERH/) ZERHUSEN B D.
PA   (PEYM/) PEYMAN J A.
PA   (ELLE/) ELLERMAN K.
PA   (STON/) STONE D J.
PA   (GROS/) GROSSE W M.
PA   (ALSO/) ALSOBROOK J P.
PA   (LEPL/) LEPLEY D M.
PA   (RIEG/) RIEGER D K.
PA   (BURG/) BURGESS C E.
PA   (EDIN/) EDINGER S R.
PA   (VOSS/) VOSS E Z.
PA   (MILL/) MILLER C E.
  Query Match             6.7%;  Score 82;  DB 10;  Length 858;
  Best Local Similarity   25.0%;  Pred. No. 12;
RESULT 1287
ID   ADG42639 standard; protein; 867 AA.
DE   Mouse prominin 1 precursor.
PN   US2003204052-A1.
PD   30-OCT-2003.
PA   (HERR/) HERRMANN J L.
PA   (RAST/) RASTELLI L.
PA   (SHIM/) SHIMKETS R A.
  Query Match             6.7%;  Score 82;  DB 7;  Length 867;
  Best Local Similarity   25.0%;  Pred. No. 13;
RESULT 1288
ID   AEF35385 standard; protein; 867 AA.
DE   NOV7 related protein, SEQ ID 134.
PN   US2006013813-A1.
PD   19-JAN-2006.
PA   (MEZE/) MEZES P S.
PA   (RAST/) RASTELLI L.
PA   (HERR/) HERRMANN J L.
PA   (MACD/) MACDOUGALL J R.
PA   (ZHON/) ZHONG H.
PA   (CASM/) CASMAN S J.
PA   (BOLD/) BOLDOG F L.
PA   (SHIM/) SHIMKETS R A.
PA   (GORM/) GORMAN L.
PA   (EISE/) EISEN A J.
PA   (SPAD/) SPADERNA S K.
PA   (VERN/) VERNET C A M.
PA   (BERG/) BERGHS C.
PA   (SPYT/) SPYTEK K A.
PA   (DIPI/) DIPIPPO V A.
PA   (ZERH/) ZERHUSEN B D.
PA   (PEYM/) PEYMAN J A.
PA   (ELLE/) ELLERMAN K.
PA   (STON/) STONE D J.
PA   (GROS/) GROSSE W M.
PA   (ALSO/) ALSOBROOK J P.
PA   (LEPL/) LEPLEY D M.
PA   (RIEG/) RIEGER D K.
PA   (BURG/) BURGESS C E.
PA   (EDIN/) EDINGER S R.
PA   (VOSS/) VOSS E Z.
PA   (MILL/) MILLER C E.
  Query Match             6.7%;  Score 82;  DB 10;  Length 867;
  Best Local Similarity   25.0%;  Pred. No. 13;
RESULT 1289
ID   AAE07051 standard; protein; 261 AA.
DE   Human gene 1 encoded secreted protein HTPFX16, SEQ ID NO:68.
PN   WO200154708-A1.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             6.7%;  Score 81.5;  DB 4;  Length 261;
  Best Local Similarity   25.6%;  Pred. No. 2.6;
RESULT 1290
ID   ABG65078 standard; protein; 261 AA.
DE   Human albumin fusion protein #1753.
PN   WO200177137-A1.
PD   18-OCT-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             6.7%;  Score 81.5;  DB 5;  Length 261;
  Best Local Similarity   25.6%;  Pred. No. 2.6;
RESULT 1291
ID   ADL78345 standard; protein; 261 AA.
DE   Albumin fusion protein related therapeutic protein X, SEQ ID No 1827.
PN   US2004010134-A1.
PD   15-JAN-2004.
PA   (ROSE/) ROSEN C A.
PA   (HASE/) HASELTINE W A.
  Query Match             6.7%;  Score 81.5;  DB 8;  Length 261;
  Best Local Similarity   25.6%;  Pred. No. 2.6;
RESULT 1292
ID   AAE07106 standard; protein; 276 AA.
DE   Human gene 1 encoded secreted protein fragment, SEQ ID NO:123.
PN   WO200154708-A1.
PD   02-AUG-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             6.7%;  Score 81.5;  DB 4;  Length 276;
  Best Local Similarity   25.6%;  Pred. No. 2.8;
RESULT 1293
ID   AAE10682 standard; protein; 316 AA.
DE   G-protein coupled receptor 1c (GPCR1c).
PN   WO200164879-A2.
PD   07-SEP-2001.
PA   (CURA-) CURAGEN CORP.
  Query Match             6.7%;  Score 81.5;  DB 4;  Length 316;
  Best Local Similarity   21.8%;  Pred. No. 3.4;
RESULT 1294
ID   AAE09449 standard; protein; 1694 AA.
DE   Human sbg24878SIa protein #2.
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PN WO200160850-A1.
PD 23-AUG-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 6.7%; Score 81.5; DB 4; Length 1694;
Best Local Similarity 22.7%; Pred. No. 37;
RESULT 1295
ID AAE09448 standard; protein; 1709 AA.
DE Human sbg24878SIa protein #1.
PN WO200160850-A1.
PD 23-AUG-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 6.7%; Score 81.5; DB 4; Length 1709;
Best Local Similarity 22.7%; Pred. No. 38;
RESULT 1296
ID ABG10466 standard; protein; 1839 AA.
DE Novel human diagnostic protein #10457.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.7%; Score 81.5; DB 4; Length 1839;
Best Local Similarity 22.7%; Pred. No. 42;
RESULT 1297
ID AAR13274 standard; protein; 254 AA.
DE Petunia extracellular chitinase.
PN EP440304-A.
PD 07-AUG-1991.
PA (MOGE-) MOGEN INT NV.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 6.7%; Score 81; DB 2; Length 254;
Best Local Similarity 24.0%; Pred. No. 2.9;
RESULT 1298
ID AAW31296 standard; protein; 254 AA.
DE Petunia hybrida extracellular chitinase protein.
PN US5670706-A.
PD 23-SEP-1997.
PA (UYLE-) RIJKSUNIV LEIDEN.
PA (MOGE-) MOGEN INT NV.
Query Match 6.7%; Score 81; DB 2; Length 254;
Best Local Similarity 24.0%; Pred. No. 2.9;
RESULT 1299
ID AAB07512 standard; protein; 254 AA.
DE Amino acid sequence of an extracellular chitinase.
PN US6087560-A.
PD 11-JUL-2000.
PA (UYLE-) RIJKSUNIV LEIDEN.
PA (MOGE-) MOGEN INT NV.
Query Match 6.7%; Score 81; DB 3; Length 254;
Best Local Similarity 24.0%; Pred. No. 2.9;
RESULT 1300
ID ADN22431 standard; protein; 461 AA.
DE Bacterial polypeptide #5084.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.7%; Score 81; DB 8; Length 461;
Best Local Similarity 24.8%; Pred. No. 6.7;
RESULT 1301
ID ABM93379 standard; protein; 706 AA.
DE M. xanthus protein sequence, seq id 12578.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 6.7%; Score 81; DB 9; Length 706;
Best Local Similarity 35.5%; Pred. No. 12;
RESULT 1302
ID AAY12855 standard; protein; 82 AA.
DE Human 5' EST secreted protein SEQ ID NO:445.
PN WO9906549-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 6.6%; Score 80.5; DB 2; Length 82;
Best Local Similarity 28.8%; Pred. No. 0.66;
RESULT 1303
ID AAG71984 standard; protein; 320 AA.
DE Human olfactory receptor polypeptide, SEQ ID NO: 1665.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 6.6%; Score 80.5; DB 4; Length 320;
Best Local Similarity 22.5%; Pred. No. 4.6;
RESULT 1304
ID ADX39596 standard; protein; 833 AA.
DE HIV Env protein #5.
PN WO2005012502-A2.
PD 10-FEB-2005.
PA (EPIM-) EPIMMUNE INC.
Query Match 6.6%; Score 80.5; DB 9; Length 833;
Best Local Similarity 18.5%; Pred. No. 18;
RESULT 1305
ID ABM69560 standard; protein; 157 AA.
DE Photorhabdus luminescens protein sequence #2657.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.6%; Score 80; DB 6; Length 157;
Best Local Similarity 29.2%; Pred. No. 1.9;
RESULT 1306
ID ADZ59470 standard; protein; 283 AA.
DE L19 antibody protein with N-terminal linker & C-terminal tagged peptide.
PN WO2005037312-A2.
PD 28-APR-2005.
PA (SCHD) SCHERING AG.
Query Match 6.6%; Score 80; DB 9; Length 283;
Best Local Similarity 23.9%; Pred. No. 4.4;
RESULT 1307
ID ABM70252 standard; protein; 391 AA.
DE Photorhabdus luminescens protein sequence #3349.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.5%; Score 79.5; DB 6; Length 391;
Best Local Similarity 21.6%; Pred. No. 7.9;
RESULT 1308
ID ABP38136 standard; protein; 430 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:2981.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.5%; Score 79.5; DB 5; Length 430;
Best Local Similarity 19.1%; Pred. No. 9.1;
RESULT 1309
ID ADS07662 standard; protein; 430 AA.
DE Staphylococcus epidermis polypeptide seqid 6957.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
Query Match 6.5%; Score 79.5; DB 8; Length 430;
Best Local Similarity 19.1%; Pred. No. 9.1;
RESULT 1310
ID ABB92528 standard; protein; 558 AA.
DE Herbicidally active polypeptide SEQ ID NO 1739.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 6.5%; Score 79.5; DB 5; Length 558;
Best Local Similarity 22.7%; Pred. No. 13;

RESULT 1311
ID AED85341 standard; protein; 558 AA.
DE Nitrogen responsive protein SEQ ID NO 60.
PN WO2005103270-A2.
PD 03-NOV-2005.
PA (CERE-) CERES INC.
Query Match 6.5%; Score 79.5; DB 9; Length 558;
Best Local Similarity 22.7%; Pred. No. 13;
RESULT 1312
ID AED85635 standard; protein; 558 AA.
DE Nitrogen responsive protein #92.
PN WO2005103270-A2.
PD 03-NOV-2005.
PA (CERE-) CERES INC.
Query Match 6.5%; Score 79.5; DB 9; Length 558;
Best Local Similarity 22.7%; Pred. No. 13;
RESULT 1313
ID AED85634 standard; protein; 558 AA.
DE Nitrogen responsive protein #91.
PN WO2005103270-A2.
PD 03-NOV-2005.
PA (CERE-) CERES INC.
Query Match 6.5%; Score 79.5; DB 9; Length 558;
Best Local Similarity 22.7%; Pred. No. 13;
RESULT 1314
ID AED85340 standard; protein; 558 AA.
DE Nitrogen responsive protein SEQ ID NO 59.
PN WO2005103270-A2.
PD 03-NOV-2005.
PA (CERE-) CERES INC.
Query Match 6.5%; Score 79.5; DB 9; Length 558;
Best Local Similarity 22.7%; Pred. No. 13;
RESULT 1315
ID ABB93024 standard; protein; 1143 AA.
DE Herbicidally active polypeptide SEQ ID NO 2235.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 6.5%; Score 79.5; DB 5; Length 1143;
Best Local Similarity 24.6%; Pred. No. 36;
RESULT 1316
ID ADA35539 standard; protein; 1160 AA.
DE Acinetobacter baumannii protein #2700.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.5%; Score 79.5; DB 6; Length 1160;
Best Local Similarity 22.8%; Pred. No. 37;
RESULT 1317
ID ADM04158 standard; protein; 144 AA.
DE Human protein of the invention SEQ ID NO:2843.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.5%; Score 79; DB 7; Length 144;
Best Local Similarity 27.8%; Pred. No. 2.2;
RESULT 1318
ID AEC87088 standard; protein; 144 AA.
DE Human cDNA clone protein BRCOC20006370, SEQ ID 2843.
PN EP1580263-A1.
PD 28-SEP-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.5%; Score 79; DB 9; Length 144;
Best Local Similarity 27.8%; Pred. No. 2.2;
RESULT 1319
ID ABP40601 standard; protein; 315 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5446.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.5%; Score 79; DB 5; Length 315;
Best Local Similarity 20.9%; Pred. No. 6.7;
RESULT 1320
ID ADS07806 standard; protein; 315 AA.
DE Staphylococcus epidermis polypeptide seqid 7101.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
Query Match 6.5%; Score 79; DB 8; Length 315;
Best Local Similarity 20.9%; Pred. No. 6.7;
RESULT 1321
ID ABU40824 standard; protein; 502 AA.
DE Protein encoded by Prokaryotic essential gene #26351.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.5%; Score 79; DB 6; Length 502;
Best Local Similarity 21.4%; Pred. No. 13;
RESULT 1322
ID ABB68615 standard; protein; 546 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 32637.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.5%; Score 79; DB 4; Length 546;
Best Local Similarity 20.9%; Pred. No. 15;
RESULT 1323
ID ADF04297 standard; protein; 555 AA.
DE Bacterial polypeptide #410.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.5%; Score 79; DB 7; Length 555;
Best Local Similarity 21.4%; Pred. No. 15;
RESULT 1324
ID AEF82319 standard; protein; 595 AA.
DE Rice sucrose transport carrier-like protein OsSUT2.
PN CN1626659-A.
PD 15-JUN-2005.
PA (UYBE-) UNIV BEIJING NORMAL.
Query Match 6.5%; Score 79; DB 9; Length 595;
Best Local Similarity 24.0%; Pred. No. 16;
RESULT 1325
ID AAY41118 standard; protein; 667 AA.
DE Rice sucrose transport protein (clone rls6.pk0076.e2).
PN WO9953068-A2.
PD 21-OCT-1999.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 6.5%; Score 79; DB 2; Length 667;
Best Local Similarity 24.0%; Pred. No. 19;
RESULT 1326
ID AAW88525 standard; protein; 1305 AA.
DE Adenyl cyclase type 9 protein amno acid sequence.
PN WO9853856-A1.
PD 03-DEC-1998.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 6.5%; Score 79; DB 2; Length 1305;
Best Local Similarity 23.5%; Pred. No. 50;
RESULT 1327
ID AAR99251 standard; protein; 1353 AA.
DE Murine adenylate cyclase 9.
PN WO9625502-A1.
PD 22-AUG-1996.
PA (MEDI-) MEDICAL RES COUNCIL.
Query Match 6.5%; Score 79; DB 2; Length 1353;
Best Local Similarity 23.5%; Pred. No. 53;
RESULT 1328
ID ADE55614 standard; protein; 328 AA.
DE Rat Protein CAA08796, SEQ ID NO 1433.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.5%; Score 78.5; DB 7; Length 328;
Best Local Similarity 26.8%; Pred. No. 8.1;

RESULT 1329
ID ADE55610 standard; protein; 328 AA.
DE Rat Protein CAA08796, SEQ ID NO 1429.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.5%; Score 78.5; DB 7; Length 328;
Best Local Similarity 26.8%; Pred. No. 8.1;
RESULT 1330
ID ABP99400 standard; protein; 423 AA.
DE Arabidopsis thaliana polypeptide SEQ ID NO 85.
PN WO200266660-A2.
PD 29-AUG-2002.
PA (META-) METANOMICS GMBH & CO KGAA.
Query Match 6.5%; Score 78.5; DB 5; Length 423;
Best Local Similarity 20.7%; Pred. No. 12;
RESULT 1331
ID ADU20553 standard; protein; 423 AA.
DE A. thaliana At5g67220 homologue.
PN WO2004092349-A2.
PD 28-OCT-2004.
PA (BADI) BASF PLANT SCI GMBH.
Query Match 6.5%; Score 78.5; DB 8; Length 423;
Best Local Similarity 20.7%; Pred. No. 12;
RESULT 1332
ID ADU20400 standard; protein; 423 AA.
DE A. thaliana drought tolerance-associated protein At5g67220.
PN WO2004092349-A2.
PD 28-OCT-2004.
PA (BADI) BASF PLANT SCI GMBH.
Query Match 6.5%; Score 78.5; DB 8; Length 423;
Best Local Similarity 20.7%; Pred. No. 12;
RESULT 1333
ID ABG24464 standard; protein; 2005 AA.
DE Novel human diagnostic protein #24455.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.5%; Score 78.5; DB 4; Length 2005;
Best Local Similarity 24.7%; Pred. No. 1.1e+02;
RESULT 1334
ID ABM72364 standard; protein; 309 AA.
DE Staphylococcus aureus protein #1604.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.4%; Score 78; DB 6; Length 309;
Best Local Similarity 20.8%; Pred. No. 8.5;
RESULT 1335
ID AEB41369 standard; protein; 493 AA.
DE L. pneumophila protein SEQ ID NO 5701.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.4%; Score 78; DB 9; Length 493;
Best Local Similarity 20.0%; Pred. No. 16;
RESULT 1336
ID AEB38076 standard; protein; 506 AA.
DE L. pneumophila protein SEQ ID NO 2408.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.4%; Score 78; DB 9; Length 506;
Best Local Similarity 20.0%; Pred. No. 17;
RESULT 1337
ID ADY07028 standard; protein; 725 AA.
DE Plant full length insert polypeptide seqid 62843.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 6.4%; Score 78; DB 8; Length 725;
Best Local Similarity 22.2%; Pred. No. 28;
RESULT 1338
ID ABU39954 standard; protein; 1059 AA.
DE Protein encoded by Prokaryotic essential gene #25481.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 78; DB 6; Length 1059;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1339
ID AAU33615 standard; protein; 1062 AA.
DE Pseudomonas aeruginosa cellular proliferation protein #59.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 78; DB 4; Length 1062;
Best Local Similarity 24.5%; Pred. No. 49;
RESULT 1340
ID ABU15603 standard; protein; 1062 AA.
DE Protein encoded by Prokaryotic essential gene #1130.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 78; DB 6; Length 1062;
Best Local Similarity 24.5%; Pred. No. 49;
RESULT 1341
ID ABO82891 standard; protein; 1065 AA.
DE Pseudomonas aeruginosa polypeptide #15066.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.4%; Score 78; DB 7; Length 1065;
Best Local Similarity 24.5%; Pred. No. 49;
RESULT 1342
ID AEF10990 standard; protein; 1783 AA.
DE C. elegans VDCC alpha 1 subunit, Cav2.1.
PN US2005288489-A1.
PD 29-DEC-2005.
PA (HIRS/) HIRSCH J A.
Query Match 6.4%; Score 78; DB 10; Length 1783;
Best Local Similarity 19.4%; Pred. No. 1e+02;
RESULT 1343
ID ADN23383 standard; protein; 1917 AA.
DE Bacterial polypeptide #6036.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.4%; Score 78; DB 8; Length 1917;
Best Local Similarity 19.4%; Pred. No. 1.1e+02;
RESULT 1344
ID ABO77741 standard; protein; 222 AA.
DE Pseudomonas aeruginosa polypeptide #9916.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.4%; Score 77.5; DB 7; Length 222;
Best Local Similarity 23.6%; Pred. No. 6.1;
RESULT 1345
ID ADM35793 standard; protein; 315 AA.

DE Human novel G protein-coupled receptor,GPCR1c.
PN US2003211485-A1.
PD 13-NOV-2003.
PA (GERL/) GERLACH V L.
PA (MACD/) MACDOUGALL J R.
PA (STON/) STONE D J.
PA (SMIT/) SMITHSON G.
PA (PADI/) PADIGARU M.
PA (BURG/) BURGESS C.
PA (VERN/) VERNET C.
PA (FERN/) FERNANDES E.
PA (SHIM/) SHIMKETS R A.
PA (TCHE/) TCHERNEV V T.
PA (MISH/) MISHRA V.
PA (CASM/) CASMAN S.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B.
Query Match 6.4%; Score 77.5; DB 7; Length 315;
Best Local Similarity 21.1%; Pred. No. 10;
RESULT 1346
ID AAY19919 standard; protein; 416 AA.
DE B. burgdorferi antigenic protein, t291.aa.
PN WO9859071-A1.
PD 30-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (MEDI-) MEDIMMUNE INC.
Query Match 6.4%; Score 77.5; DB 2; Length 416;
Best Local Similarity 24.3%; Pred. No. 15;
RESULT 1347
ID ABU25897 standard; protein; 434 AA.
DE Protein encoded by Prokaryotic essential gene #11424.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 77.5; DB 6; Length 434;
Best Local Similarity 20.8%; Pred. No. 16;
RESULT 1348
ID ADC77581 standard; protein; 453 AA.
DE Mouse TMS2 amino acid sequence.
PN WO2003066829-A2.
PD 14-AUG-2003.
PA (DISC-) DISCOVERY GENOMICS INC.
Query Match 6.4%; Score 77.5; DB 7; Length 453;
Best Local Similarity 23.5%; Pred. No. 17;
RESULT 1349
ID ABR62787 standard; protein; 459 AA.
DE MRSA hexose phosphate transporter SA214.
PN WO2003062466-A2.
PD 31-JUL-2003.
PA (UYBR-) UNIV BRISTOL.
Query Match 6.4%; Score 77.5; DB 7; Length 459;
Best Local Similarity 24.2%; Pred. No. 17;
RESULT 1350
ID ABJ18956 standard; protein; 465 AA.
DE Pathogen specific antigen related staphylococcal protein SEQ ID No 102.
PN WO200259148-A2.
PD 01-AUG-2002.
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
Query Match 6.4%; Score 77.5; DB 6; Length 465;
Best Local Similarity 24.2%; Pred. No. 17;
RESULT 1351
ID ABM72036 standard; protein; 465 AA.
DE Staphylococcus aureus protein #1276.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.4%; Score 77.5; DB 6; Length 465;
Best Local Similarity 24.2%; Pred. No. 17;
RESULT 1352
ID AAY19918 standard; protein; 500 AA.
DE B. burgdorferi antigenic protein, f291.aa.
PN WO9859071-A1.
PD 30-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (MEDI-) MEDIMMUNE INC.
Query Match 6.4%; Score 77.5; DB 2; Length 500;
Best Local Similarity 24.3%; Pred. No. 19;
RESULT 1353
ID AAU50487 standard; protein; 349 AA.
DE Propionibacterium acnes immunogenic protein #11383.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 6.3%; Score 77; DB 4; Length 349;
Best Local Similarity 27.4%; Pred. No. 13;
RESULT 1354
ID ABM47006 standard; protein; 349 AA.
DE Propionibacterium acnes transporter-related polypeptide #11682.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 6.3%; Score 77; DB 6; Length 349;
Best Local Similarity 27.4%; Pred. No. 13;
RESULT 1355
ID ADN21166 standard; protein; 515 AA.
DE Bacterial polypeptide #3819.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.3%; Score 77; DB 8; Length 515;
Best Local Similarity 23.2%; Pred. No. 23;
RESULT 1356
ID AAU35552 standard; protein; 1032 AA.
DE Haemophilus influenzae cellular proliferation protein #193.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.3%; Score 77; DB 4; Length 1032;
Best Local Similarity 22.6%; Pred. No. 61;
RESULT 1357
ID ABU30420 standard; protein; 1032 AA.
DE Protein encoded by Prokaryotic essential gene #15947.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.3%; Score 77; DB 6; Length 1032;
Best Local Similarity 22.6%; Pred. No. 61;
RESULT 1358
ID AED83230 standard; protein; 1032 AA.
DE Haemophilus influenzae AcrB protein.
PN US2005255538-A1.
PD 17-NOV-2005.
PA (BUXS/) BUXSER S E.
PA (POOL/) POOLE K.
PA (DECK/) DECKER D E.
PA (LIXX/) LI X.
Query Match 6.3%; Score 77; DB 9; Length 1032;
Best Local Similarity 22.6%; Pred. No. 61;
RESULT 1359
ID AAG30768 standard; protein; 1200 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36843.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.3%; Score 77; DB 3; Length 1200;
Best Local Similarity 28.4%; Pred. No. 76;
RESULT 1360
ID AAG30767 standard; protein; 1207 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36842.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.3%; Score 77; DB 3; Length 1207;
Best Local Similarity 28.4%; Pred. No. 77;

RESULT 1361
ID AAG30766 standard; protein; 1215 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36841.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.3%; Score 77; DB 3; Length 1215;
Best Local Similarity 28.4%; Pred. No. 77;
RESULT 1362
ID AEB00351 standard; protein; 9913 AA.
DE SARS coronavirus CCTCC-V200303 complement frame 2 translated proteins.
PN WO2005054473-A1.
PD 16-JUN-2005.
PA (UYHK-) UNIV HONG KONG.
Query Match 6.3%; Score 77; DB 9; Length 9913;
Best Local Similarity 20.9%; Pred. No. 1.5e+03;
RESULT 1363
ID ADT40602 standard; protein; 9914 AA.
DE hSARS virus protein, SEQ ID 1590.
PN WO2004085650-A1.
PD 07-OCT-2004.
PA (UYHK-) UNIV HONG KONG.
Query Match 6.3%; Score 77; DB 8; Length 9914;
Best Local Similarity 20.9%; Pred. No. 1.5e+03;
RESULT 1364
ID ADT38132 standard; protein; 9914 AA.
DE hSARS virus protein, SEQ ID 1590.
PN WO2004085633-A1.
PD 07-OCT-2004.
PA (UYHK-) UNIV HONG KONG.
Query Match 6.3%; Score 77; DB 8; Length 9914;
Best Local Similarity 20.9%; Pred. No. 1.5e+03;
RESULT 1365
ID ABB71131 standard; protein; 426 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40185.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.3%; Score 76.5; DB 4; Length 426;
Best Local Similarity 23.6%; Pred. No. 20;
RESULT 1366
ID ABP73987 standard; protein; 468 AA.
DE Candida albicans essential protein SEQ ID NO 7824.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.3%; Score 76.5; DB 5; Length 468;
Best Local Similarity 23.5%; Pred. No. 23;
RESULT 1367
ID AAY41125 standard; protein; 563 AA.
DE Wheat sucrose transport protein (clone wlmk1.pk0002.e11).
PN WO9953068-A2.
PD 21-OCT-1999.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 6.3%; Score 76.5; DB 2; Length 563;
Best Local Similarity 21.9%; Pred. No. 30;
RESULT 1368
ID ABO66088 standard; protein; 614 AA.
DE Klebsiella pneumoniae polypeptide seqid 12605.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.3%; Score 76.5; DB 7; Length 614;
Best Local Similarity 26.1%; Pred. No. 34;
RESULT 1369
ID ABM87753 standard; protein; 959 AA.
DE Rice abiotic stress responsive polypeptide SEQ ID NO:5999.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 6.3%; Score 76.5; DB 7; Length 959;
Best Local Similarity 21.1%; Pred. No. 63;
RESULT 1370
ID ABP71102 standard; protein; 1378 AA.
DE Murine homologue of attractin/mahogany (HAM) polypeptide.
PN WO200297120-A1.
PD 05-DEC-2002.
PA (IMMV) IMMUNEX CORP.
Query Match 6.3%; Score 76.5; DB 6; Length 1378;
Best Local Similarity 22.6%; Pred. No. 1.1e+02;
RESULT 1371
ID ABB98398 standard; protein; 19938 AA.
DE Streptomyces viridochromogenes Avi gene cluster polypeptide frame 1.
PN WO200268436-A1.
PD 06-SEP-2002.
PA (COMB-) COMBINATURE BIOPHARM AG.
Query Match 6.3%; Score 76.5; DB 6; Length 19938;
Best Local Similarity 24.4%; Pred. No. 4.7e+03;
RESULT 1372
ID AAW56388 standard; protein; 315 AA.
DE Fragment of the human GlyT-2 transporter encoded by clone phG2-9b.
PN WO9807854-A1.
PD 26-FEB-1998.
PA (ALLX) ALLELIX NEUROSCIENCE INC.
Query Match 6.3%; Score 76; DB 2; Length 315;
Best Local Similarity 21.4%; Pred. No. 15;
RESULT 1373
ID AAG81675 standard; protein; 337 AA.
DE S. epidermidis open reading frame protein sequence SEQ ID NO:444.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 6.3%; Score 76; DB 4; Length 337;
Best Local Similarity 25.7%; Pred. No. 16;
RESULT 1374
ID ABB48085 standard; protein; 431 AA.
DE Listeria monocytogenes protein #789.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 6.3%; Score 76; DB 5; Length 431;
Best Local Similarity 25.6%; Pred. No. 23;
RESULT 1375
ID ABM73417 standard; protein; 447 AA.
DE Staphylococcus aureus protein #2657.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.3%; Score 76; DB 6; Length 447;
Best Local Similarity 19.5%; Pred. No. 24;
RESULT 1376
ID ABG10541 standard; protein; 480 AA.
DE Novel human diagnostic protein #10532.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 76; DB 4; Length 480;
Best Local Similarity 24.2%; Pred. No. 27;
RESULT 1377
ID ADF04316 standard; protein; 500 AA.
DE Bacterial polypeptide #429.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.3%; Score 76; DB 7; Length 500;
Best Local Similarity 25.0%; Pred. No. 29;
RESULT 1378
ID AAB61263 standard; protein; 631 AA.
DE Human monocyte inhibitory receptor precursor.
PN WO200100810-A1.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.3%; Score 76; DB 4; Length 631;
Best Local Similarity 23.9%; Pred. No. 40;
RESULT 1379
ID ABJ19062 standard; protein; 643 AA.
DE Pathogen specific antigen related staphylococcal protein SEQ ID No 339.

PN WO200259148-A2.
PD 01-AUG-2002.
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
Query Match 6.3%; Score 76; DB 6; Length 643;
Best Local Similarity 22.6%; Pred. No. 41;
RESULT 1380
ID ADZ10717 standard; protein; 701 AA.
DE Rice metal complex transporter OsYSL12.
PN WO2005030950-A1.
PD 07-APR-2005.
PA (NISC-) JAPAN SCI & TECHNOLOGY AGENCY.
Query Match 6.3%; Score 76; DB 9; Length 701;
Best Local Similarity 22.2%; Pred. No. 46;
RESULT 1381
ID ABB71337 standard; protein; 1079 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40803.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.3%; Score 76; DB 4; Length 1079;
Best Local Similarity 26.0%; Pred. No. 85;
RESULT 1382
ID ADB10794 standard; protein; 93 AA.
DE Alloiococcus otitis antigenic protein SEQ ID NO:4266.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 6.2%; Score 75.5; DB 6; Length 93;
Best Local Similarity 31.4%; Pred. No. 3;
RESULT 1383
ID ADB10762 standard; protein; 93 AA.
DE Alloiococcus otitis antigenic protein SEQ ID NO:4298.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 6.2%; Score 75.5; DB 6; Length 93;
Best Local Similarity 31.4%; Pred. No. 3;
RESULT 1384
ID ADB11392 standard; protein; 93 AA.
DE Alloiococcus otitis antigenic protein SEQ ID NO:5668.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 6.2%; Score 75.5; DB 6; Length 93;
Best Local Similarity 31.4%; Pred. No. 3;
RESULT 1385
ID ABP63103 standard; protein; 397 AA.
DE FLO11 gene expression regulator At18.
PN WO200257456-A2.
PD 25-JUL-2002.
PA (MICR-) MICROBIA.
Query Match 6.2%; Score 75.5; DB 5; Length 397;
Best Local Similarity 26.3%; Pred. No. 24;
RESULT 1386
ID ABP35575 standard; protein; 397 AA.
DE Fungal ZBC protein sequence #1.
PN WO200224865-A2.
PD 28-MAR-2002.
PA (MICR-) MICROBIA INC.
Query Match 6.2%; Score 75.5; DB 5; Length 397;
Best Local Similarity 26.3%; Pred. No. 24;
RESULT 1387
ID ABU49908 standard; protein; 409 AA.
DE Protein encoded by Prokaryotic essential gene #35435.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.2%; Score 75.5; DB 6; Length 409;
Best Local Similarity 23.2%; Pred. No. 25;
RESULT 1388
ID ADN73661 standard; protein; 476 AA.
DE Thale cress protein repressed in E2Fa/Dpa expressing plants SeqID 1556.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Query Match 6.2%; Score 75.5; DB 8; Length 476;
Best Local Similarity 21.5%; Pred. No. 31;
RESULT 1389
ID AEF31284 standard; protein; 825 AA.
DE Rice blast resistance protein.
PN CN1629293-A.
PD 22-JUN-2005.
PA (GENE-) INST GENETICS & DEV BIOL CAS.
Query Match 6.2%; Score 75.5; DB 9; Length 825;
Best Local Similarity 21.6%; Pred. No. 67;
RESULT 1390
ID AEE80572 standard; protein; 1928 AA.
DE Human ovarian cancer marker fragment SEQ ID NO 939.
PN WO2005116850-A2.
PD 08-DEC-2005.
PA (COMP-) COMPUGEN LTD.
Query Match 6.2%; Score 75.5; DB 10; Length 1928;
Best Local Similarity 29.6%; Pred. No. 2.2e+02;
RESULT 1391
ID ADA36649 standard; protein; 277 AA.
DE Acinetobacter baumannii protein #3810.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.2%; Score 75; DB 6; Length 277;
Best Local Similarity 39.2%; Pred. No. 16;
RESULT 1392
ID AEE08883 standard; protein; 288 AA.
DE Yeast aquaporin, Aqu2-1.
PN WO2005108422-A2.
PD 17-NOV-2005.
PA (UYRO-) UNIV ROYAL VETERINARY & AGRIC.
Query Match 6.2%; Score 75; DB 9; Length 288;
Best Local Similarity 25.2%; Pred. No. 17;
RESULT 1393
ID ABB98338 standard; protein; 292 AA.
DE Human anti-tenascin C monoclonal antibody SEQ ID NO 2.
PN JP2002234900-A.
PD 23-AUG-2002.
PA (MIED-) MIE DAIGAKUCHO.
Query Match 6.2%; Score 75; DB 6; Length 292;
Best Local Similarity 34.7%; Pred. No. 18;
RESULT 1394
ID ADP04284 standard; protein; 292 AA.
DE Human tenascin C fibronectin III-like domain BCD domain polypeptide.
PN JP2004138489-A.
PD 13-MAY-2004.
PA (MENE-) MENEKI SEIBUTSU KENKYUSHO KK.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match 6.2%; Score 75; DB 8; Length 292;
Best Local Similarity 34.7%; Pred. No. 18;
RESULT 1395
ID AEE60240 standard; protein; 379 AA.
DE Cat chlamydia inclusion body membrane protein SEQ ID NO: 35.
PN JP2005333964-A.
PD 08-DEC-2005.
PA (UYYA-) UNIV YAMAGUCHI.
Query Match 6.2%; Score 75; DB 10; Length 379;
Best Local Similarity 22.6%; Pred. No. 25;
RESULT 1396
ID ABM84660 standard; protein; 452 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4909.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.2%; Score 75; DB 8; Length 452;
Best Local Similarity 23.6%; Pred. No. 33;
RESULT 1397
ID ABU29147 standard; protein; 527 AA.
DE Protein encoded by Prokaryotic essential gene #14674.
PN WO200277183-A2.

PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.2%; Score 75; DB 6; Length 527;
Best Local Similarity 21.2%; Pred. No. 40;
RESULT 1398
ID ADX77029 standard; protein; 588 AA.
DE Plant full length insert polypeptide seqid 46395.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 6.2%; Score 75; DB 8; Length 588;
Best Local Similarity 21.1%; Pred. No. 47;
RESULT 1399
ID AEE80568 standard; protein; 1658 AA.
DE Human ovarian cancer marker fragment SEQ ID NO 935.
PN WO2005116850-A2.
PD 08-DEC-2005.
PA (COMP-) COMPUGEN LTD.
Query Match 6.2%; Score 75; DB 10; Length 1658;
Best Local Similarity 34.7%; Pred. No. 2e+02;
RESULT 1400
ID AEE80569 standard; protein; 1673 AA.
DE Human ovarian cancer marker fragment SEQ ID NO 936.
PN WO2005116850-A2.
PD 08-DEC-2005.
PA (COMP-) COMPUGEN LTD.
Query Match 6.2%; Score 75; DB 10; Length 1673;
Best Local Similarity 34.7%; Pred. No. 2.1e+02;
RESULT 1401
ID AEE80579 standard; protein; 1730 AA.
DE Human ovarian cancer marker fragment SEQ ID NO 946.
PN WO2005116850-A2.
PD 08-DEC-2005.
PA (COMP-) COMPUGEN LTD.
Query Match 6.2%; Score 75; DB 10; Length 1730;
Best Local Similarity 34.7%; Pred. No. 2.2e+02;
RESULT 1402
ID ADN05803 standard; protein; 2000 AA.
DE Antipsoriatic protein sequence #1065.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 75; DB 8; Length 2000;
Best Local Similarity 34.7%; Pred. No. 2.7e+02;
RESULT 1403
ID AEE80578 standard; protein; 2065 AA.
DE Human ovarian cancer marker fragment SEQ ID NO 945.
PN WO2005116850-A2.
PD 08-DEC-2005.
PA (COMP-) COMPUGEN LTD.
Query Match 6.2%; Score 75; DB 10; Length 2065;
Best Local Similarity 34.7%; Pred. No. 2.8e+02;
RESULT 1404
ID AEE80577 standard; protein; 2067 AA.
DE Human ovarian cancer marker fragment SEQ ID NO 944.
PN WO2005116850-A2.
PD 08-DEC-2005.
PA (COMP-) COMPUGEN LTD.
Query Match 6.2%; Score 75; DB 10; Length 2067;
Best Local Similarity 34.7%; Pred. No. 2.8e+02;
RESULT 1405
ID AEE80574 standard; protein; 2091 AA.
DE Human ovarian cancer marker fragment SEQ ID NO 941.
PN WO2005116850-A2.
PD 08-DEC-2005.
PA (COMP-) COMPUGEN LTD.
Query Match 6.2%; Score 75; DB 10; Length 2091;
Best Local Similarity 34.7%; Pred. No. 2.8e+02;
RESULT 1406
ID ABO01379 standard; protein; 2108 AA.
DE Human protein NOV35b.
PN WO2003023008-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.2%; Score 75; DB 6; Length 2108;
Best Local Similarity 34.7%; Pred. No. 2.9e+02;
RESULT 1407
ID ADN96130 standard; protein; 2108 AA.
DE Human NOVX polypeptide #92.
PN US2004067490-A1.
PD 08-APR-2004.
PA (ZHON/) ZHONG M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (SPYT/) SPYTEK K A.
PA (KEKU/) KEKUDA R.
PA (TAUP/) TAUPIER R J.
PA (ANDE/) ANDERSON D W.
PA (VERN/) VERNET C A M.
PA (CATT/) CATTERTON E.
PA (MILL/) MILLER C E.
PA (SHEN/) SHENOY S G.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (TCHE/) TCHERNEV V T.
PA (PADI/) PADIGARU M.
PA (GUSE/) GUSEV V Y.
PA (MALY/) MALYANKAR U M.
PA (BURG/) BURGESS C E.
PA (GERL/) GERLACH V.
PA (CASM/) CASMAN S J.
PA (RIEG/) RIEGER D K.
PA (GROS/) GROSSE W M.
PA (SMIT/) SMITHSON G.
PA (PEYM/) PEYMAN J A.
PA (STAR/) STARLING G.
PA (ROTH/) ROTHENBERG M E.
PA (LARO/) LAROCHELLE W J.
PA (SHIM/) SHIMKETS R A.
PA (CRAB/) CRABTREE J.
PA (RAST/) RASTELLI L.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (MACD/) MACDOUGALL J R.
PA (ELLE/) ELLERMAN K.
PA (CHAP/) CHAPOVAL A.
Query Match 6.2%; Score 75; DB 8; Length 2108;
Best Local Similarity 34.7%; Pred. No. 2.9e+02;
RESULT 1408
ID AAO30847 standard; protein; 2110 AA.
DE Human cell adhesion and extracellular matrix protein (CADECM)-37.
PN WO2003047526-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.2%; Score 75; DB 7; Length 2110;
Best Local Similarity 34.7%; Pred. No. 2.9e+02;
RESULT 1409
ID ADM80773 standard; protein; 2110 AA.
DE Human CADECM-2 protein SEQ ID NO:2.
PN WO2004015396-A2.
PD 19-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.2%; Score 75; DB 8; Length 2110;
Best Local Similarity 34.7%; Pred. No. 2.9e+02;
RESULT 1410
ID AEE80570 standard; protein; 2110 AA.
DE Human ovarian cancer marker fragment SEQ ID NO 937.
PN WO2005116850-A2.
PD 08-DEC-2005.

PA (COMP-) COMPUGEN LTD.
Query Match 6.2%; Score 75; DB 10; Length 2110;
Best Local Similarity 34.7%; Pred. No. 2.9e+02;
RESULT 1411
ID AEE80571 standard; protein; 2110 AA.
DE Human ovarian cancer marker fragment SEQ ID NO 938.
PN WO2005116850-A2.
PD 08-DEC-2005.
PA (COMP-) COMPUGEN LTD.
Query Match 6.2%; Score 75; DB 10; Length 2110;
Best Local Similarity 34.7%; Pred. No. 2.9e+02;
RESULT 1412
ID ABM83292 standard; protein; 2116 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3541.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.2%; Score 75; DB 8; Length 2116;
Best Local Similarity 34.7%; Pred. No. 2.9e+02;
RESULT 1413
ID ABM83291 standard; protein; 2122 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3540.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.2%; Score 75; DB 8; Length 2122;
Best Local Similarity 34.7%; Pred. No. 2.9e+02;
RESULT 1414
ID ABG70361 standard; protein; 2167 AA.
DE Novel human thrombopoietin variant protein, NV-20.
PN US2002068342-A1.
PD 06-JUN-2002.
PA (KHOS/) KHOSRAVI R.
PA (BERN/) BERNSTEIN J.
Query Match 6.2%; Score 75; DB 5; Length 2167;
Best Local Similarity 34.7%; Pred. No. 3e+02;
RESULT 1415
ID AAR94562 standard; protein; 2199 AA.
DE Human cytotactin.
PN WO9608513-A1.
PD 21-MAR-1996.
PA (SCRI) SCRIPPS RES INST.
Query Match 6.2%; Score 75; DB 2; Length 2199;
Best Local Similarity 34.7%; Pred. No. 3.1e+02;
RESULT 1416
ID ABO01378 standard; protein; 2199 AA.
DE Human protein NOV35a.
PN WO2003023008-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.2%; Score 75; DB 6; Length 2199;
Best Local Similarity 34.7%; Pred. No. 3.1e+02;
RESULT 1417
ID ADN96128 standard; protein; 2199 AA.
DE Human NOVX polypeptide #91.
PN US2004067490-A1.
PD 08-APR-2004.
PA (ZHON/) ZHONG M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (SPYT/) SPYTEK K A.
PA (KEKU/) KEKUDA R.
PA (TAUP/) TAUPIER R J.
PA (ANDE/) ANDERSON D W.
PA (VERN/) VERNET C A M.
PA (CATT/) CATTERTON E.
PA (MILL/) MILLER C E.
PA (SHEN/) SHENOY S G.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (TCHE/) TCHERNEV V T.
PA (PADI/) PADIGARU M.
PA (GUSE/) GUSEV V Y.
PA (MALY/) MALYANKAR U M.
PA (BURG/) BURGESS C E.
PA (GERL/) GERLACH V.
PA (CASM/) CASMAN S J.
PA (RIEG/) RIEGER D K.
PA (GROS/) GROSSE W M.
PA (SMIT/) SMITHSON G.
PA (PEYM/) PEYMAN J A.
PA (STAR/) STARLING G.
PA (ROTH/) ROTHENBERG M E.
PA (LARO/) LAROCHELLE W J.
PA (SHIM/) SHIMKETS R A.
PA (CRAB/) CRABTREE J.
PA (RAST/) RASTELLI L.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (MACD/) MACDOUGALL J R.
PA (ELLE/) ELLERMAN K.
PA (CHAP/) CHAPOVAL A.
Query Match 6.2%; Score 75; DB 8; Length 2199;
Best Local Similarity 34.7%; Pred. No. 3.1e+02;
RESULT 1418
ID AAB36935 standard; protein; 2201 AA.
DE Human tenascin-C.
PN WO200066628-A1.
PD 09-NOV-2000.
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
Query Match 6.2%; Score 75; DB 4; Length 2201;
Best Local Similarity 34.7%; Pred. No. 3.1e+02;
RESULT 1419
ID ABP97745 standard; protein; 2201 AA.
DE Amino acid sequence of human HXB polypeptide.
PN WO2003010205-A1.
PD 06-FEB-2003.
PA (UYDU-) UNIV DUKE MEDICAL CENT.
Query Match 6.2%; Score 75; DB 6; Length 2201;
Best Local Similarity 34.7%; Pred. No. 3.1e+02;
RESULT 1420
ID ABM78955 standard; protein; 2201 AA.
DE Breast cancer specific marker under-expressed in breast cancer.
PN WO2003073911-A2.
PD 12-SEP-2003.
PA (GEOU) UNIV GEORGETOWN.
Query Match 6.2%; Score 75; DB 7; Length 2201;
Best Local Similarity 34.7%; Pred. No. 3.1e+02;
RESULT 1421
ID ADD69400 standard; protein; 2201 AA.
DE Human tenascin protein - SEQ ID 136.
PN WO2003048185-A2.
PD 12-JUN-2003.
PA (GENV-) GENVEC INC.
Query Match 6.2%; Score 75; DB 7; Length 2201;
Best Local Similarity 34.7%; Pred. No. 3.1e+02;
RESULT 1422
ID ADD47935 standard; protein; 2201 AA.
DE Human Protein XP_005348, SEQ ID NO 13631.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.2%; Score 75; DB 7; Length 2201;
Best Local Similarity 34.7%; Pred. No. 3.1e+02;
RESULT 1423
ID ADE62224 standard; protein; 2201 AA.
DE Human Protein P24821, SEQ ID NO 8153.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.2%; Score 75; DB 7; Length 2201;
Best Local Similarity 34.7%; Pred. No. 3.1e+02;

RESULT 1424
ID ADO17766 standard; protein; 2201 AA.
DE Differentially expressed protein Lu1, SEQ ID 1.
PN WO2004015390-A2.
PD 19-FEB-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.2%; Score 75; DB 8; Length 2201;
Best Local Similarity 34.7%; Pred. No. 3.1e+02;
RESULT 1425
ID ADQ19756 standard; protein; 2201 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2575.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 6.2%; Score 75; DB 8; Length 2201;
Best Local Similarity 34.7%; Pred. No. 3.1e+02;
RESULT 1426
ID ADU06359 standard; protein; 2201 AA.
DE Novel bronchial cancer-associated human protein SeqID583.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 6.2%; Score 75; DB 8; Length 2201;
Best Local Similarity 34.7%; Pred. No. 3.1e+02;
RESULT 1427
ID ADV70208 standard; protein; 2201 AA.
DE Tumor-associated antigenic target polypeptide TAT450.
PN WO2004112829-A2.
PD 29-DEC-2004.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 75; DB 9; Length 2201;
Best Local Similarity 34.7%; Pred. No. 3.1e+02;
RESULT 1428
ID ADW88533 standard; peptide; 2201 AA.
DE Human tenascin-C.
PN WO2005009366-A2.
PD 03-FEB-2005.
PA (CORR) CORNELL RES FOUND INC.
Query Match 6.2%; Score 75; DB 9; Length 2201;
Best Local Similarity 34.7%; Pred. No. 3.1e+02;
RESULT 1429
ID AED07152 standard; protein; 2201 AA.
DE Respiratory disease-associated protein, TNC.
PN WO2005092383-A1.
PD 06-OCT-2005.
PA (TAKE) TAKEDA PHARM CO LTD.
Query Match 6.2%; Score 75; DB 9; Length 2201;
Best Local Similarity 34.7%; Pred. No. 3.1e+02;
RESULT 1430
ID AEE80566 standard; protein; 2201 AA.
DE Human ovarian cancer marker fragment SEQ ID NO 933.
PN WO2005116850-A2.
PD 08-DEC-2005.
PA (COMP-) COMPUGEN LTD.
Query Match 6.2%; Score 75; DB 10; Length 2201;
Best Local Similarity 34.7%; Pred. No. 3.1e+02;
RESULT 1431
ID AEE80565 standard; protein; 2201 AA.
DE Human ovarian cancer marker fragment SEQ ID NO 932.
PN WO2005116850-A2.
PD 08-DEC-2005.
PA (COMP-) COMPUGEN LTD.
Query Match 6.2%; Score 75; DB 10; Length 2201;
Best Local Similarity 34.7%; Pred. No. 3.1e+02;
RESULT 1432
ID ABM83294 standard; protein; 2207 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3543.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.2%; Score 75; DB 8; Length 2207;
Best Local Similarity 34.7%; Pred. No. 3.1e+02;
RESULT 1433
ID ABM83293 standard; protein; 2207 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3542.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.2%; Score 75; DB 8; Length 2207;
Best Local Similarity 34.7%; Pred. No. 3.1e+02;
RESULT 1434
ID ABM83295 standard; protein; 2207 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3544.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.2%; Score 75; DB 8; Length 2207;
Best Local Similarity 34.7%; Pred. No. 3.1e+02;
RESULT 1435
ID AEE80567 standard; protein; 2293 AA.
DE Human ovarian cancer marker fragment SEQ ID NO 934.
PN WO2005116850-A2.
PD 08-DEC-2005.
PA (COMP-) COMPUGEN LTD.
Query Match 6.2%; Score 75; DB 10; Length 2293;
Best Local Similarity 34.7%; Pred. No. 3.2e+02;
RESULT 1436
ID ADQ65800 standard; protein; 202 AA.
DE Novel human protein sequence #773.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.1%; Score 74.5; DB 8; Length 202;
Best Local Similarity 22.8%; Pred. No. 12;
RESULT 1437
ID AAM41065 standard; protein; 210 AA.
DE Human polypeptide SEQ ID NO 5996.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 74.5; DB 4; Length 210;
Best Local Similarity 22.8%; Pred. No. 13;
RESULT 1438
ID AAM41066 standard; protein; 210 AA.
DE Human polypeptide SEQ ID NO 5997.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 74.5; DB 4; Length 210;
Best Local Similarity 22.8%; Pred. No. 13;
RESULT 1439
ID AAM41067 standard; protein; 210 AA.
DE Human polypeptide SEQ ID NO 5998.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 74.5; DB 4; Length 210;
Best Local Similarity 22.8%; Pred. No. 13;
RESULT 1440
ID AAB46359 standard; protein; 255 AA.
DE H. pylori HPC104 protein.
PN WO200073502-A2.
PD 07-DEC-2000.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PA (CREA-) CREATOGEN GMBH.
Query Match 6.1%; Score 74.5; DB 4; Length 255;
Best Local Similarity 18.6%; Pred. No. 17;
RESULT 1441
ID ABP58049 standard; protein; 289 AA.
DE Saccharomyces cerevisiae aquaporin.
PN WO200290557-A2.
PD 14-NOV-2002.
PA (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
Query Match 6.1%; Score 74.5; DB 6; Length 289;

Best Local Similarity 26.8%; Pred. No. 20;
RESULT 1442
ID ADR41511 standard; protein; 355 AA.
DE Human CD-like molecule HRDFA94, SEQ ID NO:310.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 74.5; DB 5; Length 355;
Best Local Similarity 22.2%; Pred. No. 26;
RESULT 1443
ID AAB78974 standard; protein; 364 AA.
DE C. glutamicum SRT protein sequence SEQ ID NO:208.
PN WO200100804-A2.
PD 04-JAN-2001.
PA (BADI) BASF AG.
Query Match 6.1%; Score 74.5; DB 4; Length 364;
Best Local Similarity 20.3%; Pred. No. 27;
RESULT 1444
ID AAG92975 standard; protein; 378 AA.
DE C glutamicum protein fragment SEQ ID NO: 6729.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 6.1%; Score 74.5; DB 4; Length 378;
Best Local Similarity 20.3%; Pred. No. 29;
RESULT 1445
ID AAB78973 standard; protein; 412 AA.
DE C. glutamicum SRT protein sequence SEQ ID NO:206.
PN WO200100804-A2.
PD 04-JAN-2001.
PA (BADI) BASF AG.
Query Match 6.1%; Score 74.5; DB 4; Length 412;
Best Local Similarity 20.3%; Pred. No. 33;
RESULT 1446
ID ABU49116 standard; protein; 468 AA.
DE Protein encoded by Prokaryotic essential gene #34643.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 74.5; DB 6; Length 468;
Best Local Similarity 25.7%; Pred. No. 39;
RESULT 1447
ID ABB60065 standard; protein; 473 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 6987.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.1%; Score 74.5; DB 4; Length 473;
Best Local Similarity 16.5%; Pred. No. 40;
RESULT 1448
ID AAU18057 standard; protein; 524 AA.
DE Human immunoglobulin polypeptide SEQ ID No 202.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 74.5; DB 4; Length 524;
Best Local Similarity 22.2%; Pred. No. 46;
RESULT 1449
ID ABB10423 standard; protein; 524 AA.
DE Human cDNA SEQ ID NO: 731.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 74.5; DB 4; Length 524;
Best Local Similarity 22.2%; Pred. No. 46;
RESULT 1450
ID ABP67010 standard; protein; 524 AA.
DE Human polypeptide SEQ ID NO 731.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 6.1%; Score 74.5; DB 5; Length 524;
Best Local Similarity 22.2%; Pred. No. 46;
RESULT 1451
ID ADB31681 standard; protein; 524 AA.
DE Human novel protein SEQ ID NO 202.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 74.5; DB 7; Length 524;
Best Local Similarity 22.2%; Pred. No. 46;
RESULT 1452
ID ABU20338 standard; protein; 541 AA.
DE Protein encoded by Prokaryotic essential gene #5865.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 74.5; DB 6; Length 541;
Best Local Similarity 20.3%; Pred. No. 48;
RESULT 1453
ID ABB90801 standard; protein; 618 AA.
DE Herbicidally active polypeptide SEQ ID NO 12.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 6.1%; Score 74.5; DB 5; Length 618;
Best Local Similarity 27.7%; Pred. No. 58;
RESULT 1454
ID ADN74317 standard; protein; 618 AA.
DE Thale cress protein repressed in E2Fa/Dpa expressing plants SeqID 2212.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Query Match 6.1%; Score 74.5; DB 8; Length 618;
Best Local Similarity 27.7%; Pred. No. 58;
RESULT 1455
ID ABB10186 standard; protein; 654 AA.
DE Human cDNA SEQ ID NO: 494.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 74.5; DB 4; Length 654;
Best Local Similarity 22.2%; Pred. No. 63;
RESULT 1456
ID ABP66773 standard; protein; 654 AA.
DE Human polypeptide SEQ ID NO 494.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 6.1%; Score 74.5; DB 5; Length 654;
Best Local Similarity 22.2%; Pred. No. 63;
RESULT 1457
ID ADP04132 standard; protein; 705 AA.
DE Human colon specific protein SEQ ID NO:113.
PN WO2004050858-A2.
PD 17-JUN-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 6.1%; Score 74.5; DB 8; Length 705;
Best Local Similarity 23.1%; Pred. No. 70;
RESULT 1458
ID ADT56083 standard; protein; 837 AA.
DE Plant polypeptide, SEQ ID 6160.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 6.1%; Score 74.5; DB 8; Length 837;
Best Local Similarity 27.7%; Pred. No. 89;
RESULT 1459
ID AAG38915 standard; protein; 1030 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48077.
PN EP1033405-A2.
PD 06-SEP-2000.

Query Match 6.1%; Score 74.5; DB 3; Length 1030;
Best Local Similarity 27.7%; Pred. No. 1.2e+02;

RESULT 1460
ID AAG38914 standard; protein; 1133 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48076.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.1%; Score 74.5; DB 3; Length 1133;
Best Local Similarity 27.7%; Pred. No. 1.4e+02;

RESULT 1461
ID AAG38913 standard; protein; 1193 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48075.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.1%; Score 74.5; DB 3; Length 1193;
Best Local Similarity 27.7%; Pred. No. 1.5e+02;

RESULT 1462
ID ABU79090 standard; protein; 1709 AA.
DE Human sialic acid binding Ig-superfamily lectin, siglec-1.
PN US2002177551-A1.
PD 28-NOV-2002.
PA (TERM/) TERMAN D S.
Query Match 6.1%; Score 74.5; DB 6; Length 1709;
Best Local Similarity 22.2%; Pred. No. 2.4e+02;

RESULT 1463
ID ADF43331 standard; protein; 1709 AA.
DE Superantigen associated protein seq id 51.
PN US2003157113-A1.
PD 21-AUG-2003.
PA (TERM/) TERMAN D S.
Query Match 6.1%; Score 74.5; DB 7; Length 1709;
Best Local Similarity 22.2%; Pred. No. 2.4e+02;

RESULT 1464
ID ADJ69756 standard; protein; 1709 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1562.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 6.1%; Score 74.5; DB 7; Length 1709;
Best Local Similarity 22.2%; Pred. No. 2.4e+02;

RESULT 1465
ID ADH71514 standard; protein; 1709 AA.
DE Human protein of the invention NOV14g SEQ ID NO:410.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.1%; Score 74.5; DB 8; Length 1709;
Best Local Similarity 22.2%; Pred. No. 2.4e+02;

RESULT 1466
ID ADR14167 standard; protein; 1709 AA.
DE Human NF-kappaB pathway-associated protein SeqID168.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 6.1%; Score 74.5; DB 8; Length 1709;
Best Local Similarity 22.2%; Pred. No. 2.4e+02;

RESULT 1467
ID AEA23641 standard; protein; 1709 AA.
DE Human PRO polypeptide SEQ ID NO 183.
PN WO2005051988-A2.
PD 09-JUN-2005.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 74.5; DB 9; Length 1709;
Best Local Similarity 22.2%; Pred. No. 2.4e+02;

RESULT 1468
ID AEA23470 standard; protein; 1709 AA.
DE Human PRO polypeptide SEQ ID NO 12.
PN WO2005051988-A2.
PD 09-JUN-2005.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 74.5; DB 9; Length 1709;
Best Local Similarity 22.2%; Pred. No. 2.4e+02;

RESULT 1469
ID ABG01737 standard; protein; 161 AA.
DE Novel human diagnostic protein #1728.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 74; DB 4; Length 161;
Best Local Similarity 30.0%; Pred. No. 9.8;

RESULT 1470
ID ADS21994 standard; protein; 421 AA.
DE Bacterial polypeptide #11027.
PN US20032336 75-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.1%; Score 74; DB 8; Length 421;
Best Local Similarity 20.8%; Pred. No. 38;

RESULT 1471
ID AAB92492 standard; protein; 448 AA.
DE Human protein sequence SEQ ID NO:10589.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.1%; Score 74; DB 4; Length 448;
Best Local Similarity 23.5%; Pred. No. 42;

RESULT 1472
ID ABB97449 standard; protein; 448 AA.
DE Novel human protein SEQ ID NO: 717.
PN WO200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 74; DB 5; Length 448;
Best Local Similarity 23.5%; Pred. No. 42;

RESULT 1473
ID ABB82639 standard; protein; 448 AA.
DE Human hypothetical protein FLJ10060.
PN WO200286060-A2.
PD 31-OCT-2002.
PA (IMME-) IMMERGE BIOTHERAPEUTICS INC.
Query Match 6.1%; Score 74; DB 6; Length 448;
Best Local Similarity 23.5%; Pred. No. 42;

RESULT 1474
ID ABB92535 standard; protein; 555 AA.
DE Herbicidally active polypeptide SEQ ID NO 1746.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 6.1%; Score 74; DB 5; Length 555;
Best Local Similarity 26.4%; Pred. No. 57;

RESULT 1475
ID AED85632 standard; protein; 555 AA.
DE Nitrogen responsive protein #89.
PN WO2005103270-A2.
PD 03-NOV-2005.
PA (CERE-) CERES INC.
Query Match 6.1%; Score 74; DB 9; Length 555;
Best Local Similarity 26.4%; Pred. No. 57;

RESULT 1476
ID AED85338 standard; protein; 555 AA.
DE Nitrogen responsive protein SEQ ID NO 57.
PN WO2005103270-A2.
PD 03-NOV-2005.
PA (CERE-) CERES INC.
Query Match 6.1%; Score 74; DB 9; Length 555;
Best Local Similarity 26.4%; Pred. No. 57;

RESULT 1477
ID ADY12557 standard; protein; 733 AA.
DE Plant full length insert polypeptide seqid 68372.
PN US2004034888-A1.
PD 19-FEB-2004.

PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 6.1%; Score 74; DB 8; Length 733;
Best Local Similarity 19.7%; Pred. No. 84;
RESULT 1478
ID ADG42638 standard; protein; 857 AA.
DE Rat prominin.
PN US2003204052-A1.
PD 30-OCT-2003.
PA (HERR/) HERRMANN J L.
PA (RAST/) RASTELLI L.
PA (SHIM/) SHIMKETS R A.
Query Match 6.1%; Score 74; DB 7; Length 857;
Best Local Similarity 23.0%; Pred. No. 1.1e+02;
RESULT 1479
ID AEF35384 standard; protein; 857 AA.
DE NOV7 related protein, SEQ ID 133.
PN US2006013813-A1.
PD 19-JAN-2006.
PA (MEZE/) MEZES P S.
PA (RAST/) RASTELLI L.
PA (HERR/) HERRMANN J L.
PA (MACD/) MACDOUGALL J R.
PA (ZHON/) ZHONG H.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (SHIM/) SHIMKETS R A.
PA (GORM/) GORMAN L.
PA (EISE/) EISEN A J.
PA (SPAD/) SPADERNA S K.
PA (VERN/) VERNET C A M.
PA (BERG/) BERGHS C.
PA (SPYT/) SPYTEK K A.
PA (DIPI/) DIPIPPO V A.
PA (ZERH/) ZERHUSEN B D.
PA (PEYM/) PEYMAN J A.
PA (ELLE/) ELLERMAN K.
PA (STON/) STONE D J.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
PA (EDIN/) EDINGER S R.
PA (VOSS/) VOSS E Z.
PA (MILL/) MILLER C E.
Query Match 6.1%; Score 74; DB 10; Length 857;
Best Local Similarity 23.0%; Pred. No. 1.1e+02;
RESULT 1480
ID AAB40566 standard; protein; 261 AA.
DE Human ORFX ORF330 polypeptide sequence SEQ ID NO:660.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 6.0%; Score 73.5; DB 3; Length 261;
Best Local Similarity 23.8%; Pred. No. 22;
RESULT 1481
ID AAY70675 standard; protein; 261 AA.
DE Human stomach protein zsig28.
PN WO200015659-A2.
PD 23-MAR-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 6.0%; Score 73.5; DB 3; Length 261;
Best Local Similarity 23.8%; Pred. No. 22;
RESULT 1482
ID AAY92235 standard; protein; 261 AA.
DE Claudin homologue from clone 3224646 cDNA.
PN WO200020447-A2.
PD 13-APR-2000.
PA (CURA-) CURAGEN CORP.
Query Match 6.0%; Score 73.5; DB 3; Length 261;
Best Local Similarity 23.8%; Pred. No. 22;
RESULT 1483
ID AAY99432 standard; protein; 261 AA.
DE Human PRO1572 (UNQ778) amino acid sequence SEQ ID NO:326.
PN WO200012708-A2.
PD 09-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 6.0%; Score 73.5; DB 3; Length 261;
Best Local Similarity 23.8%; Pred. No. 22;
RESULT 1484
ID AAB66181 standard; protein; 261 AA.
DE Protein of the invention #93.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 6.0%; Score 73.5; DB 4; Length 261;
Best Local Similarity 23.8%; Pred. No. 22;
RESULT 1485
ID AAU29201 standard; protein; 261 AA.
DE Human PRO polypeptide sequence #178.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 6.0%; Score 73.5; DB 4; Length 261;
Best Local Similarity 23.8%; Pred. No. 22;
RESULT 1486
ID AAB87584 standard; protein; 261 AA.
DE Human PRO1572.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 6.0%; Score 73.5; DB 4; Length 261;
Best Local Similarity 23.8%; Pred. No. 22;
RESULT 1487
ID ABG60912 standard; protein; 261 AA.
DE Protein encoded by lung specific gene #2.
PN WO200218576-A2.
PD 07-MAR-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 6.0%; Score 73.5; DB 5; Length 261;
Best Local Similarity 23.8%; Pred. No. 22;
RESULT 1488
ID ABG95909 standard; protein; 261 AA.
DE Human secreted/transmembrane protein PRO1572.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 6.0%; Score 73.5; DB 5; Length 261;
Best Local Similarity 23.8%; Pred. No. 22;
RESULT 1489
ID ABU58577 standard; protein; 261 AA.
DE Human PRO polypeptide #178.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 22;
RESULT 1490
ID ABU88125 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 22;
RESULT 1491
ID ABU84440 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 22;
RESULT 1492

ID ABR66314 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 22;
RESULT 1493
ID ABR65704 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 22;
RESULT 1494
ID ABU99644 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 22;
RESULT 1495
ID ABU82883 standard; protein; 261 AA.
DE Human PRO polypeptide #178.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 22;
RESULT 1496
ID ABU90004 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 22;
RESULT 1497
ID ABR68253 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 22;
RESULT 1498
ID ABU96306 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 22;
RESULT 1499
ID ABU92737 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 22;
RESULT 1500
ID ABO08814 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 6.0%; Score 73.5; DB 6; Length 261;
Best Local Similarity 23.8%; Pred. No. 22;

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OM protein - protein search, using sw model

Run on: November 21, 2006, 20:09:55 ; Search time 67.2294 Seconds
(without alignments)
298.151 Million cell updates/sec

Title: US-10-063-553-48
Perfect score: 1215
Sequence: 1 MTCCEGWTSCNGFSLLVLLL.....IVIGFLGCLCGVSKRRSQIV 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued_Patents_AA:*
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6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1215	100.0	229	2	US-09-991-181-258	Sequence 258, App
2	1215	100.0	229	2	US-09-990-444-258	Sequence 258, App
3	1215	100.0	229	2	US-09-997-333-258	Sequence 258, App
4	1215	100.0	229	2	US-09-992-598-258	Sequence 258, App
5	1215	100.0	229	2	US-09-989-735-258	Sequence 258, App
6	1215	100.0	229	3	US-09-989-726-258	Sequence 258, App
7	1215	100.0	229	3	US-09-997-514-258	Sequence 258, App
8	1215	100.0	229	3	US-09-989-728-258	Sequence 258, App
9	1215	100.0	229	3	US-09-997-349-258	Sequence 258, App
10	1215	100.0	229	3	US-09-997-653-258	Sequence 258, App
11	1215	100.0	229	3	US-09-989-293A-258	Sequence 258, App
12	175.5	14.4	200	2	US-09-949-016-9937	Sequence 9937, Ap
13	170	14.0	197	1	US-08-855-261A-1	Sequence 1, Appli
14	170	14.0	197	2	US-09-227-224-1	Sequence 1, Appli
15	170	14.0	197	2	US-09-855-288-1	Sequence 1, Appli
16	170	14.0	197	2	US-09-973-278-154	Sequence 154, App
17	170	14.0	198	2	US-09-227-357-232	Sequence 232, App
18	170	14.0	202	1	US-08-048-700-2	Sequence 2, Appli
19	170	14.0	202	1	US-08-855-261A-3	Sequence 3, Appli
20	170	14.0	202	2	US-08-839-711-3	Sequence 3, Appli
21	170	14.0	202	2	US-09-227-224-3	Sequence 3, Appli
22	170	14.0	202	2	US-09-855-288-9	Sequence 9, Appli
23	160	13.2	202	1	US-08-855-261A-4	Sequence 4, Appli
24	160	13.2	202	2	US-08-839-711-4	Sequence 4, Appli
25	160	13.2	202	2	US-09-227-224-4	Sequence 4, Appli
26	160	13.2	202	2	US-09-855-288-10	Sequence 10, Appl
27	125	10.3	205	2	US-08-839-711-1	Sequence 1, Appli
28	87.5	7.2	117	2	US-10-104-047-3823	Sequence 3823, Ap
29	85.5	7.0	344	1	US-08-689-974-1	Sequence 1, Appli
30	85.5	7.0	344	2	US-09-058-376-1	Sequence 1, Appli
31	85.5	7.0	356	2	US-10-144-929-114	Sequence 114, App
32	85.5	7.0	453	2	US-09-991-181-73	Sequence 73, Appl
33	85.5	7.0	453	2	US-09-990-444-73	Sequence 73, Appl
34	85.5	7.0	453	2	US-09-997-333-73	Sequence 73, Appl
35	85.5	7.0	453	2	US-09-992-598-73	Sequence 73, Appl
36	85.5	7.0	453	2	US-09-989-735-73	Sequence 73, Appl
37	85.5	7.0	453	3	US-09-989-726-73	Sequence 73, Appl
38	85.5	7.0	453	3	US-09-997-514-73	Sequence 73, Appl
39	85.5	7.0	453	3	US-09-989-728-73	Sequence 73, Appl
40	85.5	7.0	453	3	US-09-997-349-73	Sequence 73, Appl
41	85.5	7.0	453	3	US-09-997-653-73	Sequence 73, Appl
42	85.5	7.0	453	3	US-09-989-293A-73	Sequence 73, Appl
43	82.5	6.8	180	2	US-09-949-016-6478	Sequence 6478, Ap
44	82	6.7	858	2	US-10-099-322-135	Sequence 135, App
45	82	6.7	858	2	US-10-044-564-135	Sequence 135, App
46	82	6.7	867	2	US-10-099-322-134	Sequence 134, App
47	82	6.7	867	2	US-10-044-564-134	Sequence 134, App
48	81	6.7	254	1	US-08-047-413-9	Sequence 9, Appli
49	81	6.7	254	2	US-08-229-050-9	Sequence 9, Appli
50	81	6.7	254	2	US-08-801-563-9	Sequence 9, Appli
51	81	6.7	706	2	US-09-902-540-12578	Sequence 12578, A
52	79.5	6.5	430	2	US-09-134-001C-2981	Sequence 2981, Ap
53	79.5	6.5	1160	2	US-09-328-352-6826	Sequence 6826, Ap
54	79	6.5	315	2	US-09-134-001C-5446	Sequence 5446, Ap
55	79	6.5	555	2	US-09-543-681A-4582	Sequence 4582, Ap
56	79	6.5	1305	2	US-08-864-785-3	Sequence 3, Appli
57	79	6.5	1353	2	US-08-894-173-2	Sequence 2, Appli
58	79	6.5	1353	2	US-09-398-193-2	Sequence 2, Appli
59	78	6.4	1065	2	US-09-252-991A-31637	Sequence 31637, A
60	78	6.4	1353	2	US-09-473-717-3	Sequence 3, Appli
61	78	6.4	1353	2	US-10-071-223-3	Sequence 3, Appli
62	77.5	6.4	222	2	US-09-252-991A-26487	Sequence 26487, A
63	77.5	6.4	416	2	US-09-830-230A-290	Sequence 290, App
64	77.5	6.4	500	2	US-09-830-230A-289	Sequence 289, App
65	76.5	6.3	614	2	US-09-489-039A-12605	Sequence 12605, A
66	76	6.3	144	2	US-09-949-016-11102	Sequence 11102, A
67	76	6.3	337	2	US-09-710-279-444	Sequence 444, App
68	76	6.3	500	2	US-09-543-681A-4601	Sequence 4601, Ap
69	75.5	6.2	397	2	US-10-029-180-40	Sequence 40, Appl
70	75	6.2	277	2	US-09-328-352-7936	Sequence 7936, Ap
71	75	6.2	2199	2	US-08-793-273C-2	Sequence 2, Appli
72	75	6.2	2199	5	PCT-US95-11684-2	Sequence 2, Appli
73	75	6.2	2200	2	US-09-796-575-2	Sequence 2, Appli
74	74.5	6.1	364	2	US-09-603-208A-208	Sequence 208, App
75	74.5	6.1	412	2	US-09-603-208A-206	Sequence 206, App
76	74.5	6.1	1709	2	US-09-949-016-10503	Sequence 10503, A
77	74	6.1	857	2	US-10-099-322-133	Sequence 133, App
78	74	6.1	857	2	US-10-044-564-133	Sequence 133, App
79	73.5	6.0	261	2	US-10-012-231A-326	Sequence 326, App
80	73.5	6.0	261	2	US-10-015-389A-326	Sequence 326, App
81	73.5	6.0	261	2	US-10-006-768A-326	Sequence 326, App
82	73.5	6.0	261	2	US-10-015-671A-326	Sequence 326, App
83	73.5	6.0	261	2	US-10-015-393A-326	Sequence 326, App
84	73.5	6.0	261	2	US-10-011-833A-326	Sequence 326, App
85	73.5	6.0	261	2	US-10-006-041A-326	Sequence 326, App
86	73.5	6.0	261	2	US-10-012-064A-326	Sequence 326, App
87	73.5	6.0	261	2	US-10-015-392A-326	Sequence 326, App
88	73.5	6.0	261	3	US-10-011-795B-326	Sequence 326, App
89	73.5	6.0	261	3	US-10-015-386A-326	Sequence 326, App
90	73.5	6.0	261	3	US-10-012-121A-326	Sequence 326, App
91	73.5	6.0	261	3	US-10-006-485A-326	Sequence 326, App
92	73.5	6.0	261	3	US-10-006-746A-326	Sequence 326, App
93	73.5	6.0	261	3	US-10-012-752A-326	Sequence 326, App
94	73.5	6.0	261	3	US-10-017-253A-326	Sequence 326, App
95	73.5	6.0	261	3	US-10-015-519A-326	Sequence 326, App
96	73.5	6.0	261	3	US-10-015-715A-326	Sequence 326, App
97	73.5	6.0	261	3	US-10-007-236A-326	Sequence 326, App
98	73.5	6.0	624	2	US-09-543-681A-4343	Sequence 4343, Ap
99	73	6.0	203	2	US-09-252-991A-22678	Sequence 22678, A

100	73	6.0	631	2	US-09-345-468-12	Sequence 12, Appl
101	73	6.0	631	2	US-09-414-453A-12	Sequence 12, Appl
102	73	6.0	631	2	US-09-610-118-12	Sequence 12, Appl
103	73	6.0	707	2	US-10-094-749-2466	Sequence 2466, Ap
104	72.5	6.0	180	2	US-09-270-767-32589	Sequence 32589, A
105	72.5	6.0	180	2	US-09-270-767-47806	Sequence 47806, A
106	72.5	6.0	616	1	US-08-149-100-2	Sequence 2, Appli
107	72	5.9	296	2	US-09-489-039A-10219	Sequence 10219, A
108	72	5.9	332	2	US-09-270-767-43166	Sequence 43166, A
109	72	5.9	475	2	US-09-543-681A-4458	Sequence 4458, Ap
110	72	5.9	741	2	US-09-248-796A-18963	Sequence 18963, A
111	72	5.9	1253	2	US-08-864-785-2	Sequence 2, Appli
112	71.5	5.9	250	2	US-09-270-767-42724	Sequence 42724, A
113	71.5	5.9	353	2	US-08-838-151A-49	Sequence 49, Appl
114	71.5	5.9	398	1	US-08-288-663A-1	Sequence 1, Appli
115	71.5	5.9	445	2	US-09-710-279-2644	Sequence 2644, Ap
116	71.5	5.9	450	2	US-09-134-001C-4858	Sequence 4858, Ap
117	71	5.8	286	2	US-09-902-540-10462	Sequence 10462, A
118	71	5.8	299	2	US-09-393-634-5	Sequence 5, Appli
119	71	5.8	299	3	US-10-770-127-81	Sequence 81, Appl
120	70.5	5.8	235	2	US-09-769-787-58	Sequence 58, Appl
121	70.5	5.8	235	2	US-09-769-787-59	Sequence 59, Appl
122	70.5	5.8	286	2	US-09-333-521-1	Sequence 1, Appli
123	70.5	5.8	286	2	US-09-899-863A-1	Sequence 1, Appli
124	70.5	5.8	319	2	US-09-543-681A-5398	Sequence 5398, Ap
125	70.5	5.8	600	2	US-09-198-452A-397	Sequence 397, App
126	70.5	5.8	600	2	US-09-438-185A-383	Sequence 383, App
127	70.5	5.8	712	2	US-09-949-016-8130	Sequence 8130, Ap
128	70	5.8	255	2	US-09-302-626B-76	Sequence 76, Appl
129	70	5.8	485	2	US-09-602-787A-614	Sequence 614, App
130	70	5.8	512	2	US-09-303-518D-118	Sequence 118, App
131	70	5.8	625	2	US-09-489-039A-10099	Sequence 10099, A
132	70	5.8	715	2	US-09-792-024-85	Sequence 85, Appl
133	70	5.8	735	2	US-09-270-767-40232	Sequence 40232, A
134	70	5.8	735	2	US-09-270-767-55448	Sequence 55448, A
135	70	5.8	797	2	US-09-191-468-120	Sequence 120, App
136	70	5.8	797	2	US-09-191-468-122	Sequence 122, App
137	70	5.8	1058	1	US-08-687-289A-5	Sequence 5, Appli
138	70	5.8	1058	2	US-09-435-897-5	Sequence 5, Appli
139	69.5	5.7	172	2	US-09-248-796A-21509	Sequence 21509, A
140	69.5	5.7	235	2	US-09-472-087-14	Sequence 14, Appl
141	69.5	5.7	235	2	US-09-472-087-65	Sequence 65, Appl
142	69.5	5.7	320	2	US-09-543-681A-6667	Sequence 6667, Ap
143	69.5	5.7	347	1	US-08-118-270-47	Sequence 47, Appl
144	69.5	5.7	347	5	PCT-US93-08528-47	Sequence 47, Appl
145	69.5	5.7	724	2	US-10-104-047-2224	Sequence 2224, Ap
146	69.5	5.7	1019	2	US-09-252-991A-24417	Sequence 24417, A
147	69	5.7	160	2	US-09-248-796A-24377	Sequence 24377, A
148	69	5.7	245	2	US-09-325-932A-89	Sequence 89, Appl
149	69	5.7	405	1	US-08-700-013B-6	Sequence 6, Appli
150	69	5.7	454	2	US-09-303-518D-120	Sequence 120, App
151	69	5.7	493	2	US-09-134-001C-3486	Sequence 3486, Ap
152	69	5.7	500	2	US-09-252-991A-25053	Sequence 25053, A
153	69	5.7	512	2	US-09-303-518D-116	Sequence 116, App
154	69	5.7	512	2	US-09-303-518D-122	Sequence 122, App
155	69	5.7	797	1	US-08-700-013B-19	Sequence 19, Appl
156	69	5.7	797	2	US-09-182-728A-2	Sequence 2, Appli
157	69	5.7	797	2	US-09-191-468-124	Sequence 124, App
158	69	5.7	797	2	US-09-795-232-2	Sequence 2, Appli
159	69	5.7	2496	2	US-09-125-028-2	Sequence 2, Appli
160	68.5	5.6	208	2	US-09-583-110-4112	Sequence 4112, Ap
161	68.5	5.6	212	2	US-09-107-433-2936	Sequence 2936, Ap
162	68.5	5.6	305	2	US-10-376-397B-8	Sequence 8, Appli
163	68.5	5.6	305	3	US-10-889-526-8	Sequence 8, Appli
164	68.5	5.6	305	3	US-10-889-527-8	Sequence 8, Appli
165	68.5	5.6	323	2	US-09-619-353-4	Sequence 4, Appli
166	68.5	5.6	356	2	US-09-134-000C-4914	Sequence 4914, Ap
167	68.5	5.6	465	2	US-09-710-279-2928	Sequence 2928, Ap
168	68.5	5.6	467	2	US-09-107-532A-6175	Sequence 6175, Ap
169	68.5	5.6	473	2	US-09-134-001C-3564	Sequence 3564, Ap
170	68.5	5.6	1091	2	US-09-949-016-6688	Sequence 6688, Ap
171	68.5	5.6	1091	2	US-09-644-947A-2	Sequence 2, Appli
172	68.5	5.6	2032	2	US-09-071-035-458	Sequence 458, App
173	68.5	5.6	2032	2	US-09-071-035-462	Sequence 462, App
174	68.5	5.6	2032	2	US-09-071-035-466	Sequence 466, App
175	68.5	5.6	2032	2	US-10-206-576-458	Sequence 458, App
176	68.5	5.6	2032	2	US-10-206-576-462	Sequence 462, App
177	68.5	5.6	2032	2	US-10-206-576-466	Sequence 466, App
178	68.5	5.6	2054	2	US-09-134-000C-6612	Sequence 6612, Ap
179	68	5.6	205	2	US-09-191-468-55	Sequence 55, Appl
180	68	5.6	271	2	US-09-248-796A-14877	Sequence 14877, A
181	68	5.6	320	2	US-09-489-039A-10551	Sequence 10551, A
182	68	5.6	354	1	US-08-700-013B-9	Sequence 9, Appli
183	68	5.6	392	2	US-09-902-540-12860	Sequence 12860, A
184	68	5.6	443	2	US-09-711-164-462	Sequence 462, App
185	68	5.6	443	2	US-09-492-709A-276	Sequence 276, App
186	68	5.6	498	5	PCT-US94-01101-2	Sequence 2, Appli
187	68	5.6	596	1	US-08-392-806A-2	Sequence 2, Appli
188	68	5.6	596	2	US-09-257-490-2	Sequence 2, Appli
189	68	5.6	694	2	US-09-252-991A-22637	Sequence 22637, A
190	68	5.6	797	1	US-08-700-013B-21	Sequence 21, Appl
191	68	5.6	799	1	US-08-700-013B-27	Sequence 27, Appl
192	68	5.6	1810	2	US-08-793-273C-4	Sequence 4, Appli
193	68	5.6	1810	5	PCT-US95-11684-4	Sequence 4, Appli
194	67.5	5.6	155	2	US-09-107-532A-6942	Sequence 6942, Ap
195	67.5	5.6	202	2	US-09-605-703B-350	Sequence 350, App
196	67.5	5.6	312	2	US-09-393-634-51	Sequence 51, Appl
197	67.5	5.6	312	3	US-10-770-127-17	Sequence 17, Appl
198	67.5	5.6	317	1	US-08-619-362A-8	Sequence 8, Appli
199	67.5	5.6	326	2	US-09-605-703B-346	Sequence 346, App
200	67.5	5.6	372	2	US-09-252-991A-26719	Sequence 26719, A
201	67.5	5.6	431	2	US-09-875-076-38	Sequence 38, Appl
202	67.5	5.6	431	2	US-09-899-532-2	Sequence 2, Appli
203	67.5	5.6	449	2	US-09-543-681A-6546	Sequence 6546, Ap
204	67.5	5.6	855	2	US-10-290-579A-255	Sequence 255, App
205	67.5	5.6	2161	1	US-07-745-206A-2	Sequence 2, Appli
206	67.5	5.6	2161	1	US-08-455-543A-49	Sequence 49, Appl
207	67.5	5.6	2161	1	US-08-455-543A-51	Sequence 51, Appl
208	67.5	5.6	2161	1	US-08-223-305C-49	Sequence 49, Appl
209	67.5	5.6	2161	1	US-08-223-305C-51	Sequence 51, Appl
210	67.5	5.6	2161	1	US-08-311-363-2	Sequence 2, Appli
211	67.5	5.6	2181	2	US-09-949-016-5981	Sequence 5981, Ap
212	67.5	5.6	2188	2	US-09-949-016-8295	Sequence 8295, Ap
213	67	5.5	147	2	US-09-134-000C-6018	Sequence 6018, Ap
214	67	5.5	167	2	US-09-191-468-65	Sequence 65, Appl
215	67	5.5	199	2	US-09-248-796A-14467	Sequence 14467, A
216	67	5.5	203	2	US-09-270-767-38554	Sequence 38554, A
217	67	5.5	203	2	US-09-270-767-53771	Sequence 53771, A
218	67	5.5	205	2	US-09-191-468-63	Sequence 63, Appl
219	67	5.5	205	2	US-09-191-468-68	Sequence 68, Appl
220	67	5.5	205	2	US-09-191-468-70	Sequence 70, Appl
221	67	5.5	283	2	US-09-134-000C-4870	Sequence 4870, Ap
222	67	5.5	287	2	US-09-252-991A-31548	Sequence 31548, A
223	67	5.5	297	2	US-09-540-236-3296	Sequence 3296, Ap
224	67	5.5	339	2	US-09-328-352-4674	Sequence 4674, Ap
225	67	5.5	342	2	US-09-540-236-2385	Sequence 2385, Ap
226	67	5.5	345	2	US-09-248-796A-26951	Sequence 26951, A
227	67	5.5	376	2	US-09-540-236-3121	Sequence 3121, Ap
228	67	5.5	393	1	US-07-629-104I-3	Sequence 3, Appli
229	67	5.5	448	2	US-09-792-024-101	Sequence 101, App
230	67	5.5	454	2	US-09-303-518D-114	Sequence 114, App
231	67	5.5	486	2	US-09-178-093B-1	Sequence 1, Appli
232	67	5.5	630	2	US-09-538-092-384	Sequence 384, App
233	67	5.5	1791	2	US-09-354-147C-42	Sequence 42, Appl
234	67	5.5	2958	2	US-08-894-344C-2	Sequence 2, Appli
235	67	5.5	2958	2	US-09-678-023A-2	Sequence 2, Appli
236	66.5	5.5	208	2	US-10-188-495-85	Sequence 85, Appl
237	66.5	5.5	222	2	US-10-037-417-81	Sequence 81, Appl
238	66.5	5.5	225	2	US-10-188-495-83	Sequence 83, Appl
239	66.5	5.5	280	2	US-09-270-767-32524	Sequence 32524, A
240	66.5	5.5	280	2	US-09-270-767-47741	Sequence 47741, A
241	66.5	5.5	346	2	US-10-152-886-91	Sequence 91, Appl
242	66.5	5.5	353	2	US-08-838-151A-44	Sequence 44, Appl
243	66.5	5.5	353	2	US-08-838-151A-46	Sequence 46, Appl
244	66.5	5.5	376	2	US-09-404-296B-32	Sequence 32, Appl
245	66.5	5.5	478	2	US-09-949-016-6543	Sequence 6543, Ap

246	66.5	5.5	485	2	US-09-949-016-10465	Sequence 10465, A
247	66.5	5.5	517	2	US-09-540-236-2403	Sequence 2403, Ap
248	66.5	5.5	562	2	US-09-328-352-4694	Sequence 4694, Ap
249	66.5	5.5	572	2	US-10-154-419-13	Sequence 13, Appl
250	66.5	5.5	585	2	US-09-328-352-6133	Sequence 6133, Ap
251	66.5	5.5	1027	2	US-09-162-021B-2	Sequence 2, Appli
252	66.5	5.5	1027	2	US-10-268-051-8	Sequence 8, Appli
253	66.5	5.5	1027	2	US-10-125-772-2	Sequence 2, Appli
254	66.5	5.5	1027	2	US-10-125-778-2	Sequence 2, Appli
255	66.5	5.5	1027	2	US-10-125-792-2	Sequence 2, Appli
256	66.5	5.5	1078	1	US-08-485-588-7	Sequence 7, Appli
257	66.5	5.5	1078	1	US-08-484-565-7	Sequence 7, Appli
258	66.5	5.5	1078	1	US-08-480-751-7	Sequence 7, Appli
259	66.5	5.5	1078	1	US-08-943-986-7	Sequence 7, Appli
260	66.5	5.5	1078	2	US-08-353-784-7	Sequence 7, Appli
261	66.5	5.5	1078	2	US-08-484-719B-7	Sequence 7, Appli
262	66.5	5.5	1078	2	US-08-484-159-7	Sequence 7, Appli
263	66.5	5.5	1088	1	US-08-485-588-6	Sequence 6, Appli
264	66.5	5.5	1088	1	US-08-484-565-6	Sequence 6, Appli
265	66.5	5.5	1088	1	US-08-480-751-6	Sequence 6, Appli
266	66.5	5.5	1088	1	US-08-943-986-6	Sequence 6, Appli
267	66.5	5.5	1088	2	US-08-353-784-6	Sequence 6, Appli
268	66.5	5.5	1088	2	US-08-484-719B-6	Sequence 6, Appli
269	66.5	5.5	1088	2	US-08-484-159-6	Sequence 6, Appli
270	66.5	5.5	1627	2	US-09-902-540-11280	Sequence 11280, A
271	66	5.4	160	2	US-09-270-767-36568	Sequence 36568, A
272	66	5.4	160	2	US-09-270-767-51785	Sequence 51785, A
273	66	5.4	205	2	US-09-191-468-57	Sequence 57, Appl
274	66	5.4	217	2	US-09-270-767-33957	Sequence 33957, A
275	66	5.4	217	2	US-09-270-767-49174	Sequence 49174, A
276	66	5.4	236	2	US-09-598-401C-72	Sequence 72, Appl
277	66	5.4	250	2	US-09-710-279-1124	Sequence 1124, Ap
278	66	5.4	255	2	US-09-302-626B-78	Sequence 78, Appl
279	66	5.4	268	2	US-09-710-279-1830	Sequence 1830, Ap
280	66	5.4	273	2	US-09-134-001C-3917	Sequence 3917, Ap
281	66	5.4	342	2	US-09-054-272-2	Sequence 2, Appli
282	66	5.4	342	2	US-09-826-509-555	Sequence 555, App
283	66	5.4	345	2	US-09-602-787A-544	Sequence 544, App
284	66	5.4	352	2	US-09-029-027B-2	Sequence 2, Appli
285	66	5.4	376	2	US-09-710-279-490	Sequence 490, App
286	66	5.4	376	2	US-09-710-279-2260	Sequence 2260, Ap
287	66	5.4	482	1	US-07-792-885A-1	Sequence 1, Appli
288	66	5.4	482	1	US-08-142-439A-7	Sequence 7, Appli
289	66	5.4	482	1	US-08-869-477-7	Sequence 7, Appli
290	66	5.4	594	2	US-09-107-532A-7250	Sequence 7250, Ap
291	66	5.4	646	2	US-09-949-016-7344	Sequence 7344, Ap
292	66	5.4	718	2	US-09-657-960-3	Sequence 3, Appli
293	66	5.4	877	2	US-09-206-551-20	Sequence 20, Appl
294	66	5.4	1353	2	US-09-398-193-99	Sequence 99, Appl
295	66	5.4	1451	2	US-09-060-299-25	Sequence 25, Appl
296	66	5.4	1451	2	US-09-402-923A-25	Sequence 25, Appl
297	66	5.4	1584	2	US-09-060-299-39	Sequence 39, Appl
298	66	5.4	1584	2	US-09-402-923A-39	Sequence 39, Appl
299	66	5.4	1591	2	US-09-060-299-4	Sequence 4, Appli
300	66	5.4	1591	2	US-09-060-299-43	Sequence 43, Appl
301	66	5.4	1591	2	US-09-402-923A-4	Sequence 4, Appli
302	66	5.4	1591	2	US-09-402-923A-43	Sequence 43, Appl
303	66	5.4	1615	2	US-09-060-299-3	Sequence 3, Appli
304	66	5.4	1615	2	US-09-402-923A-3	Sequence 3, Appli
305	66	5.4	1615	2	US-09-544-398B-3	Sequence 3, Appli
306	66	5.4	1615	2	US-09-544-398B-4	Sequence 4, Appli
307	66	5.4	1615	2	US-09-543-771B-3	Sequence 3, Appli
308	66	5.4	1615	2	US-09-543-771B-4	Sequence 4, Appli
309	66	5.4	1639	2	US-09-060-299-29	Sequence 29, Appl
310	66	5.4	1639	2	US-09-402-923A-29	Sequence 29, Appl
311	65.5	5.4	176	2	US-09-252-991A-25290	Sequence 25290, A
312	65.5	5.4	230	2	US-10-104-047-3554	Sequence 3554, Ap
313	65.5	5.4	268	2	US-08-965-056-70	Sequence 70, Appl
314	65.5	5.4	318	1	US-08-619-362A-9	Sequence 9, Appli
315	65.5	5.4	353	2	US-08-838-151A-52	Sequence 52, Appl
316	65.5	5.4	353	2	US-08-838-151A-55	Sequence 55, Appl
317	65.5	5.4	398	2	US-09-543-681A-5007	Sequence 5007, Ap
318	65.5	5.4	536	2	US-09-107-532A-5507	Sequence 5507, Ap
319	65.5	5.4	650	1	US-08-121-713D-60	Sequence 60, Appl
320	65.5	5.4	650	1	US-08-835-268-60	Sequence 60, Appl
321	65.5	5.4	650	1	US-09-060-692-60	Sequence 60, Appl
322	65.5	5.4	650	2	US-08-833-391-60	Sequence 60, Appl
323	65.5	5.4	650	2	US-09-060-610-60	Sequence 60, Appl
324	65.5	5.4	650	5	PCT-US94-10151A-60	Sequence 60, Appl
325	65.5	5.4	928	2	US-09-487-558B-282	Sequence 282, App
326	65.5	5.4	1033	2	US-09-252-991A-20611	Sequence 20611, A
327	65.5	5.4	1041	2	US-09-949-016-9618	Sequence 9618, Ap
328	65.5	5.4	1058	2	US-09-328-352-4276	Sequence 4276, Ap
329	65.5	5.4	1085	1	US-08-485-588-5	Sequence 5, Appli
330	65.5	5.4	1085	1	US-08-484-565-5	Sequence 5, Appli
331	65.5	5.4	1085	1	US-08-480-751-5	Sequence 5, Appli
332	65.5	5.4	1085	1	US-08-943-986-5	Sequence 5, Appli
333	65.5	5.4	1085	2	US-08-353-784-5	Sequence 5, Appli
334	65.5	5.4	1085	2	US-08-484-719B-5	Sequence 5, Appli
335	65.5	5.4	1085	2	US-08-484-159-5	Sequence 5, Appli
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337	65	5.3	88	2	US-09-621-976-5007	Sequence 5007, Ap
338	65	5.3	105	2	US-09-489-039A-11705	Sequence 11705, A
339	65	5.3	234	2	US-09-848-832-4	Sequence 4, Appli
340	65	5.3	273	2	US-09-893-737-294	Sequence 294, App
341	65	5.3	289	2	US-09-489-039A-12627	Sequence 12627, A
342	65	5.3	367	2	US-09-543-681A-4184	Sequence 4184, Ap
343	65	5.3	371	2	US-10-188-495-11	Sequence 11, Appl
344	65	5.3	434	2	US-09-328-352-4563	Sequence 4563, Ap
345	65	5.3	491	2	US-09-543-681A-8251	Sequence 8251, Ap
346	65	5.3	509	1	US-09-031-392-6	Sequence 6, Appli
347	65	5.3	509	2	US-09-299-549-6	Sequence 6, Appli
348	65	5.3	509	2	US-09-610-417-6	Sequence 6, Appli
349	65	5.3	509	2	US-09-981-947B-6	Sequence 6, Appli
350	65	5.3	580	1	US-08-677-049-12	Sequence 12, Appl
351	65	5.3	588	2	US-09-265-585C-34	Sequence 34, Appl
352	65	5.3	657	2	US-10-411-076-20	Sequence 20, Appl
353	65	5.3	749	2	US-09-562-737-97	Sequence 97, Appl
354	65	5.3	863	2	US-09-894-927B-9	Sequence 9, Appli
355	64.5	5.3	112	2	US-10-360-101-261	Sequence 261, App
356	64.5	5.3	186	2	US-09-248-796A-24150	Sequence 24150, A
357	64.5	5.3	190	2	US-09-543-681A-8168	Sequence 8168, Ap
358	64.5	5.3	230	2	US-09-270-767-44365	Sequence 44365, A
359	64.5	5.3	247	2	US-10-104-047-2014	Sequence 2014, Ap
360	64.5	5.3	253	1	US-08-162-475A-5	Sequence 5, Appli
361	64.5	5.3	253	2	US-10-300-819B-18	Sequence 18, Appl
362	64.5	5.3	258	2	US-09-248-796A-25815	Sequence 25815, A
363	64.5	5.3	271	2	US-09-479-040-23	Sequence 23, Appl
364	64.5	5.3	282	2	US-09-247-890-16	Sequence 16, Appl
365	64.5	5.3	282	2	US-09-724-969-16	Sequence 16, Appl
366	64.5	5.3	282	2	US-09-724-852-16	Sequence 16, Appl
367	64.5	5.3	317	1	US-08-790-572-3	Sequence 3, Appli
368	64.5	5.3	317	1	US-09-213-398-3	Sequence 3, Appli
369	64.5	5.3	327	2	US-08-748-506-22	Sequence 22, Appl
370	64.5	5.3	327	2	US-08-748-506-23	Sequence 23, Appl
371	64.5	5.3	331	2	US-09-830-217-18	Sequence 18, Appl
372	64.5	5.3	331	2	US-10-278-946-18	Sequence 18, Appl
373	64.5	5.3	338	2	US-09-252-991A-27402	Sequence 27402, A
374	64.5	5.3	615	1	US-08-663-566A-17	Sequence 17, Appl
375	64.5	5.3	615	1	US-08-023-610-17	Sequence 17, Appl
376	64.5	5.3	615	1	US-08-288-065A-17	Sequence 17, Appl
377	64.5	5.3	615	1	US-08-362-240A-17	Sequence 17, Appl
378	64.5	5.3	615	5	PCT-US95-10245-17	Sequence 17, Appl
379	64.5	5.3	620	1	US-08-301-722A-2	Sequence 2, Appli
380	64.5	5.3	620	2	US-09-949-016-6017	Sequence 6017, Ap
381	64.5	5.3	662	2	US-09-949-016-7095	Sequence 7095, Ap
382	64.5	5.3	718	2	US-09-252-991A-28229	Sequence 28229, A
383	64.5	5.3	934	2	US-09-949-016-7286	Sequence 7286, Ap
384	64.5	5.3	1078	2	US-10-125-772-28	Sequence 28, Appl
385	64.5	5.3	1078	2	US-10-125-778-28	Sequence 28, Appl
386	64.5	5.3	1078	2	US-10-125-792-28	Sequence 28, Appl
387	64.5	5.3	1165	2	US-09-487-558B-76	Sequence 76, Appl
388	64.5	5.3	1580	2	US-08-726-320-1	Sequence 1, Appli
389	64.5	5.3	1580	2	US-09-208-716-1	Sequence 1, Appli
390	64.5	5.3	3177	1	US-08-477-451-4	Sequence 4, Appli
391	64	5.3	167	1	US-08-627-610-6	Sequence 6, Appli

392	64	5.3	168	1	US-08-508-735-46	Sequence 46, Appl
393	64	5.3	168	2	US-09-201-139-46	Sequence 46, Appl
394	64	5.3	195	2	US-09-134-000C-5992	Sequence 5992, Ap
395	64	5.3	205	2	US-09-191-468-61	Sequence 61, Appl
396	64	5.3	322	2	US-09-543-681A-6839	Sequence 6839, Ap
397	64	5.3	379	2	US-09-248-796A-22533	Sequence 22533, A
398	64	5.3	456	2	US-09-328-352-6174	Sequence 6174, Ap
399	64	5.3	484	2	US-09-328-352-7797	Sequence 7797, Ap
400	64	5.3	484	2	US-09-489-039A-7690	Sequence 7690, Ap
401	64	5.3	579	2	US-09-252-991A-32124	Sequence 32124, A
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403	64	5.3	808	2	US-09-248-796A-17196	Sequence 17196, A
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405	64	5.3	1182	2	US-09-060-939A-7	Sequence 7, Appli
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407	64	5.3	1203	2	US-09-060-939A-2	Sequence 2, Appli
408	63.5	5.2	178	2	US-09-248-796A-21678	Sequence 21678, A
409	63.5	5.2	211	2	US-09-248-796A-20685	Sequence 20685, A
410	63.5	5.2	220	2	US-09-602-787A-608	Sequence 608, App
411	63.5	5.2	236	2	US-09-315-926A-79	Sequence 79, Appl
412	63.5	5.2	240	2	US-09-328-352-7537	Sequence 7537, Ap
413	63.5	5.2	268	2	US-08-965-056-71	Sequence 71, Appl
414	63.5	5.2	297	2	US-09-902-540-13203	Sequence 13203, A
415	63.5	5.2	327	3	US-10-770-127-105	Sequence 105, App
416	63.5	5.2	350	2	US-09-252-991A-32358	Sequence 32358, A
417	63.5	5.2	398	1	US-08-288-663A-15	Sequence 15, Appl
418	63.5	5.2	400	1	US-08-103-170-9	Sequence 9, Appli
419	63.5	5.2	403	2	US-09-602-787A-606	Sequence 606, App
420	63.5	5.2	433	2	US-09-328-352-5746	Sequence 5746, Ap
421	63.5	5.2	448	2	US-09-134-000C-3794	Sequence 3794, Ap
422	63.5	5.2	467	2	US-09-134-000C-6048	Sequence 6048, Ap
423	63.5	5.2	467	2	US-09-540-236-2469	Sequence 2469, Ap
424	63.5	5.2	482	2	US-09-107-532A-6644	Sequence 6644, Ap
425	63.5	5.2	531	2	US-10-154-419-81	Sequence 81, Appl
426	63.5	5.2	575	2	US-09-248-796A-20353	Sequence 20353, A
427	63.5	5.2	585	2	US-10-104-047-2739	Sequence 2739, Ap
428	63.5	5.2	590	2	US-09-248-796A-18826	Sequence 18826, A
429	63.5	5.2	597	2	US-09-252-991A-24252	Sequence 24252, A
430	63.5	5.2	1179	2	US-09-792-024-89	Sequence 89, Appl
431	63	5.2	103	2	US-09-248-796A-27772	Sequence 27772, A
432	63	5.2	210	2	US-09-710-279-708	Sequence 708, App
433	63	5.2	216	2	US-09-248-796A-14175	Sequence 14175, A
434	63	5.2	224	2	US-09-134-001C-4608	Sequence 4608, Ap
435	63	5.2	275	2	US-09-489-039A-13172	Sequence 13172, A
436	63	5.2	295	1	US-08-679-765-5	Sequence 5, Appli
437	63	5.2	295	1	US-09-196-525-5	Sequence 5, Appli
438	63	5.2	295	2	US-09-318-317-5	Sequence 5, Appli
439	63	5.2	295	2	US-09-177-165A-22	Sequence 22, Appl
440	63	5.2	295	2	US-09-538-092-137	Sequence 137, App
441	63	5.2	337	2	US-09-949-016-10573	Sequence 10573, A
442	63	5.2	337	3	US-09-944-049-10	Sequence 10, Appl
443	63	5.2	341	2	US-09-248-796A-16208	Sequence 16208, A
444	63	5.2	356	2	US-09-134-000C-6394	Sequence 6394, Ap
445	63	5.2	364	2	US-09-252-991A-31716	Sequence 31716, A
446	63	5.2	376	1	US-08-758-621-10	Sequence 10, Appl
447	63	5.2	376	2	US-09-107-858-10	Sequence 10, Appl
448	63	5.2	376	2	US-09-579-174-10	Sequence 10, Appl
449	63	5.2	391	2	US-09-107-532A-4615	Sequence 4615, Ap
450	63	5.2	394	2	US-09-252-991A-18502	Sequence 18502, A
451	63	5.2	400	2	US-09-303-518D-256	Sequence 256, App
452	63	5.2	437	2	US-09-830-433A-12	Sequence 12, Appl
453	63	5.2	445	2	US-09-328-352-6669	Sequence 6669, Ap
454	63	5.2	458	1	US-08-310-271-2	Sequence 2, Appli
455	63	5.2	458	2	US-09-292-071-27	Sequence 27, Appl
456	63	5.2	458	2	US-09-292-071-29	Sequence 29, Appl
457	63	5.2	458	2	US-09-292-069A-27	Sequence 27, Appl
458	63	5.2	458	2	US-09-292-069A-29	Sequence 29, Appl
459	63	5.2	458	2	US-09-032-742-10	Sequence 10, Appl
460	63	5.2	458	2	US-09-767-013-27	Sequence 27, Appl
461	63	5.2	458	2	US-09-767-013-29	Sequence 29, Appl
462	63	5.2	458	2	US-09-341-446B-11	Sequence 11, Appl
463	63	5.2	458	2	US-09-292-072-27	Sequence 27, Appl
464	63	5.2	458	2	US-09-292-072-29	Sequence 29, Appl
465	63	5.2	458	2	US-09-170-496D-126	Sequence 126, App
466	63	5.2	458	2	US-09-170-496D-230	Sequence 230, App
467	63	5.2	458	2	US-10-176-255-27	Sequence 27, Appl
468	63	5.2	458	2	US-10-176-255-29	Sequence 29, Appl
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473	63	5.2	532	2	US-09-911-514-2	Sequence 2, Appli
474	63	5.2	532	2	US-09-911-513-2	Sequence 2, Appli
475	63	5.2	556	2	US-09-538-092-712	Sequence 712, App
476	63	5.2	556	2	US-09-487-558B-426	Sequence 426, App
477	63	5.2	571	2	US-09-973-180A-2	Sequence 2, Appli
478	63	5.2	571	2	US-09-973-180A-3	Sequence 3, Appli
479	63	5.2	571	2	US-09-973-180A-4	Sequence 4, Appli
480	63	5.2	571	2	US-09-949-016-6878	Sequence 6878, Ap
481	63	5.2	572	2	US-09-943-075A-2	Sequence 2, Appli
482	63	5.2	596	2	US-09-902-540-13814	Sequence 13814, A
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484	63	5.2	606	2	US-09-041-236-4	Sequence 4, Appli
485	63	5.2	606	2	US-09-771-467C-4	Sequence 4, Appli
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487	63	5.2	682	1	US-08-453-274B-107	Sequence 107, App
488	63	5.2	682	1	US-08-453-695A-107	Sequence 107, App
489	63	5.2	682	1	US-08-268-161A-107	Sequence 107, App
490	63	5.2	682	1	US-08-453-702A-107	Sequence 107, App
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492	63	5.2	682	5	PCT-US93-12588-107	Sequence 107, App
493	63	5.2	682	5	PCT-US95-08071-107	Sequence 107, App
494	63	5.2	706	2	US-09-303-518D-258	Sequence 258, App
495	63	5.2	804	2	US-09-270-767-46146	Sequence 46146, A
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497	63	5.2	836	1	US-08-453-274B-105	Sequence 105, App
498	63	5.2	836	1	US-08-453-695A-105	Sequence 105, App
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502	63	5.2	836	5	PCT-US93-12588-105	Sequence 105, App
503	63	5.2	836	5	PCT-US95-08071-105	Sequence 105, App
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513	63	5.2	1243	2	US-09-354-147C-8	Sequence 8, Appli
514	63	5.2	1294	2	US-09-473-717-2	Sequence 2, Appli
515	63	5.2	1294	2	US-09-949-016-6023	Sequence 6023, Ap
516	63	5.2	1294	2	US-10-071-223-2	Sequence 2, Appli
517	63	5.2	3119	1	US-08-246-982A-16	Sequence 16, Appl
518	63	5.2	3119	1	US-08-453-265-16	Sequence 16, Appl
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525	62.5	5.1	222	2	US-09-270-767-49626	Sequence 49626, A
526	62.5	5.1	269	1	US-08-484-905-116	Sequence 116, App
527	62.5	5.1	269	2	US-08-481-985B-116	Sequence 116, App
528	62.5	5.1	269	2	US-08-370-476-116	Sequence 116, App
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550	62.5	5.1	386	2	US-09-130-491-6	Sequence 6, Appli
551	62.5	5.1	386	2	US-09-580-212-2	Sequence 2, Appli
552	62.5	5.1	386	2	US-09-769-402-2	Sequence 2, Appli
553	62.5	5.1	386	2	US-09-949-002-357	Sequence 357, App
554	62.5	5.1	386	2	US-10-280-047-2	Sequence 2, Appli
555	62.5	5.1	391	2	US-09-949-016-7325	Sequence 7325, Ap
556	62.5	5.1	399	2	US-09-949-002-437	Sequence 437, App
557	62.5	5.1	405	2	US-09-543-681A-6109	Sequence 6109, Ap
558	62.5	5.1	416	2	US-09-949-016-7087	Sequence 7087, Ap
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576	62.5	5.1	716	2	US-09-402-936-11	Sequence 11, Appl
577	62.5	5.1	851	2	US-09-543-681A-7277	Sequence 7277, Ap
578	62.5	5.1	856	2	US-09-605-703B-2760	Sequence 2760, Ap
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581	62.5	5.1	1079	1	US-08-484-565-8	Sequence 8, Appli
582	62.5	5.1	1079	1	US-08-480-751-8	Sequence 8, Appli
583	62.5	5.1	1079	1	US-08-943-986-8	Sequence 8, Appli
584	62.5	5.1	1079	2	US-08-353-784-8	Sequence 8, Appli
585	62.5	5.1	1079	2	US-08-484-719B-8	Sequence 8, Appli
586	62.5	5.1	1079	2	US-08-484-159-8	Sequence 8, Appli
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588	62	5.1	113	2	US-09-328-352-7133	Sequence 7133, Ap
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590	62	5.1	150	2	US-08-862-124-5	Sequence 5, Appli
591	62	5.1	185	2	US-09-324-910-6	Sequence 6, Appli
592	62	5.1	185	2	US-09-793-495-6	Sequence 6, Appli
593	62	5.1	216	2	US-09-294-298A-7	Sequence 7, Appli
594	62	5.1	230	2	US-09-663-600A-186	Sequence 186, App
595	62	5.1	230	2	US-10-037-417-135	Sequence 135, App
596	62	5.1	230	2	US-10-012-231A-134	Sequence 134, App
597	62	5.1	230	2	US-10-015-389A-134	Sequence 134, App
598	62	5.1	230	2	US-10-006-768A-134	Sequence 134, App
599	62	5.1	230	2	US-10-015-671A-134	Sequence 134, App
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602	62	5.1	230	2	US-10-006-041A-134	Sequence 134, App
603	62	5.1	230	2	US-10-012-064A-134	Sequence 134, App
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611	62	5.1	230	3	US-10-017-253A-134	Sequence 134, App
612	62	5.1	230	3	US-10-015-519A-134	Sequence 134, App
613	62	5.1	230	3	US-10-015-715A-134	Sequence 134, App
614	62	5.1	230	3	US-10-007-236A-134	Sequence 134, App
615	62	5.1	261	2	US-09-248-796A-18760	Sequence 18760, A
616	62	5.1	266	2	US-09-540-236-2374	Sequence 2374, Ap
617	62	5.1	287	1	US-08-433-783-37	Sequence 37, Appl
618	62	5.1	287	1	US-08-337-358-37	Sequence 37, Appl
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620	62	5.1	287	5	PCT-US95-07537-37	Sequence 37, Appl
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624	62	5.1	294	2	US-09-326-157-1	Sequence 1, Appli
625	62	5.1	294	2	US-10-135-755-1	Sequence 1, Appli
626	62	5.1	302	2	US-09-270-767-40028	Sequence 40028, A
627	62	5.1	302	2	US-09-270-767-55244	Sequence 55244, A
628	62	5.1	318	1	US-08-628-291-16	Sequence 16, Appl
629	62	5.1	318	1	US-09-128-722-16	Sequence 16, Appl
630	62	5.1	319	2	US-09-324-910-12	Sequence 12, Appl
631	62	5.1	319	2	US-09-793-495-12	Sequence 12, Appl
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635	62	5.1	388	2	US-10-125-778-6	Sequence 6, Appli
636	62	5.1	388	2	US-10-125-792-6	Sequence 6, Appli
637	62	5.1	395	3	US-09-609-146-25	Sequence 25, Appl
638	62	5.1	399	2	US-09-489-039A-8272	Sequence 8272, Ap
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640	62	5.1	448	2	US-09-583-110-4040	Sequence 4040, Ap
641	62	5.1	448	2	US-09-769-787-56	Sequence 56, Appl
642	62	5.1	452	2	US-09-107-433-5105	Sequence 5105, Ap
643	62	5.1	516	2	US-09-489-039A-12893	Sequence 12893, A
644	62	5.1	574	2	US-09-943-075A-5	Sequence 5, Appli
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647	62	5.1	631	3	US-10-143-618-20	Sequence 20, Appl
648	62	5.1	850	2	US-10-125-772-12	Sequence 12, Appl
649	62	5.1	850	2	US-10-125-778-12	Sequence 12, Appl
650	62	5.1	850	2	US-10-125-792-12	Sequence 12, Appl
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652	62	5.1	941	2	US-09-949-016-10983	Sequence 10983, A
653	62	5.1	941	2	US-09-949-016-10984	Sequence 10984, A
654	62	5.1	941	2	US-09-949-016-10985	Sequence 10985, A
655	62	5.1	941	2	US-10-125-772-8	Sequence 8, Appli
656	62	5.1	941	2	US-10-125-772-10	Sequence 10, Appl
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659	62	5.1	941	2	US-10-125-792-8	Sequence 8, Appli
660	62	5.1	941	2	US-10-125-792-10	Sequence 10, Appl
661	62	5.1	1091	2	US-09-900-237-26	Sequence 26, Appl
662	62	5.1	1135	2	US-09-294-298A-21	Sequence 21, Appl
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664	62	5.1	1376	2	US-09-294-298A-4	Sequence 4, Appli
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666	62	5.1	3118	1	US-08-457-273B-8	Sequence 8, Appli
667	61.5	5.1	78	2	US-09-543-681A-5110	Sequence 5110, Ap
668	61.5	5.1	86	2	US-09-270-767-58811	Sequence 58811, A
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670	61.5	5.1	182	2	US-09-710-279-1354	Sequence 1354, Ap
671	61.5	5.1	186	2	US-09-134-001C-4741	Sequence 4741, Ap
672	61.5	5.1	205	7	5482709-4	Patent No. 5482709
673	61.5	5.1	249	2	US-09-328-352-6476	Sequence 6476, Ap
674	61.5	5.1	252	3	US-09-907-155B-10	Sequence 10, Appl
675	61.5	5.1	267	2	US-09-134-000C-5723	Sequence 5723, Ap
676	61.5	5.1	268	2	US-09-248-796A-18304	Sequence 18304, A
677	61.5	5.1	298	2	US-09-134-000C-5845	Sequence 5845, Ap
678	61.5	5.1	317	2	US-09-134-001C-5199	Sequence 5199, Ap
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680	61.5	5.1	326	5	PCT-US93-08528-39	Sequence 39, Appl
681	61.5	5.1	355	2	US-09-489-039A-9302	Sequence 9302, Ap
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683	61.5	5.1	370	5	PCT-US93-08528-18	Sequence 18, Appl

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687	61.5	5.1	502	2	US-09-134-000C-6114	Sequence 6114, Ap
688	61.5	5.1	524	1	US-08-529-654-4	Sequence 4, Appli
689	61.5	5.1	542	2	US-09-449-632-4	Sequence 4, Appli
690	61.5	5.1	780	2	US-09-785-381-11	Sequence 11, Appl
691	61.5	5.1	826	2	US-09-134-000C-4999	Sequence 4999, Ap
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693	61.5	5.1	856	2	US-10-044-564-116	Sequence 116, App
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695	61	5.0	83	2	US-09-621-976-4085	Sequence 4085, Ap
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697	61	5.0	108	2	US-10-608-504-5	Sequence 5, Appli
698	61	5.0	135	2	US-09-270-767-34805	Sequence 34805, A
699	61	5.0	135	2	US-09-270-767-50022	Sequence 50022, A
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701	61	5.0	174	2	US-09-823-038A-12	Sequence 12, Appl
702	61	5.0	199	2	US-08-737-248-13	Sequence 13, Appl
703	61	5.0	203	2	US-09-248-796A-16898	Sequence 16898, A
704	61	5.0	208	2	US-10-094-749-2828	Sequence 2828, Ap
705	61	5.0	213	2	US-08-807-300-4	Sequence 4, Appli
706	61	5.0	219	2	US-08-311-731A-305	Sequence 305, App
707	61	5.0	220	2	US-09-205-258-1129	Sequence 1129, Ap
708	61	5.0	220	2	US-10-004-860-1129	Sequence 1129, Ap
709	61	5.0	221	2	US-09-248-796A-15458	Sequence 15458, A
710	61	5.0	234	2	US-09-472-087-17	Sequence 17, Appl
711	61	5.0	234	2	US-09-472-087-69	Sequence 69, Appl
712	61	5.0	255	2	US-09-107-532A-4920	Sequence 4920, Ap
713	61	5.0	296	2	US-09-270-767-37980	Sequence 37980, A
714	61	5.0	296	2	US-09-270-767-53197	Sequence 53197, A
715	61	5.0	297	2	US-09-489-039A-8466	Sequence 8466, Ap
716	61	5.0	299	2	US-09-252-991A-17878	Sequence 17878, A
717	61	5.0	299	3	US-10-770-127-139	Sequence 139, App
718	61	5.0	300	2	US-09-134-000C-3733	Sequence 3733, Ap
719	61	5.0	308	2	US-09-252-991A-23958	Sequence 23958, A
720	61	5.0	325	2	US-09-461-325-141	Sequence 141, App
721	61	5.0	325	2	US-10-012-542-141	Sequence 141, App
722	61	5.0	325	2	US-10-115-123-141	Sequence 141, App
723	61	5.0	365	2	US-09-801-874-5	Sequence 5, Appli
724	61	5.0	391	2	US-09-107-532A-4209	Sequence 4209, Ap
725	61	5.0	426	2	US-09-491-577-46	Sequence 46, Appl
726	61	5.0	435	2	US-09-252-991A-17254	Sequence 17254, A
727	61	5.0	441	2	US-09-252-991A-32306	Sequence 32306, A
728	61	5.0	446	2	US-09-543-681A-6579	Sequence 6579, Ap
729	61	5.0	453	2	US-09-489-039A-8916	Sequence 8916, Ap
730	61	5.0	460	2	US-09-543-681A-8195	Sequence 8195, Ap
731	61	5.0	494	2	US-09-126-420A-26	Sequence 26, Appl
732	61	5.0	506	2	US-09-543-681A-8246	Sequence 8246, Ap
733	61	5.0	518	2	US-09-248-796A-20772	Sequence 20772, A
734	61	5.0	529	2	US-09-500-063-2	Sequence 2, Appli
735	61	5.0	568	2	US-09-543-681A-5958	Sequence 5958, Ap
736	61	5.0	574	2	US-09-383-586-36	Sequence 36, Appl
737	61	5.0	574	2	US-09-823-038A-36	Sequence 36, Appl
738	61	5.0	595	2	US-09-252-991A-17469	Sequence 17469, A
739	61	5.0	661	2	US-09-438-185A-415	Sequence 415, App
740	61	5.0	685	2	US-09-720-317A-31	Sequence 31, Appl
741	61	5.0	694	2	US-09-902-540-10624	Sequence 10624, A
742	61	5.0	771	3	US-10-199-229-16	Sequence 16, Appl
743	61	5.0	852	2	US-09-206-551-19	Sequence 19, Appl
744	61	5.0	1146	2	US-09-807-007-1	Sequence 1, Appli
745	61	5.0	1279	2	US-09-170-496D-293	Sequence 293, App
746	61	5.0	1279	2	US-09-364-425B-58	Sequence 58, Appl
747	61	5.0	1666	2	US-09-949-016-8322	Sequence 8322, Ap
748	61	5.0	1765	2	US-09-354-147C-5	Sequence 5, Appli
749	61	5.0	3169	1	US-08-477-451-6	Sequence 6, Appli
750	60.5	5.0	102	2	US-09-270-767-58664	Sequence 58664, A
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752	60.5	5.0	142	2	US-09-248-796A-25278	Sequence 25278, A
753	60.5	5.0	162	2	US-09-621-976-4128	Sequence 4128, Ap
754	60.5	5.0	202	2	US-09-248-796A-19348	Sequence 19348, A
755	60.5	5.0	269	2	US-08-965-056-42	Sequence 42, Appl
756	60.5	5.0	277	2	US-09-583-110-2944	Sequence 2944, Ap
757	60.5	5.0	278	2	US-09-769-787-19	Sequence 19, Appl
758	60.5	5.0	290	2	US-09-107-433-4262	Sequence 4262, Ap
759	60.5	5.0	369	2	US-09-252-991A-18429	Sequence 18429, A
760	60.5	5.0	379	2	US-09-605-703B-2672	Sequence 2672, Ap
761	60.5	5.0	381	2	US-09-248-796A-19481	Sequence 19481, A
762	60.5	5.0	381	2	US-09-273-164-50	Sequence 50, Appl
763	60.5	5.0	390	2	US-09-198-452A-254	Sequence 254, App
764	60.5	5.0	390	2	US-09-438-185A-243	Sequence 243, App
765	60.5	5.0	424	2	US-09-252-991A-18895	Sequence 18895, A
766	60.5	5.0	439	2	US-09-107-433-4351	Sequence 4351, Ap
767	60.5	5.0	448	2	US-09-361-443-4	Sequence 4, Appli
768	60.5	5.0	467	2	US-09-361-443-2	Sequence 2, Appli
769	60.5	5.0	469	2	US-09-198-452A-793	Sequence 793, App
770	60.5	5.0	469	2	US-09-438-185A-745	Sequence 745, App
771	60.5	5.0	487	2	US-10-074-547-5	Sequence 5, Appli
772	60.5	5.0	492	2	US-09-949-016-10677	Sequence 10677, A
773	60.5	5.0	533	2	US-09-107-532A-5244	Sequence 5244, Ap
774	60.5	5.0	583	2	US-09-700-687-2	Sequence 2, Appli
775	60.5	5.0	681	2	US-08-760-615-4	Sequence 4, Appli
776	60.5	5.0	681	2	US-09-336-910A-2	Sequence 2, Appli
777	60.5	5.0	681	3	US-09-762-224B-6	Sequence 6, Appli
778	60.5	5.0	805	2	US-08-989-299-2	Sequence 2, Appli
779	60.5	5.0	805	2	US-10-158-847-142	Sequence 142, App
780	60.5	5.0	805	2	US-09-407-427-2	Sequence 2, Appli
781	60.5	5.0	805	2	US-09-635-501-2	Sequence 2, Appli
782	60.5	5.0	805	2	US-09-635-501-106	Sequence 106, App
783	60.5	5.0	805	2	US-10-158-825-142	Sequence 142, App
784	60.5	5.0	805	2	US-09-163-648-2	Sequence 2, Appli
785	60.5	5.0	819	2	US-09-949-016-11284	Sequence 11284, A
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787	60.5	5.0	905	1	US-08-072-574-2	Sequence 2, Appli
788	60.5	5.0	914	2	US-10-104-047-2923	Sequence 2923, Ap
789	60.5	5.0	1088	2	US-09-949-016-8011	Sequence 8011, Ap
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791	60	4.9	87	2	US-09-252-991A-30361	Sequence 30361, A
792	60	4.9	87	2	US-09-107-532A-6457	Sequence 6457, Ap
793	60	4.9	125	2	US-09-198-452A-1172	Sequence 1172, Ap
794	60	4.9	134	2	US-09-605-703B-1756	Sequence 1756, Ap
795	60	4.9	141	2	US-09-198-452A-1173	Sequence 1173, Ap
796	60	4.9	149	2	US-09-902-540-10481	Sequence 10481, A
797	60	4.9	153	2	US-09-438-185A-229	Sequence 229, App
798	60	4.9	153	2	US-09-640-211A-910	Sequence 910, App
799	60	4.9	158	2	US-09-270-767-38728	Sequence 38728, A
800	60	4.9	158	2	US-09-270-767-53945	Sequence 53945, A
801	60	4.9	205	2	US-09-191-468-59	Sequence 59, Appl
802	60	4.9	211	2	US-09-130-491-4	Sequence 4, Appli
803	60	4.9	211	2	US-09-603-552-12	Sequence 12, Appl
804	60	4.9	211	2	US-09-886-683A-4	Sequence 4, Appli
805	60	4.9	211	2	US-09-949-016-6992	Sequence 6992, Ap
806	60	4.9	211	2	US-09-999-833A-270	Sequence 270, App
807	60	4.9	211	2	US-10-020-445A-270	Sequence 270, App
808	60	4.9	211	2	US-09-978-189-270	Sequence 270, App
809	60	4.9	211	2	US-10-017-085A-270	Sequence 270, App
810	60	4.9	211	3	US-10-145-129A-270	Sequence 270, App
811	60	4.9	211	3	US-10-013-929A-270	Sequence 270, App
812	60	4.9	211	3	US-10-013-917A-270	Sequence 270, App
813	60	4.9	213	2	US-10-147-849-8	Sequence 8, Appli
814	60	4.9	213	2	US-10-147-849-9	Sequence 9, Appli
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816	60	4.9	218	2	US-09-252-991A-22136	Sequence 22136, A
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819	60	4.9	227	1	US-08-453-925-6	Sequence 6, Appli
820	60	4.9	227	2	US-08-403-253A-6	Sequence 6, Appli
821	60	4.9	227	2	US-08-435-816A-6	Sequence 6, Appli
822	60	4.9	227	2	US-09-350-202-6	Sequence 6, Appli
823	60	4.9	227	2	US-08-592-711-6	Sequence 6, Appli
824	60	4.9	227	2	US-09-349-915B-6	Sequence 6, Appli
825	60	4.9	227	3	US-08-253-964-6	Sequence 6, Appli
826	60	4.9	228	1	US-08-408-222B-1	Sequence 1, Appli
827	60	4.9	233	1	US-09-024-848-4	Sequence 4, Appli
828	60	4.9	233	2	US-09-348-116A-4	Sequence 4, Appli
829	60	4.9	239	2	US-09-270-767-44514	Sequence 44514, A

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831	60	4.9	259	2	US-09-270-767-38568	Sequence 38568, A
832	60	4.9	259	2	US-09-270-767-53785	Sequence 53785, A
833	60	4.9	275	2	US-09-270-767-48250	Sequence 48250, A
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835	60	4.9	365	2	US-08-155-005A-8	Sequence 8, Appli
836	60	4.9	365	2	US-09-363-783-8	Sequence 8, Appli
837	60	4.9	365	2	US-09-661-758A-8	Sequence 8, Appli
838	60	4.9	388	2	US-08-155-005A-6	Sequence 6, Appli
839	60	4.9	388	2	US-09-363-783-6	Sequence 6, Appli
840	60	4.9	388	2	US-09-661-758A-6	Sequence 6, Appli
841	60	4.9	390	2	US-08-155-005A-4	Sequence 4, Appli
842	60	4.9	390	2	US-08-155-005A-17	Sequence 17, Appl
843	60	4.9	390	2	US-09-363-783-4	Sequence 4, Appli
844	60	4.9	390	2	US-09-363-783-17	Sequence 17, Appl
845	60	4.9	390	2	US-09-661-758A-4	Sequence 4, Appli
846	60	4.9	390	2	US-09-661-758A-17	Sequence 17, Appl
847	60	4.9	397	2	US-10-243-468-8	Sequence 8, Appli
848	60	4.9	405	2	US-09-134-001C-4999	Sequence 4999, Ap
849	60	4.9	437	2	US-09-830-433A-59	Sequence 59, Appl
850	60	4.9	455	2	US-09-489-039A-12823	Sequence 12823, A
851	60	4.9	462	2	US-09-710-279-906	Sequence 906, App
852	60	4.9	491	2	US-09-134-001C-4612	Sequence 4612, Ap
853	60	4.9	571	2	US-09-328-352-4633	Sequence 4633, Ap
854	60	4.9	633	2	US-09-248-796A-20407	Sequence 20407, A
855	60	4.9	744	2	US-09-252-991A-30945	Sequence 30945, A
856	60	4.9	838	2	US-09-894-998A-45	Sequence 45, Appl
857	60	4.9	838	2	US-10-237-551-45	Sequence 45, Appl
858	60	4.9	838	2	US-10-237-551-249	Sequence 249, App
859	60	4.9	902	3	US-09-958-359-36	Sequence 36, Appl
860	60	4.9	934	2	US-09-252-991A-19515	Sequence 19515, A
861	60	4.9	1059	2	US-09-489-039A-10044	Sequence 10044, A
862	60	4.9	1527	2	US-09-647-140B-6	Sequence 6, Appli
863	60	4.9	1527	2	US-09-939-853A-83	Sequence 83, Appl
864	60	4.9	1527	2	US-09-939-853A-84	Sequence 84, Appl
865	60	4.9	1530	2	US-09-647-140B-33	Sequence 33, Appl
866	60	4.9	1543	2	US-09-904-987-7	Sequence 7, Appli
867	60	4.9	1781	2	US-09-995-749A-2	Sequence 2, Appli
868	60	4.9	2476	1	US-08-276-967-2	Sequence 2, Appli
869	60	4.9	3144	1	US-08-246-982A-6	Sequence 6, Appli
870	60	4.9	3144	1	US-08-453-265-6	Sequence 6, Appli
871	60	4.9	3144	1	US-08-457-273B-42	Sequence 42, Appl
872	60	4.9	3144	2	US-08-556-419-21	Sequence 21, Appl
873	60	4.9	3144	2	US-09-041-886-15	Sequence 15, Appl
874	60	4.9	3144	2	US-09-538-092-1118	Sequence 1118, Ap
875	59.5	4.9	123	2	US-09-893-737-90	Sequence 90, Appl
876	59.5	4.9	144	2	US-09-107-532A-4029	Sequence 4029, Ap
877	59.5	4.9	169	2	US-09-489-039A-8944	Sequence 8944, Ap
878	59.5	4.9	178	2	US-09-446-959-10	Sequence 10, Appl
879	59.5	4.9	189	2	US-09-134-000C-5408	Sequence 5408, Ap
880	59.5	4.9	208	2	US-09-991-181-416	Sequence 416, App
881	59.5	4.9	208	2	US-09-990-444-416	Sequence 416, App
882	59.5	4.9	208	2	US-09-832-129-36	Sequence 36, Appl
883	59.5	4.9	208	2	US-09-997-333-416	Sequence 416, App
884	59.5	4.9	208	2	US-09-992-598-416	Sequence 416, App
885	59.5	4.9	208	2	US-09-989-735-416	Sequence 416, App
886	59.5	4.9	208	3	US-09-989-726-416	Sequence 416, App
887	59.5	4.9	208	3	US-09-997-514-416	Sequence 416, App
888	59.5	4.9	208	3	US-09-989-728-416	Sequence 416, App
889	59.5	4.9	208	3	US-09-997-349-416	Sequence 416, App
890	59.5	4.9	208	3	US-09-997-653-416	Sequence 416, App
891	59.5	4.9	208	3	US-09-989-293A-416	Sequence 416, App
892	59.5	4.9	243	2	US-08-965-056-73	Sequence 73, Appl
893	59.5	4.9	279	2	US-09-248-796A-25140	Sequence 25140, A
894	59.5	4.9	283	2	US-10-198-053-624	Sequence 624, App
895	59.5	4.9	329	2	US-09-198-452A-363	Sequence 363, App
896	59.5	4.9	329	2	US-09-438-185A-348	Sequence 348, App
897	59.5	4.9	337	2	US-08-448-722A-2	Sequence 2, Appli
898	59.5	4.9	337	2	US-08-189-309B-2	Sequence 2, Appli
899	59.5	4.9	373	2	US-09-134-000C-4099	Sequence 4099, Ap
900	59.5	4.9	384	2	US-10-029-180-50	Sequence 50, Appl
901	59.5	4.9	406	2	US-09-489-039A-8267	Sequence 8267, Ap
902	59.5	4.9	419	2	US-09-489-039A-12928	Sequence 12928, A
903	59.5	4.9	427	2	US-09-252-991A-31904	Sequence 31904, A
904	59.5	4.9	433	2	US-10-152-886-11	Sequence 11, Appl
905	59.5	4.9	470	2	US-09-543-681A-4625	Sequence 4625, Ap
906	59.5	4.9	477	2	US-09-134-000C-6123	Sequence 6123, Ap
907	59.5	4.9	480	1	US-08-724-394A-11	Sequence 11, Appl
908	59.5	4.9	483	1	US-08-307-485A-1	Sequence 1, Appli
909	59.5	4.9	483	1	US-08-465-809-2	Sequence 2, Appli
910	59.5	4.9	483	2	US-08-477-928A-2	Sequence 2, Appli
911	59.5	4.9	483	2	US-08-477-928A-40	Sequence 40, Appl
912	59.5	4.9	483	2	US-08-467-605-2	Sequence 2, Appli
913	59.5	4.9	555	2	US-09-270-767-43300	Sequence 43300, A
914	59.5	4.9	562	2	US-09-328-352-4802	Sequence 4802, Ap
915	59.5	4.9	563	2	US-09-535-315-23	Sequence 23, Appl
916	59.5	4.9	577	1	US-07-820-154A-30	Sequence 30, Appl
917	59.5	4.9	577	1	US-08-663-566A-11	Sequence 11, Appl
918	59.5	4.9	577	1	US-08-097-554A-30	Sequence 30, Appl
919	59.5	4.9	577	1	US-08-023-610-11	Sequence 11, Appl
920	59.5	4.9	577	1	US-08-288-065A-11	Sequence 11, Appl
921	59.5	4.9	577	1	US-08-362-240A-11	Sequence 11, Appl
922	59.5	4.9	577	2	US-08-480-640A-30	Sequence 30, Appl
923	59.5	4.9	577	2	US-08-295-802-30	Sequence 30, Appl
924	59.5	4.9	577	2	US-08-804-372A-9	Sequence 9, Appli
925	59.5	4.9	577	2	US-08-488-237A-30	Sequence 30, Appl
926	59.5	4.9	577	2	US-08-375-992A-30	Sequence 30, Appl
927	59.5	4.9	577	2	US-08-472-679H-30	Sequence 30, Appl
928	59.5	4.9	577	5	PCT-US93-00324-30	Sequence 30, Appl
929	59.5	4.9	577	5	PCT-US95-10245-11	Sequence 11, Appl
930	59.5	4.9	581	1	US-08-484-575A-13	Sequence 13, Appl
931	59.5	4.9	581	2	US-08-477-459-13	Sequence 13, Appl
932	59.5	4.9	581	2	US-08-479-869-13	Sequence 13, Appl
933	59.5	4.9	581	2	US-08-486-414-13	Sequence 13, Appl
934	59.5	4.9	581	5	PCT-US94-01826A-13	Sequence 13, Appl
935	59.5	4.9	581	5	PCT-US94-02252A-13	Sequence 13, Appl
936	59.5	4.9	586	2	US-09-583-110-3470	Sequence 3470, Ap
937	59.5	4.9	599	2	US-09-107-433-3182	Sequence 3182, Ap
938	59.5	4.9	618	3	US-10-479-787-6	Sequence 6, Appli
939	59.5	4.9	621	2	US-09-720-317A-16	Sequence 16, Appl
940	59.5	4.9	646	2	US-09-720-317A-26	Sequence 26, Appl
941	59.5	4.9	658	2	US-09-720-317A-24	Sequence 24, Appl
942	59.5	4.9	673	3	US-10-433-794-2	Sequence 2, Appli
943	59.5	4.9	711	2	US-10-158-847-138	Sequence 138, App
944	59.5	4.9	711	2	US-10-158-825-138	Sequence 138, App
945	59.5	4.9	717	2	US-09-583-110-4629	Sequence 4629, Ap
946	59.5	4.9	721	2	US-09-107-433-2819	Sequence 2819, Ap
947	59.5	4.9	746	2	US-09-548-797B-4	Sequence 4, Appli
948	59.5	4.9	747	2	US-09-489-039A-12856	Sequence 12856, A
949	59.5	4.9	852	2	US-09-897-427A-6	Sequence 6, Appli
950	59.5	4.9	852	3	US-10-770-127-199	Sequence 199, App
951	59.5	4.9	913	3	US-09-907-155B-2	Sequence 2, Appli
952	59.5	4.9	920	2	US-09-538-092-1197	Sequence 1197, Ap
953	59.5	4.9	994	2	US-09-902-540-13822	Sequence 13822, A
954	59.5	4.9	1053	2	US-09-328-352-5058	Sequence 5058, Ap
955	59.5	4.9	1081	2	US-09-369-364A-17	Sequence 17, Appl
956	59.5	4.9	1237	1	US-08-241-853-2	Sequence 2, Appli
957	59.5	4.9	1237	1	US-08-850-917-2	Sequence 2, Appli
958	59.5	4.9	1289	1	US-08-542-003-2	Sequence 2, Appli
959	59.5	4.9	1289	1	US-08-322-760A-2	Sequence 2, Appli
960	59.5	4.9	1289	2	US-09-236-949-2	Sequence 2, Appli
961	59.5	4.9	1522	2	US-09-939-853A-85	Sequence 85, Appl
962	59.5	4.9	1584	2	US-09-457-040B-27	Sequence 27, Appl
963	59.5	4.9	1709	2	US-09-949-016-11345	Sequence 11345, A
964	59	4.9	155	1	US-08-801-972-1	Sequence 1, Appli
965	59	4.9	155	2	US-09-178-881-1	Sequence 1, Appli
966	59	4.9	225	2	US-09-107-532A-4090	Sequence 4090, Ap
967	59	4.9	230	2	US-09-663-600A-92	Sequence 92, Appl
968	59	4.9	278	2	US-09-270-767-59700	Sequence 59700, A
969	59	4.9	292	1	US-09-024-848-2	Sequence 2, Appli
970	59	4.9	292	2	US-09-348-116A-2	Sequence 2, Appli
971	59	4.9	292	2	US-09-583-110-4530	Sequence 4530, Ap
972	59	4.9	293	2	US-09-252-991A-33017	Sequence 33017, A
973	59	4.9	300	2	US-09-252-991A-26038	Sequence 26038, A
974	59	4.9	304	2	US-09-134-000C-5201	Sequence 5201, Ap
975	59	4.9	308	2	US-09-107-433-3470	Sequence 3470, Ap

976	59	4.9	310	2	US-09-907-794A-423	Sequence 423, App
977	59	4.9	310	2	US-09-905-125A-423	Sequence 423, App
978	59	4.9	310	2	US-09-902-775A-423	Sequence 423, App
979	59	4.9	310	2	US-09-906-700-423	Sequence 423, App
980	59	4.9	310	2	US-09-903-603A-423	Sequence 423, App
981	59	4.9	310	2	US-09-904-920A-423	Sequence 423, App
982	59	4.9	310	2	US-09-909-064-423	Sequence 423, App
983	59	4.9	310	2	US-09-905-381A-423	Sequence 423, App
984	59	4.9	310	2	US-09-906-618-423	Sequence 423, App
985	59	4.9	310	2	US-09-906-646-423	Sequence 423, App
986	59	4.9	310	2	US-09-904-462-423	Sequence 423, App
987	59	4.9	310	2	US-09-902-736A-423	Sequence 423, App
988	59	4.9	310	2	US-10-033-301-20	Sequence 20, Appl
989	59	4.9	310	2	US-09-906-722A-423	Sequence 423, App
990	59	4.9	310	2	US-09-905-449-423	Sequence 423, App
991	59	4.9	310	2	US-09-903-562B-423	Sequence 423, App
992	59	4.9	310	2	US-10-033-435-20	Sequence 20, Appl
993	59	4.9	310	2	US-09-906-679A-423	Sequence 423, App
994	59	4.9	310	3	US-09-907-841-423	Sequence 423, App
995	59	4.9	318	2	US-09-540-236-2086	Sequence 2086, Ap
996	59	4.9	339	2	US-09-252-991A-19350	Sequence 19350, A
997	59	4.9	342	2	US-09-134-001C-4190	Sequence 4190, Ap
998	59	4.9	368	1	US-07-977-630-4	Sequence 4, Appli
999	59	4.9	368	2	US-09-252-991A-29907	Sequence 29907, A
1000	59	4.9	374	1	US-08-820-170A-25	Sequence 25, Appl
1001	59	4.9	374	2	US-09-055-699-25	Sequence 25, Appl
1002	59	4.9	374	2	US-09-273-565-25	Sequence 25, Appl
1003	59	4.9	374	2	US-09-565-538-25	Sequence 25, Appl
1004	59	4.9	374	2	US-09-661-468-25	Sequence 25, Appl
1005	59	4.9	374	2	US-09-976-165-25	Sequence 25, Appl
1006	59	4.9	374	2	US-09-227-853A-2	Sequence 2, Appli
1007	59	4.9	374	5	PCT-US95-06385-2	Sequence 2, Appli
1008	59	4.9	381	2	US-10-012-896-941	Sequence 941, App
1009	59	4.9	381	3	US-10-144-678A-941	Sequence 941, App
1010	59	4.9	405	2	US-09-270-767-45879	Sequence 45879, A
1011	59	4.9	405	2	US-09-603-208A-262	Sequence 262, App
1012	59	4.9	410	2	US-09-270-767-44276	Sequence 44276, A
1013	59	4.9	416	2	US-09-252-991A-24117	Sequence 24117, A
1014	59	4.9	417	2	US-09-252-991A-25870	Sequence 25870, A
1015	59	4.9	426	2	US-09-902-540-12172	Sequence 12172, A
1016	59	4.9	430	2	US-09-134-000C-4819	Sequence 4819, Ap
1017	59	4.9	444	2	US-09-721-870-42	Sequence 42, Appl
1018	59	4.9	454	2	US-09-455-486-6	Sequence 6, Appli
1019	59	4.9	454	2	US-10-104-047-3155	Sequence 3155, Ap
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1022	59	4.9	471	2	US-09-492-709A-284	Sequence 284, App
1023	59	4.9	476	2	US-09-529-157-4	Sequence 4, Appli
1024	59	4.9	505	2	US-09-328-352-4724	Sequence 4724, Ap
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1026	59	4.9	566	1	US-08-272-255-8	Sequence 8, Appli
1027	59	4.9	566	5	PCT-US95-08565-8	Sequence 8, Appli
1028	59	4.9	570	2	US-09-489-039A-9421	Sequence 9421, Ap
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1030	59	4.9	577	2	US-09-514-245-3	Sequence 3, Appli
1031	59	4.9	591	2	US-09-949-016-10026	Sequence 10026, A
1032	59	4.9	639	2	US-09-538-092-17	Sequence 17, Appl
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1036	59	4.9	694	2	US-09-846-996A-1	Sequence 1, Appli
1037	59	4.9	694	2	US-10-246-085A-1	Sequence 1, Appli
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1040	59	4.9	875	3	US-10-199-229-10	Sequence 10, Appl
1041	59	4.9	1203	2	US-09-207-857-2	Sequence 2, Appli
1042	59	4.9	1203	2	US-09-909-280A-2	Sequence 2, Appli
1043	59	4.9	1296	2	US-08-857-636-60	Sequence 60, Appl
1044	59	4.9	1692	2	US-09-263-933-4	Sequence 4, Appli
1045	59	4.9	1692	2	US-09-263-933-11	Sequence 11, Appl
1046	59	4.9	1692	2	US-09-263-933-18	Sequence 18, Appl
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1054	59	4.9	2307	2	US-09-263-933-9	Sequence 9, Appli
1055	59	4.9	2307	2	US-09-263-933-16	Sequence 16, Appl
1056	59	4.9	2307	2	US-09-919-901-2	Sequence 2, Appli
1057	59	4.9	2307	2	US-09-919-901-9	Sequence 9, Appli
1058	59	4.9	2307	2	US-09-919-901-16	Sequence 16, Appl
1059	59	4.9	2307	2	US-10-191-966-2	Sequence 2, Appli
1060	59	4.9	2307	2	US-10-191-966-9	Sequence 9, Appli
1061	59	4.9	2307	2	US-10-191-966-16	Sequence 16, Appl
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1064	58.5	4.8	108	2	US-09-270-767-53122	Sequence 53122, A
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1066	58.5	4.8	130	2	US-09-248-796A-18320	Sequence 18320, A
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1068	58.5	4.8	142	2	US-09-380-882-9	Sequence 9, Appli
1069	58.5	4.8	163	2	US-09-489-039A-12148	Sequence 12148, A
1070	58.5	4.8	169	1	US-08-828-832-4	Sequence 4, Appli
1071	58.5	4.8	174	2	US-09-270-767-46903	Sequence 46903, A
1072	58.5	4.8	180	2	US-09-270-767-38798	Sequence 38798, A
1073	58.5	4.8	180	2	US-09-270-767-54015	Sequence 54015, A
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1075	58.5	4.8	198	2	US-08-737-248-6	Sequence 6, Appli
1076	58.5	4.8	226	1	US-08-505-058-6	Sequence 6, Appli
1077	58.5	4.8	226	1	US-08-459-818-26	Sequence 26, Appl
1078	58.5	4.8	226	1	US-08-889-666-26	Sequence 26, Appl
1079	58.5	4.8	226	1	US-08-465-078-26	Sequence 26, Appl
1080	58.5	4.8	226	1	US-08-725-776-26	Sequence 26, Appl
1081	58.5	4.8	226	1	US-08-488-062-26	Sequence 26, Appl
1082	58.5	4.8	233	2	US-09-472-087-15	Sequence 15, Appl
1083	58.5	4.8	233	2	US-09-472-087-67	Sequence 67, Appl
1084	58.5	4.8	234	2	US-09-252-991A-22915	Sequence 22915, A
1085	58.5	4.8	238	2	US-09-270-767-41693	Sequence 41693, A
1086	58.5	4.8	242	2	US-09-489-039A-13487	Sequence 13487, A
1087	58.5	4.8	252	2	US-09-522-714-20	Sequence 20, Appl
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1089	58.5	4.8	263	2	US-09-270-767-43668	Sequence 43668, A
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1092	58.5	4.8	281	2	US-09-489-039A-8675	Sequence 8675, Ap
1093	58.5	4.8	282	2	US-09-270-767-41535	Sequence 41535, A
1094	58.5	4.8	294	2	US-09-710-279-1688	Sequence 1688, Ap
1095	58.5	4.8	299	2	US-09-393-634-41	Sequence 41, Appl
1096	58.5	4.8	299	3	US-10-770-127-7	Sequence 7, Appli
1097	58.5	4.8	306	2	US-09-252-991A-22636	Sequence 22636, A
1098	58.5	4.8	338	2	US-09-248-796A-23866	Sequence 23866, A
1099	58.5	4.8	338	2	US-09-902-540-10905	Sequence 10905, A
1100	58.5	4.8	339	1	US-08-758-621-2	Sequence 2, Appli
1101	58.5	4.8	339	2	US-09-107-858-2	Sequence 2, Appli
1102	58.5	4.8	339	2	US-09-579-174-2	Sequence 2, Appli
1103	58.5	4.8	348	1	US-08-454-196-8	Sequence 8, Appli
1104	58.5	4.8	348	1	US-08-454-196-17	Sequence 17, Appl
1105	58.5	4.8	348	2	US-09-064-033-8	Sequence 8, Appli
1106	58.5	4.8	348	2	US-09-064-033-17	Sequence 17, Appl
1107	58.5	4.8	348	2	US-09-291-046-8	Sequence 8, Appli
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1114	58.5	4.8	397	2	US-09-270-767-43356	Sequence 43356, A
1115	58.5	4.8	420	2	US-09-198-452A-533	Sequence 533, App
1116	58.5	4.8	420	2	US-09-438-185A-493	Sequence 493, App
1117	58.5	4.8	425	2	US-09-134-000C-5971	Sequence 5971, Ap
1118	58.5	4.8	426	2	US-09-583-110-4102	Sequence 4102, Ap
1119	58.5	4.8	428	2	US-10-104-047-2468	Sequence 2468, Ap
1120	58.5	4.8	431	2	US-09-583-110-4734	Sequence 4734, Ap
1121	58.5	4.8	432	2	US-09-769-787-21	Sequence 21, Appl

1122	58.5	4.8	441	2	US-09-107-433-3441	Sequence 3441, Ap
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1125	58.5	4.8	469	2	US-09-489-039A-10214	Sequence 10214, A
1126	58.5	4.8	486	2	US-08-622-191-7	Sequence 7, Appli
1127	58.5	4.8	488	2	US-10-162-012-46	Sequence 46, Appl
1128	58.5	4.8	511	2	US-09-107-532A-6112	Sequence 6112, Ap
1129	58.5	4.8	545	2	US-09-572-147-2	Sequence 2, Appli
1130	58.5	4.8	550	2	US-09-330-245A-2	Sequence 2, Appli
1131	58.5	4.8	550	2	US-09-614-891-7	Sequence 7, Appli
1132	58.5	4.8	554	2	US-08-943-714-2	Sequence 2, Appli
1133	58.5	4.8	555	2	US-09-712-338-2	Sequence 2, Appli
1134	58.5	4.8	563	2	US-09-424-347B-2	Sequence 2, Appli
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1136	58.5	4.8	578	2	US-09-248-796A-19477	Sequence 19477, A
1137	58.5	4.8	589	2	US-09-949-016-9431	Sequence 9431, Ap
1138	58.5	4.8	595	2	US-08-842-079-18	Sequence 18, Appl
1139	58.5	4.8	595	2	US-08-842-079-20	Sequence 20, Appl
1140	58.5	4.8	595	2	US-09-638-857-18	Sequence 18, Appl
1141	58.5	4.8	595	2	US-09-638-857-20	Sequence 20, Appl
1142	58.5	4.8	627	2	US-09-538-092-760	Sequence 760, App
1143	58.5	4.8	635	1	US-09-014-969-11	Sequence 11, Appl
1144	58.5	4.8	635	2	US-09-949-016-6991	Sequence 6991, Ap
1145	58.5	4.8	660	2	US-09-720-317A-30	Sequence 30, Appl
1146	58.5	4.8	666	2	US-09-341-587-1	Sequence 1, Appli
1147	58.5	4.8	668	2	US-09-252-991A-22341	Sequence 22341, A
1148	58.5	4.8	681	2	US-09-248-796A-20857	Sequence 20857, A
1149	58.5	4.8	686	2	US-09-949-016-7874	Sequence 7874, Ap
1150	58.5	4.8	691	2	US-09-575-081B-2	Sequence 2, Appli
1151	58.5	4.8	903	2	US-09-252-991A-17937	Sequence 17937, A
1152	58.5	4.8	907	2	US-09-170-496D-264	Sequence 264, App
1153	58.5	4.8	907	2	US-09-170-496D-278	Sequence 278, App
1154	58.5	4.8	1012	1	US-08-475-891A-4	Sequence 4, Appli
1155	58.5	4.8	1025	1	US-08-567-375-4	Sequence 4, Appli
1156	58.5	4.8	1025	1	US-08-587-680A-4	Sequence 4, Appli
1157	58.5	4.8	1026	2	US-09-623-551-18	Sequence 18, Appl
1158	58.5	4.8	1724	1	US-08-325-547-3	Sequence 3, Appli
1159	58.5	4.8	1785	2	US-09-341-587-3	Sequence 3, Appli
1160	58.5	4.8	1912	1	US-08-409-995-4	Sequence 4, Appli
1161	58.5	4.8	1912	2	US-08-685-467-4	Sequence 4, Appli
1162	58.5	4.8	1964	2	US-09-467-997-1	Sequence 1, Appli
1163	58.5	4.8	2353	2	US-09-377-155-33	Sequence 33, Appl
1164	58.5	4.8	2353	2	US-08-913-942-4	Sequence 4, Appli
1165	58.5	4.8	2353	2	US-09-669-974-33	Sequence 33, Appl
1166	58.5	4.8	2353	2	US-09-797-862-33	Sequence 33, Appl
1167	58.5	4.8	2353	2	US-09-684-707-4	Sequence 4, Appli
1168	58.5	4.8	2354	2	US-09-268-347-47	Sequence 47, Appl
1169	58.5	4.8	2411	2	US-09-268-347-36	Sequence 36, Appl
1170	58	4.8	125	2	US-09-248-796A-26907	Sequence 26907, A
1171	58	4.8	141	2	US-09-270-767-32327	Sequence 32327, A
1172	58	4.8	143	2	US-09-830-230A-222	Sequence 222, App
1173	58	4.8	153	2	US-09-769-787-39	Sequence 39, Appl
1174	58	4.8	155	2	US-09-830-230A-221	Sequence 221, App
1175	58	4.8	170	2	US-09-107-532A-5197	Sequence 5197, Ap
1176	58	4.8	176	2	US-10-094-749-2950	Sequence 2950, Ap
1177	58	4.8	178	2	US-09-809-665A-12	Sequence 12, Appl
1178	58	4.8	199	2	US-08-737-248-2	Sequence 2, Appli
1179	58	4.8	199	2	US-08-737-248-11	Sequence 11, Appl
1180	58	4.8	213	2	US-08-397-411-12	Sequence 12, Appl
1181	58	4.8	219	2	US-10-094-749-2381	Sequence 2381, Ap
1182	58	4.8	225	2	US-09-270-767-40689	Sequence 40689, A
1183	58	4.8	225	2	US-09-270-767-55905	Sequence 55905, A
1184	58	4.8	234	2	US-08-944-483-46	Sequence 46, Appl
1185	58	4.8	239	1	US-08-916-902A-1	Sequence 1, Appli
1186	58	4.8	239	1	US-09-213-389-1	Sequence 1, Appli
1187	58	4.8	239	2	US-10-164-595-74	Sequence 74, Appl
1188	58	4.8	254	2	US-09-107-532A-4025	Sequence 4025, Ap
1189	58	4.8	268	2	US-09-949-016-10712	Sequence 10712, A
1190	58	4.8	274	2	US-09-902-540-14629	Sequence 14629, A
1191	58	4.8	288	2	US-09-248-796A-16494	Sequence 16494, A
1192	58	4.8	294	2	US-09-710-279-46	Sequence 46, Appl
1193	58	4.8	315	2	US-09-270-767-33342	Sequence 33342, A
1194	58	4.8	315	2	US-09-270-767-48559	Sequence 48559, A
1195	58	4.8	316	1	US-08-846-762-9	Sequence 9, Appli
1196	58	4.8	316	2	US-09-393-634-39	Sequence 39, Appl
1197	58	4.8	316	2	US-09-949-016-8207	Sequence 8207, Ap
1198	58	4.8	316	3	US-10-770-127-5	Sequence 5, Appli
1199	58	4.8	348	2	US-09-248-796A-14883	Sequence 14883, A
1200	58	4.8	386	2	US-09-107-532A-4764	Sequence 4764, Ap
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1202	58	4.8	401	2	US-09-391-958-1	Sequence 1, Appli
1203	58	4.8	401	2	US-10-104-047-3800	Sequence 3800, Ap
1204	58	4.8	418	2	US-09-252-991A-30786	Sequence 30786, A
1205	58	4.8	426	2	US-08-737-248-4	Sequence 4, Appli
1206	58	4.8	426	2	US-08-311-731A-109	Sequence 109, App
1207	58	4.8	445	2	US-09-252-991A-28655	Sequence 28655, A
1208	58	4.8	446	2	US-09-489-039A-7920	Sequence 7920, Ap
1209	58	4.8	447	2	US-09-555-093-7	Sequence 7, Appli
1210	58	4.8	448	1	US-08-366-779-5	Sequence 5, Appli
1211	58	4.8	448	1	US-08-789-936-5	Sequence 5, Appli
1212	58	4.8	448	2	US-08-934-254-5	Sequence 5, Appli
1213	58	4.8	448	2	US-09-685-775-5	Sequence 5, Appli
1214	58	4.8	448	2	US-09-583-110-4257	Sequence 4257, Ap
1215	58	4.8	448	2	US-09-857-583B-15	Sequence 15, Appl
1216	58	4.8	448	2	US-09-857-524B-11	Sequence 11, Appl
1217	58	4.8	448	2	US-09-769-787-42	Sequence 42, Appl
1218	58	4.8	452	2	US-09-107-433-4995	Sequence 4995, Ap
1219	58	4.8	457	2	US-09-999-833A-19	Sequence 19, Appl
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1221	58	4.8	457	2	US-09-978-189-19	Sequence 19, Appl
1222	58	4.8	457	2	US-10-017-085A-19	Sequence 19, Appl
1223	58	4.8	457	3	US-10-145-129A-19	Sequence 19, Appl
1224	58	4.8	457	3	US-10-013-929A-19	Sequence 19, Appl
1225	58	4.8	457	3	US-10-013-917A-19	Sequence 19, Appl
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1229	58	4.8	467	2	US-09-489-039A-9693	Sequence 9693, Ap
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1235	58	4.8	485	1	US-08-452-930-15	Sequence 15, Appl
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1238	58	4.8	486	1	US-08-942-423-3	Sequence 3, Appli
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1240	58	4.8	486	2	US-09-879-957-26	Sequence 26, Appl
1241	58	4.8	486	2	US-09-538-092-926	Sequence 926, App
1242	58	4.8	504	2	US-09-919-497-67	Sequence 67, Appl
1243	58	4.8	505	2	US-09-949-016-11556	Sequence 11556, A
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1251	58	4.8	598	2	US-09-438-185A-476	Sequence 476, App
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1264	58	4.8	706	2	US-09-303-518D-254	Sequence 254, App
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1272	58	4.8	837	2	US-10-044-564-38	Sequence 38, Appl
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1276	58	4.8	865	2	US-09-608-821-2	Sequence 2, Appli
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1278	58	4.8	865	2	US-10-044-564-132	Sequence 132, App
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1293	58	4.8	2261	2	US-09-595-526C-8	Sequence 8, Appli
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1341	57.5	4.7	340	3	US-10-062-831-174	Sequence 174, App
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1343	57.5	4.7	341	2	US-10-062-548-132	Sequence 132, App
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1352	57.5	4.7	431	2	US-09-944-944-83	Sequence 83, Appl
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1354	57.5	4.7	431	2	US-09-945-587-83	Sequence 83, Appl
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1356	57.5	4.7	431	2	US-09-992-598-515	Sequence 515, App
1357	57.5	4.7	431	2	US-09-989-735-515	Sequence 515, App
1358	57.5	4.7	431	3	US-09-989-726-515	Sequence 515, App
1359	57.5	4.7	431	3	US-09-944-884-83	Sequence 83, Appl
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1362	57.5	4.7	431	3	US-09-997-349-515	Sequence 515, App
1363	57.5	4.7	431	3	US-09-997-653-515	Sequence 515, App
1364	57.5	4.7	431	3	US-09-989-293A-515	Sequence 515, App
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1378	57.5	4.7	489	2	US-09-997-333-138	Sequence 138, App
1379	57.5	4.7	489	2	US-09-992-598-138	Sequence 138, App
1380	57.5	4.7	489	2	US-09-989-735-138	Sequence 138, App
1381	57.5	4.7	489	3	US-09-989-726-138	Sequence 138, App
1382	57.5	4.7	489	3	US-09-997-514-138	Sequence 138, App
1383	57.5	4.7	489	3	US-09-989-728-138	Sequence 138, App
1384	57.5	4.7	489	3	US-09-997-349-138	Sequence 138, App
1385	57.5	4.7	489	3	US-09-997-653-138	Sequence 138, App
1386	57.5	4.7	489	3	US-09-989-293A-138	Sequence 138, App
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1398	57.5	4.7	693	2	US-09-978-189-483	Sequence 483, App
1399	57.5	4.7	693	2	US-10-017-085A-483	Sequence 483, App
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1408	57.5	4.7	771	2	US-09-717-888-8	Sequence 8, Appli
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1412	57.5	4.7	896	2	US-08-618-957A-10	Sequence 10, Appl
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1487	57	4.7	125	2	US-09-270-767-54759	Sequence 54759, A
1488	57	4.7	127	2	US-09-252-991A-18412	Sequence 18412, A
1489	57	4.7	136	2	US-09-615-192A-293	Sequence 293, App
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1491	57	4.7	139	1	US-08-444-733-177	Sequence 177, App
1492	57	4.7	139	1	US-08-464-134-177	Sequence 177, App
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1494	57	4.7	139	1	US-08-485-910-177	Sequence 177, App
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ALIGNMENTS

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;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
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;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C53
;  CURRENT APPLICATION NUMBER: US/09/991,181
;  CURRENT FILING DATE:  2001-11-16
;  PRIOR APPLICATION NUMBER: 60/049787
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;  PRIOR FILING DATE: 1998-07-09

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; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
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;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C19
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RESULT 3
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
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; APPLICANT: Paoni,Nicholas F.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C27
; CURRENT APPLICATION NUMBER: US/09/997,333
; CURRENT FILING DATE: 2001-11-15
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Query Match 100.0%; Score 1215; DB 2; Length 229;
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RESULT 4
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; Sequence 258, Application US/09992598
; Patent No. 6956108
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
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; APPLICANT: Kljavin,Ivar J.
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; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C20
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; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1215; DB 2; Length 229;
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RESULT 5
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; Patent No. 6972185
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
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; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR FILING DATE: 1998-07-07
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1215; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 7.9e-131;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
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; Sequence 258, Application US/09989726
; Patent No. 7018811
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C60
; CURRENT APPLICATION NUMBER: US/09/989,726
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
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; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
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; Patent No. 7029873
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C72
; CURRENT APPLICATION NUMBER: US/09/989,728
; CURRENT FILING DATE: 2001-11-20
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1215; DB 3; Length 229;
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RESULT 9
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; Patent No. 7034106
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C37
; CURRENT APPLICATION NUMBER: US/09/997,349
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
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RESULT 10
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; Patent No. 7034122
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; APPLICANT: Ashkenazi,Avi J.
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; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C38
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; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1215; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 7.9e-131;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db         61 MAIPATTMSLTARKRACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPS 120

Qy        121 NSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSE 180

Qy        181 ENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV 229
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Db        181 ENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV 229
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RESULT 11
US-09-989-293A-258
; Sequence 258, Application US/09989293A
; Patent No. 7034136

; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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;  PRIOR APPLICATION NUMBER: 60/091978
;  PRIOR FILING DATE: 1998-07-07
;  PRIOR APPLICATION NUMBER: 60/091982
;  PRIOR FILING DATE: 1998-07-07
;  PRIOR APPLICATION NUMBER: 60/092182
;  PRIOR FILING DATE: 1998-07-09

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Qy        121 NSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSE 180

Qy        181 ENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV 229
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RESULT 12
US-09-949-016-9937
; Sequence 9937, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
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;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-9937

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Qy         60 LMAIPATTMSLTARKR-----ACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPL 114
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Qy        175 FHFDSEENKHRLIHFSVFLGLLLV--GILEVLFGLSQIVIGFLGCLCGVSKRR 225
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RESULT 13
US-08-855-261A-1
; Sequence 1, Application US/08855261A
; Patent No. 5922566
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Goli, Surya K.
;    APPLICANT:  Shah, Purvi
;    APPLICANT:  Corley, Neil C.
;    TITLE OF INVENTION:  NEW TUMOR-ASSOCIATED ANTIGEN
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/855,261A
;      FILING DATE:  Filed Herewith
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0298 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  197 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  COLNNOT19
;      CLONE:  1634851
US-08-855-261A-1

  Query Match             14.0%;  Score 170;  DB 1;  Length 197;
  Best Local Similarity   26.5%;  Pred. No. 3.5e-11;
  Matches   61;  Conservative   32;  Mismatches   91;  Indels   46;  Gaps    7;

Qy          3 CCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA 62
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Qy         63 IPATTMSLTARKR-----ACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCN 117
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Db         61 LCPGIAAVRAGGKGCCGAGCCGNRCRMLRSVFSSAFGVLGAIYCLSVSGAGLRNGP---- 116

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Qy        178 DSEENKHRLIHFSVFLGLLLV--GILEVLFGLSQIVIGFLGCLCGVSKRR 225
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Db        143 DRCEAPPRVVPWNVTLFSLLVAASCLEIVLCGIQLVNATIGVFCGDCRKK 192


RESULT 14
US-09-227-224-1
; Sequence 1, Application US/09227224
; Patent No. 6350581
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Goli, Surya K.
;    APPLICANT:  Shah, Purvi
;    APPLICANT:  Corley, Neil C.
;    TITLE OF INVENTION:  NEW TUMOR-ASSOCIATED ANTIGEN
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/227,224
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/855,261
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0298 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  197 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  COLNNOT19
;      CLONE:  1634851
US-09-227-224-1

  Query Match             14.0%;  Score 170;  DB 2;  Length 197;
  Best Local Similarity   26.5%;  Pred. No. 3.5e-11;
  Matches   61;  Conservative   32;  Mismatches   91;  Indels   46;  Gaps    7;

Qy          3 CCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA 62
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Db          2 CTGKCARCVGLSLITLCLVCIVANAL-LLVPNGETSWTNTNHLSLQVWLMGGFIGGGLMV 60

Qy         63 IPATTMSLTARKR-----ACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCN 117
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Qy        118 SPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHF 177
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; Patent No. 6632617
; GENERAL INFORMATION:
;  APPLICANT: Bandman, Olga
;  APPLICANT:  Goli, Surya K.
;  APPLICANT:  Shah, Purvi
;  APPLICANT:  Corley, Neil C.
;  APPLICANT:  Streeter, David G.
;  TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN
;  FILE REFERENCE: PC-0043 CIP
;  CURRENT APPLICATION NUMBER: US/09/855,288
;  CURRENT FILING DATE:  2001-05-14
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PERL Program
; SEQ ID NO 1
;   LENGTH: 197
;   TYPE: PRT
;   ORGANISM: Homo sapiens
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;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6632617 1634851CD1
US-09-855-288-1

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Job time : 86.2294 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: November 21, 2006, 20:39:39 ; Search time 218.495 Seconds
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Scoring table: BLOSUM62
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Total number of hits satisfying chosen parameters: 2097797

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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759	173.5	14.3	205	5	US-10-821-234-968	Sequence 968, App
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761	170	14.0	197	4	US-10-156-136-27	Sequence 27, Appl
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763	170	14.0	197	6	US-11-041-419-27	Sequence 27, Appl
764	170	14.0	198	3	US-09-983-802-232	Sequence 232, App
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Total number of hits satisfying chosen parameters: 330775

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SUMMARIES

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42	74.5	6.1	720	6	US-10-953-349-4003	Sequence 4003, Ap
43	74.5	6.1	763	6	US-10-982-908-28	Sequence 28, Appl
46	73.5	6.0	261	6	US-10-574-398-95	Sequence 95, Appl
47	73.5	6.0	261	7	US-11-101-316-118	Sequence 118, App
48	73.5	6.0	261	7	US-11-376-673-118	Sequence 118, App
49	73.5	6.0	356	7	US-11-056-355B-62768	Sequence 62768, A
50	73.5	6.0	358	7	US-11-056-355B-62767	Sequence 62767, A
51	73.5	6.0	385	7	US-11-330-403-16089	Sequence 16089, A
52	73.5	6.0	396	7	US-11-056-355B-62766	Sequence 62766, A
53	73.5	6.0	432	7	US-11-056-355B-87092	Sequence 87092, A
54	73.5	6.0	445	7	US-11-056-355B-101684	Sequence 101684,
55	73.5	6.0	445	7	US-11-056-355B-112923	Sequence 112923,
56	73.5	6.0	467	7	US-11-056-355B-87091	Sequence 87091, A
57	73.5	6.0	475	7	US-11-056-355B-22057	Sequence 22057, A
58	73.5	6.0	563	7	US-11-056-355B-101683	Sequence 101683,
59	73.5	6.0	563	7	US-11-056-355B-112922	Sequence 112922,
60	73.5	6.0	574	7	US-11-056-355B-101682	Sequence 101682,
61	73.5	6.0	574	7	US-11-056-355B-112921	Sequence 112921,
62	73.5	6.0	585	7	US-11-056-355B-87090	Sequence 87090, A
63	73.5	6.0	593	7	US-11-056-355B-22056	Sequence 22056, A
64	73.5	6.0	604	7	US-11-056-355B-22055	Sequence 22055, A
65	73.5	6.0	644	6	US-10-527-191-5	Sequence 5, Appli
66	73	6.0	231	6	US-10-449-902-40046	Sequence 40046, A
67	73	6.0	231	7	US-11-330-403-13103	Sequence 13103, A
68	73	6.0	293	7	US-11-330-403-5360	Sequence 5360, Ap
69	73	6.0	327	6	US-10-953-349-11653	Sequence 11653, A
70	73	6.0	437	6	US-10-953-349-8975	Sequence 8975, Ap
71	73	6.0	440	6	US-10-953-349-8974	Sequence 8974, Ap
72	73	6.0	501	6	US-10-471-571A-3072	Sequence 3072, Ap
73	73	6.0	528	6	US-10-449-902-46397	Sequence 46397, A
74	73	6.0	631	7	US-11-447-460-12	Sequence 12, Appl
75	73	6.0	679	7	US-11-330-403-3414	Sequence 3414, Ap
76	72.5	6.0	275	6	US-10-471-571A-2828	Sequence 2828, Ap
77	72.5	6.0	297	7	US-11-330-403-3646	Sequence 3646, Ap
78	72	5.9	423	7	US-11-056-355B-40885	Sequence 40885, A
79	72	5.9	445	7	US-11-056-355B-4888	Sequence 4888, Ap
80	72	5.9	445	7	US-11-056-355B-40884	Sequence 40884, A
81	72	5.9	450	7	US-11-056-355B-4887	Sequence 4887, Ap
82	72	5.9	499	6	US-10-449-902-46724	Sequence 46724, A
83	72	5.9	583	7	US-11-056-355B-40883	Sequence 40883, A
84	71.5	5.9	243	7	US-11-056-355B-8755	Sequence 8755, Ap
85	71.5	5.9	276	6	US-10-953-349-3480	Sequence 3480, Ap
86	71.5	5.9	276	7	US-11-056-355B-35712	Sequence 35712, A
87	71.5	5.9	276	7	US-11-056-355B-102670	Sequence 102670,
88	71.5	5.9	276	7	US-11-056-355B-113909	Sequence 113909,
89	71.5	5.9	282	6	US-10-953-349-3479	Sequence 3479, Ap
90	71.5	5.9	282	7	US-11-056-355B-35711	Sequence 35711, A
91	71.5	5.9	282	7	US-11-056-355B-102669	Sequence 102669,
92	71.5	5.9	282	7	US-11-056-355B-113908	Sequence 113908,
93	71.5	5.9	287	7	US-11-056-355B-8754	Sequence 8754, Ap
94	71.5	5.9	332	6	US-10-953-349-3478	Sequence 3478, Ap
95	71.5	5.9	332	7	US-11-056-355B-35710	Sequence 35710, A
96	71.5	5.9	332	7	US-11-056-355B-102668	Sequence 102668,
97	71.5	5.9	332	7	US-11-056-355B-113907	Sequence 113907,
98	71.5	5.9	602	7	US-11-330-403-13112	Sequence 13112, A
99	71.5	5.9	1148	6	US-10-501-566B-42	Sequence 42, Appl
100	71	5.8	253	6	US-10-449-902-39560	Sequence 39560, A
101	71	5.8	432	6	US-10-471-571A-822	Sequence 822, App
102	71	5.8	441	7	US-11-330-403-2518	Sequence 2518, Ap
103	71	5.8	473	7	US-11-330-403-13590	Sequence 13590, A
104	70.5	5.8	221	7	US-11-056-355B-82119	Sequence 82119, A
105	70.5	5.8	222	7	US-11-056-355B-82118	Sequence 82118, A

106	70.5	5.8	223	7	US-11-056-355B-22973	Sequence 22973, A
107	70.5	5.8	223	7	US-11-056-355B-99673	Sequence 99673, A
108	70.5	5.8	223	7	US-11-056-355B-110912	Sequence 110912,
109	70.5	5.8	239	7	US-11-056-355B-82117	Sequence 82117, A
110	70.5	5.8	251	7	US-11-056-355B-22972	Sequence 22972, A
111	70.5	5.8	251	7	US-11-056-355B-99672	Sequence 99672, A
112	70.5	5.8	251	7	US-11-056-355B-110911	Sequence 110911,
113	70.5	5.8	367	7	US-11-056-355B-47761	Sequence 47761, A
114	70.5	5.8	373	7	US-11-056-355B-47760	Sequence 47760, A
115	70.5	5.8	385	7	US-11-330-403-1739	Sequence 1739, Ap
116	70.5	5.8	420	7	US-11-056-355B-47759	Sequence 47759, A
117	70.5	5.8	589	7	US-11-330-403-8157	Sequence 8157, Ap
118	70.5	5.8	589	7	US-11-330-403-15468	Sequence 15468, A
119	70.5	5.8	1111	6	US-10-449-902-41187	Sequence 41187, A
120	70	5.8	253	6	US-10-471-571A-2642	Sequence 2642, Ap
121	70	5.8	430	7	US-11-056-355B-97092	Sequence 97092, A
122	70	5.8	437	7	US-11-056-355B-97091	Sequence 97091, A
123	70	5.8	485	6	US-10-805-394-5126	Sequence 5126, Ap
124	70	5.8	557	7	US-11-296-657-36	Sequence 36, Appl
125	70	5.8	590	7	US-11-330-403-13125	Sequence 13125, A
126	69.5	5.7	273	7	US-11-330-403-15873	Sequence 15873, A
127	69.5	5.7	550	7	US-11-056-355B-82017	Sequence 82017, A
128	69.5	5.7	558	6	US-10-540-898-822	Sequence 822, App
129	69.5	5.7	643	6	US-10-471-571A-4394	Sequence 4394, Ap
130	69.5	5.7	658	7	US-11-056-355B-82016	Sequence 82016, A
131	69.5	5.7	675	7	US-11-056-355B-82015	Sequence 82015, A
132	69	5.7	231	7	US-11-330-403-3639	Sequence 3639, Ap
133	69	5.7	231	7	US-11-330-403-5202	Sequence 5202, Ap
134	69	5.7	231	7	US-11-330-403-11439	Sequence 11439, A
135	69	5.7	231	7	US-11-330-403-12225	Sequence 12225, A
136	69	5.7	233	7	US-11-330-403-5087	Sequence 5087, Ap
137	69	5.7	259	6	US-10-449-902-30235	Sequence 30235, A
138	69	5.7	259	6	US-10-449-902-30690	Sequence 30690, A
139	69	5.7	259	6	US-10-449-902-30761	Sequence 30761, A
140	69	5.7	259	6	US-10-449-902-30767	Sequence 30767, A
141	69	5.7	259	6	US-10-449-902-31699	Sequence 31699, A
142	69	5.7	259	6	US-10-449-902-32099	Sequence 32099, A
143	69	5.7	259	6	US-10-449-902-32375	Sequence 32375, A
144	69	5.7	259	6	US-10-449-902-32541	Sequence 32541, A
145	69	5.7	259	6	US-10-449-902-40510	Sequence 40510, A
146	69	5.7	341	7	US-11-056-355B-81786	Sequence 81786, A
147	69	5.7	346	7	US-11-056-355B-81785	Sequence 81785, A
148	69	5.7	355	7	US-11-056-355B-81784	Sequence 81784, A
149	69	5.7	494	6	US-10-953-349-32707	Sequence 32707, A
150	69	5.7	494	7	US-11-056-355B-63282	Sequence 63282, A
151	69	5.7	527	7	US-11-056-355B-44010	Sequence 44010, A
152	69	5.7	636	6	US-10-953-349-32706	Sequence 32706, A
153	69	5.7	636	7	US-11-056-355B-63281	Sequence 63281, A
154	69	5.7	690	6	US-10-953-349-32705	Sequence 32705, A
155	69	5.7	690	7	US-11-056-355B-63280	Sequence 63280, A
156	69	5.7	743	7	US-11-056-355B-69595	Sequence 69595, A
157	69	5.7	756	7	US-11-056-355B-69594	Sequence 69594, A
158	69	5.7	814	7	US-11-056-355B-69593	Sequence 69593, A
159	68.5	5.6	305	7	US-11-414-658-8	Sequence 8, Appli
160	68.5	5.6	372	7	US-11-056-355B-108174	Sequence 108174,
161	68.5	5.6	372	7	US-11-056-355B-119413	Sequence 119413,
162	68.5	5.6	402	6	US-10-953-349-20715	Sequence 20715, A
163	68.5	5.6	402	7	US-11-056-355B-55135	Sequence 55135, A
164	68.5	5.6	419	7	US-11-056-355B-108173	Sequence 108173,
165	68.5	5.6	419	7	US-11-056-355B-119412	Sequence 119412,
166	68.5	5.6	441	6	US-10-953-349-20714	Sequence 20714, A
167	68.5	5.6	441	7	US-11-056-355B-55134	Sequence 55134, A
168	68.5	5.6	441	7	US-11-056-355B-108172	Sequence 108172,
169	68.5	5.6	441	7	US-11-056-355B-119411	Sequence 119411,
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171	68.5	5.6	443	7	US-11-056-355B-55133	Sequence 55133, A
172	68.5	5.6	626	6	US-10-449-902-53701	Sequence 53701, A
173	68	5.6	280	6	US-10-953-349-853	Sequence 853, App
174	68	5.6	280	7	US-11-056-355B-27903	Sequence 27903, A
175	68	5.6	280	7	US-11-056-355B-31493	Sequence 31493, A
176	68	5.6	406	7	US-11-434-137-6814	Sequence 6814, Ap
177	68	5.6	406	7	US-11-434-137-8996	Sequence 8996, Ap
178	68	5.6	406	7	US-11-434-184-6814	Sequence 6814, Ap
179	68	5.6	406	7	US-11-434-184-8996	Sequence 8996, Ap
180	68	5.6	406	7	US-11-434-199-6814	Sequence 6814, Ap
181	68	5.6	406	7	US-11-434-199-8996	Sequence 8996, Ap
182	68	5.6	406	7	US-11-434-203-6814	Sequence 6814, Ap
183	68	5.6	406	7	US-11-434-203-8996	Sequence 8996, Ap
184	68	5.6	417	6	US-10-449-902-52716	Sequence 52716, A
185	68	5.6	433	7	US-11-434-137-3066	Sequence 3066, Ap
186	68	5.6	433	7	US-11-434-184-3066	Sequence 3066, Ap
187	68	5.6	433	7	US-11-434-199-3066	Sequence 3066, Ap
188	68	5.6	433	7	US-11-434-203-3066	Sequence 3066, Ap
189	68	5.6	459	6	US-10-612-783-4310	Sequence 4310, Ap
190	68	5.6	465	7	US-11-056-355B-6329	Sequence 6329, Ap
191	68	5.6	470	7	US-11-293-697-3139	Sequence 3139, Ap
192	68	5.6	536	7	US-11-450-517-165	Sequence 165, App
193	68	5.6	827	7	US-11-056-355B-97469	Sequence 97469, A
194	68	5.6	837	7	US-11-056-355B-97468	Sequence 97468, A
195	68	5.6	879	7	US-11-056-355B-85855	Sequence 85855, A
196	68	5.6	889	7	US-11-056-355B-85854	Sequence 85854, A
197	68	5.6	3176	7	US-11-105-233-155	Sequence 155, App
198	67.5	5.6	210	7	US-11-056-355B-53766	Sequence 53766, A
199	67.5	5.6	216	7	US-11-056-355B-53765	Sequence 53765, A
200	67.5	5.6	228	7	US-11-056-355B-53764	Sequence 53764, A
201	67.5	5.6	256	6	US-10-953-349-854	Sequence 854, App
202	67.5	5.6	256	7	US-11-056-355B-27904	Sequence 27904, A
203	67.5	5.6	256	7	US-11-056-355B-31494	Sequence 31494, A
204	67.5	5.6	299	6	US-10-560-723-178	Sequence 178, App
205	67.5	5.6	312	6	US-10-528-630-35	Sequence 35, Appl
206	67.5	5.6	312	7	US-11-339-553-5	Sequence 5, Appli
207	67.5	5.6	319	6	US-10-562-469-26	Sequence 26, Appl
208	67.5	5.6	326	6	US-10-805-394-4974	Sequence 4974, Ap
209	67.5	5.6	494	7	US-11-434-137-1958	Sequence 1958, Ap
210	67.5	5.6	494	7	US-11-434-137-8624	Sequence 8624, Ap
211	67.5	5.6	494	7	US-11-434-184-1958	Sequence 1958, Ap
212	67.5	5.6	494	7	US-11-434-184-8624	Sequence 8624, Ap
213	67.5	5.6	494	7	US-11-434-199-1958	Sequence 1958, Ap
214	67.5	5.6	494	7	US-11-434-199-8624	Sequence 8624, Ap
215	67.5	5.6	494	7	US-11-434-203-1958	Sequence 1958, Ap
216	67.5	5.6	494	7	US-11-434-203-8624	Sequence 8624, Ap
217	67.5	5.6	510	6	US-10-449-902-35691	Sequence 35691, A
218	67.5	5.6	516	7	US-11-330-403-763	Sequence 763, App
219	67.5	5.6	695	7	US-11-051-725-184	Sequence 184, App
220	67.5	5.6	884	6	US-10-449-902-56049	Sequence 56049, A
221	67.5	5.6	1379	6	US-10-502-394-46	Sequence 46, Appl
222	67.5	5.6	2152	7	US-11-051-725-22	Sequence 22, Appl
223	67.5	5.6	2161	6	US-10-829-000-4	Sequence 4, Appli
224	67.5	5.6	2161	7	US-11-051-725-188	Sequence 188, App
225	67.5	5.6	2181	6	US-10-543-503-125	Sequence 125, App
226	67	5.5	407	7	US-11-330-403-9183	Sequence 9183, Ap
227	67	5.5	408	7	US-11-330-403-9184	Sequence 9184, Ap
228	67	5.5	428	7	US-11-056-355B-101866	Sequence 101866,
229	67	5.5	428	7	US-11-056-355B-113105	Sequence 113105,
230	67	5.5	431	7	US-11-056-355B-79779	Sequence 79779, A
231	67	5.5	440	7	US-11-056-355B-79778	Sequence 79778, A
232	67	5.5	448	7	US-11-056-355B-79777	Sequence 79777, A
233	67	5.5	450	7	US-11-056-355B-101865	Sequence 101865,
234	67	5.5	450	7	US-11-056-355B-113104	Sequence 113104,
235	67	5.5	535	6	US-10-449-902-42800	Sequence 42800, A
236	67	5.5	588	7	US-11-056-355B-101864	Sequence 101864,
237	67	5.5	588	7	US-11-056-355B-113103	Sequence 113103,
238	67	5.5	653	6	US-10-449-902-42798	Sequence 42798, A
239	67	5.5	665	6	US-10-449-902-47070	Sequence 47070, A
240	67	5.5	686	6	US-10-449-902-47675	Sequence 47675, A
241	67	5.5	1791	7	US-11-313-450-18	Sequence 18, Appl
242	67	5.5	1791	7	US-11-324-768-42	Sequence 42, Appl
243	66.5	5.5	117	7	US-11-413-563-40	Sequence 40, Appl
244	66.5	5.5	226	7	US-11-056-355B-60195	Sequence 60195, A
245	66.5	5.5	244	7	US-11-056-355B-60194	Sequence 60194, A
246	66.5	5.5	259	7	US-11-056-355B-60193	Sequence 60193, A
247	66.5	5.5	261	6	US-10-449-902-29181	Sequence 29181, A
248	66.5	5.5	284	6	US-10-449-902-46240	Sequence 46240, A
249	66.5	5.5	380	6	US-10-449-902-48268	Sequence 48268, A
250	66.5	5.5	380	6	US-10-449-902-50013	Sequence 50013, A
251	66.5	5.5	384	7	US-11-056-355B-70547	Sequence 70547, A

252	66.5	5.5	384	7	US-11-056-355B-85617	Sequence 85617, A
253	66.5	5.5	407	7	US-11-330-403-12810	Sequence 12810, A
254	66.5	5.5	408	7	US-11-226-554-146	Sequence 146, App
255	66.5	5.5	408	7	US-11-248-718-146	Sequence 146, App
256	66.5	5.5	409	7	US-11-056-355B-4889	Sequence 4889, Ap
257	66.5	5.5	470	7	US-11-056-355B-70546	Sequence 70546, A
258	66.5	5.5	482	7	US-11-056-355B-70545	Sequence 70545, A
259	66.5	5.5	485	6	US-10-526-324-1611	Sequence 1611, Ap
260	66.5	5.5	505	6	US-10-449-902-41685	Sequence 41685, A
261	66.5	5.5	744	7	US-11-330-403-6236	Sequence 6236, Ap
262	66.5	5.5	867	6	US-10-725-037-19	Sequence 19, Appl
263	66.5	5.5	867	6	US-10-725-488-19	Sequence 19, Appl
264	66.5	5.5	1028	6	US-10-502-394-76	Sequence 76, Appl
265	66.5	5.5	1078	7	US-11-242-079-7	Sequence 7, Appli
266	66.5	5.5	1088	7	US-11-242-079-6	Sequence 6, Appli
267	66	5.4	140	6	US-10-538-410-92	Sequence 92, Appl
268	66	5.4	267	7	US-11-056-355B-53916	Sequence 53916, A
269	66	5.4	269	6	US-10-449-902-52682	Sequence 52682, A
270	66	5.4	342	7	US-11-404-939-555	Sequence 555, App
271	66	5.4	395	6	US-10-449-902-29254	Sequence 29254, A
272	66	5.4	431	7	US-11-330-403-7905	Sequence 7905, Ap
273	66	5.4	537	7	US-11-330-403-10206	Sequence 10206, A
274	66	5.4	749	7	US-11-056-355B-13688	Sequence 13688, A
275	66	5.4	768	7	US-11-056-355B-13687	Sequence 13687, A
276	66	5.4	785	7	US-11-056-355B-13686	Sequence 13686, A
277	66	5.4	1041	7	US-11-056-355B-96010	Sequence 96010, A
278	66	5.4	1615	7	US-11-197-665-6	Sequence 6, Appli
279	65.5	5.4	217	6	US-10-953-349-855	Sequence 855, App
280	65.5	5.4	217	7	US-11-056-355B-27905	Sequence 27905, A
281	65.5	5.4	217	7	US-11-056-355B-31495	Sequence 31495, A
282	65.5	5.4	261	6	US-10-511-937-2998	Sequence 2998, Ap
283	65.5	5.4	261	7	US-11-363-149-21	Sequence 21, Appl
284	65.5	5.4	261	7	US-11-363-151-21	Sequence 21, Appl
285	65.5	5.4	411	7	US-11-366-965-520	Sequence 520, App
286	65.5	5.4	412	6	US-10-612-783-3864	Sequence 3864, Ap
287	65.5	5.4	424	6	US-10-953-349-11588	Sequence 11588, A
288	65.5	5.4	424	7	US-11-056-355B-48861	Sequence 48861, A
289	65.5	5.4	424	7	US-11-056-355B-97952	Sequence 97952, A
290	65.5	5.4	424	7	US-11-056-355B-109191	Sequence 109191,
291	65.5	5.4	430	7	US-11-056-355B-88022	Sequence 88022, A
292	65.5	5.4	460	6	US-10-953-349-11587	Sequence 11587, A
293	65.5	5.4	460	7	US-11-056-355B-48860	Sequence 48860, A
294	65.5	5.4	460	7	US-11-056-355B-97951	Sequence 97951, A
295	65.5	5.4	460	7	US-11-056-355B-109190	Sequence 109190,
296	65.5	5.4	466	7	US-11-056-355B-88021	Sequence 88021, A
297	65.5	5.4	486	6	US-10-953-349-11586	Sequence 11586, A
298	65.5	5.4	486	7	US-11-056-355B-48859	Sequence 48859, A
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304	65.5	5.4	558	7	US-11-056-355B-45019	Sequence 45019, A
305	65.5	5.4	558	7	US-11-056-355B-47150	Sequence 47150, A
306	65.5	5.4	558	7	US-11-056-355B-49869	Sequence 49869, A
307	65.5	5.4	558	7	US-11-056-355B-108349	Sequence 108349,
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309	65.5	5.4	558	7	US-11-056-355B-108596	Sequence 108596,
310	65.5	5.4	558	7	US-11-056-355B-119588	Sequence 119588,
311	65.5	5.4	558	7	US-11-056-355B-119827	Sequence 119827,
312	65.5	5.4	558	7	US-11-056-355B-119835	Sequence 119835,
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315	65.5	5.4	559	7	US-11-056-355B-47149	Sequence 47149, A
316	65.5	5.4	559	7	US-11-056-355B-49868	Sequence 49868, A
317	65.5	5.4	559	7	US-11-056-355B-108348	Sequence 108348,
318	65.5	5.4	559	7	US-11-056-355B-108587	Sequence 108587,
319	65.5	5.4	559	7	US-11-056-355B-108595	Sequence 108595,
320	65.5	5.4	559	7	US-11-056-355B-119587	Sequence 119587,
321	65.5	5.4	559	7	US-11-056-355B-119826	Sequence 119826,
322	65.5	5.4	559	7	US-11-056-355B-119834	Sequence 119834,
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324	65.5	5.4	587	7	US-11-056-355B-45017	Sequence 45017, A
325	65.5	5.4	587	7	US-11-056-355B-47148	Sequence 47148, A
326	65.5	5.4	587	7	US-11-056-355B-49867	Sequence 49867, A
327	65.5	5.4	587	7	US-11-056-355B-108347	Sequence 108347,
328	65.5	5.4	587	7	US-11-056-355B-108586	Sequence 108586,
329	65.5	5.4	587	7	US-11-056-355B-108594	Sequence 108594,
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332	65.5	5.4	587	7	US-11-056-355B-119833	Sequence 119833,
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334	65.5	5.4	866	6	US-10-669-920-640	Sequence 640, App
335	65.5	5.4	1012	6	US-10-953-349-13624	Sequence 13624, A
336	65.5	5.4	1025	6	US-10-953-349-13623	Sequence 13623, A
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338	65.5	5.4	1587	6	US-10-669-920-1223	Sequence 1223, Ap
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340	65.5	5.4	2122	6	US-10-669-920-1229	Sequence 1229, Ap
341	65.5	5.4	2123	6	US-10-669-920-1213	Sequence 1213, Ap
342	65.5	5.4	2134	6	US-10-669-920-1217	Sequence 1217, Ap
343	65.5	5.4	2143	6	US-10-669-920-1221	Sequence 1221, Ap
344	65.5	5.4	2150	6	US-10-669-920-1227	Sequence 1227, Ap
345	65.5	5.4	2154	6	US-10-669-920-1215	Sequence 1215, Ap
346	65.5	5.4	2163	6	US-10-669-920-1231	Sequence 1231, Ap
347	65	5.3	117	6	US-10-953-349-15927	Sequence 15927, A
348	65	5.3	122	6	US-10-953-349-15926	Sequence 15926, A
349	65	5.3	124	6	US-10-953-349-15925	Sequence 15925, A
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351	65	5.3	236	6	US-10-574-398-285	Sequence 285, App
352	65	5.3	287	6	US-10-449-902-31011	Sequence 31011, A
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354	65	5.3	493	6	US-10-449-902-46021	Sequence 46021, A
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356	65	5.3	554	7	US-11-056-355B-44784	Sequence 44784, A
357	65	5.3	585	6	US-10-449-902-51010	Sequence 51010, A
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362	64.5	5.3	163	7	US-11-056-355B-44436	Sequence 44436, A
363	64.5	5.3	219	7	US-11-056-355B-44435	Sequence 44435, A
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365	64.5	5.3	260	7	US-11-434-184-4106	Sequence 4106, Ap
366	64.5	5.3	260	7	US-11-434-199-4106	Sequence 4106, Ap
367	64.5	5.3	260	7	US-11-434-203-4106	Sequence 4106, Ap
368	64.5	5.3	282	7	US-11-056-355B-77195	Sequence 77195, A
369	64.5	5.3	284	7	US-11-056-355B-77194	Sequence 77194, A
370	64.5	5.3	308	6	US-10-548-463-167	Sequence 167, App
371	64.5	5.3	308	7	US-11-434-137-324	Sequence 324, App
372	64.5	5.3	308	7	US-11-434-184-324	Sequence 324, App
373	64.5	5.3	308	7	US-11-434-199-324	Sequence 324, App
374	64.5	5.3	308	7	US-11-434-203-324	Sequence 324, App
375	64.5	5.3	331	6	US-10-471-571A-4582	Sequence 4582, Ap
376	64.5	5.3	339	7	US-11-056-355B-106804	Sequence 106804,
377	64.5	5.3	339	7	US-11-056-355B-118043	Sequence 118043,
378	64.5	5.3	402	7	US-11-056-355B-40984	Sequence 40984, A
379	64.5	5.3	441	7	US-11-056-355B-106803	Sequence 106803,
380	64.5	5.3	441	7	US-11-056-355B-118042	Sequence 118042,
381	64.5	5.3	448	7	US-11-056-355B-106802	Sequence 106802,
382	64.5	5.3	448	7	US-11-056-355B-118041	Sequence 118041,
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384	64.5	5.3	464	7	US-11-056-355B-79371	Sequence 79371, A
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395	64.5	5.3	609	7	US-11-056-355B-82923	Sequence 82923, A
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397	64.5	5.3	949	7	US-11-293-697-3033	Sequence 3033, Ap

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403	64	5.3	258	7	US-11-434-199-5312	Sequence 5312, Ap
404	64	5.3	258	7	US-11-434-203-5312	Sequence 5312, Ap
405	64	5.3	273	7	US-11-434-137-364	Sequence 364, App
406	64	5.3	273	7	US-11-434-184-364	Sequence 364, App
407	64	5.3	273	7	US-11-434-199-364	Sequence 364, App
408	64	5.3	273	7	US-11-434-203-364	Sequence 364, App
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411	64	5.3	353	7	US-11-434-184-8832	Sequence 8832, Ap
412	64	5.3	353	7	US-11-434-199-8832	Sequence 8832, Ap
413	64	5.3	353	7	US-11-434-203-8832	Sequence 8832, Ap
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415	64	5.3	362	7	US-11-434-184-4674	Sequence 4674, Ap
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417	64	5.3	362	7	US-11-434-203-4674	Sequence 4674, Ap
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423	64	5.3	497	7	US-11-434-184-6438	Sequence 6438, Ap
424	64	5.3	497	7	US-11-434-199-6438	Sequence 6438, Ap
425	64	5.3	497	7	US-11-434-203-6438	Sequence 6438, Ap
426	64	5.3	590	7	US-11-094-278-16	Sequence 16, Appl
427	64	5.3	775	6	US-10-199-229-12	Sequence 12, Appl
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430	64	5.3	953	6	US-10-953-349-9823	Sequence 9823, Ap
431	64	5.3	987	7	US-11-330-403-5885	Sequence 5885, Ap
432	64	5.3	987	7	US-11-330-403-8031	Sequence 8031, Ap
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434	63.5	5.2	171	7	US-11-434-137-6672	Sequence 6672, Ap
435	63.5	5.2	171	7	US-11-434-184-6672	Sequence 6672, Ap
436	63.5	5.2	171	7	US-11-434-199-6672	Sequence 6672, Ap
437	63.5	5.2	171	7	US-11-434-203-6672	Sequence 6672, Ap
438	63.5	5.2	211	7	US-11-302-678-23	Sequence 23, Appl
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443	63.5	5.2	299	7	US-11-056-355B-75757	Sequence 75757, A
444	63.5	5.2	317	7	US-11-330-403-3143	Sequence 3143, Ap
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446	63.5	5.2	340	7	US-11-330-403-13101	Sequence 13101, A
447	63.5	5.2	342	6	US-10-612-783-4340	Sequence 4340, Ap
448	63.5	5.2	342	7	US-11-330-403-480	Sequence 480, App
449	63.5	5.2	342	7	US-11-330-403-4107	Sequence 4107, Ap
450	63.5	5.2	346	7	US-11-330-403-11612	Sequence 11612, A
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455	63.5	5.2	389	7	US-11-056-355B-95410	Sequence 95410, A
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457	63.5	5.2	417	6	US-10-805-394-6850	Sequence 6850, Ap
458	63.5	5.2	457	7	US-11-056-355B-90060	Sequence 90060, A
459	63.5	5.2	457	7	US-11-056-355B-93816	Sequence 93816, A
460	63.5	5.2	457	7	US-11-330-403-7820	Sequence 7820, Ap
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462	63.5	5.2	462	7	US-11-056-355B-93815	Sequence 93815, A
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465	63.5	5.2	532	7	US-11-056-355B-93814	Sequence 93814, A
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468	63.5	5.2	570	6	US-10-953-349-6515	Sequence 6515, Ap
469	63.5	5.2	610	6	US-10-449-902-52679	Sequence 52679, A
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473	63	5.2	114	6	US-10-953-349-15305	Sequence 15305, A
474	63	5.2	167	7	US-11-330-403-9479	Sequence 9479, Ap
475	63	5.2	172	6	US-10-953-349-23844	Sequence 23844, A
476	63	5.2	208	6	US-10-449-902-38420	Sequence 38420, A
477	63	5.2	209	6	US-10-953-349-23843	Sequence 23843, A
478	63	5.2	212	7	US-11-056-355B-91717	Sequence 91717, A
479	63	5.2	212	7	US-11-056-355B-95473	Sequence 95473, A
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482	63	5.2	213	7	US-11-106-762-3	Sequence 3, Appli
483	63	5.2	213	7	US-11-106-762-24	Sequence 24, Appl
484	63	5.2	213	7	US-11-106-762-33	Sequence 33, Appl
485	63	5.2	213	7	US-11-106-762-35	Sequence 35, Appl
486	63	5.2	213	7	US-11-106-762-38	Sequence 38, Appl
487	63	5.2	213	7	US-11-238-281-13	Sequence 13, Appl
488	63	5.2	213	7	US-11-238-281-28	Sequence 28, Appl
489	63	5.2	213	7	US-11-238-281-30	Sequence 30, Appl
490	63	5.2	213	7	US-11-332-194-3	Sequence 3, Appli
491	63	5.2	213	7	US-11-332-194-8	Sequence 8, Appli
492	63	5.2	213	7	US-11-332-194-13	Sequence 13, Appl
493	63	5.2	213	7	US-11-332-194-16	Sequence 16, Appl
494	63	5.2	213	7	US-11-403-462-13	Sequence 13, Appl
495	63	5.2	213	7	US-11-403-462-15	Sequence 15, Appl
496	63	5.2	213	7	US-11-407-726-13	Sequence 13, Appl
497	63	5.2	213	7	US-11-407-726-15	Sequence 15, Appl
498	63	5.2	213	7	US-11-439-906-3	Sequence 3, Appli
499	63	5.2	213	7	US-11-348-609-13	Sequence 13, Appl
500	63	5.2	213	7	US-11-348-609-18	Sequence 18, Appl
501	63	5.2	213	7	US-11-348-609-23	Sequence 23, Appl
502	63	5.2	213	7	US-11-348-609-26	Sequence 26, Appl
503	63	5.2	232	6	US-10-509-131-45	Sequence 45, Appl
504	63	5.2	232	7	US-11-106-762-23	Sequence 23, Appl
505	63	5.2	232	7	US-11-291-698A-56	Sequence 56, Appl
506	63	5.2	232	7	US-11-330-403-14995	Sequence 14995, A
507	63	5.2	263	6	US-10-953-349-6420	Sequence 6420, Ap
508	63	5.2	263	7	US-11-056-355B-41151	Sequence 41151, A
509	63	5.2	263	7	US-11-056-355B-104006	Sequence 104006,
510	63	5.2	263	7	US-11-056-355B-115245	Sequence 115245,
511	63	5.2	271	7	US-11-293-697-3657	Sequence 3657, Ap
512	63	5.2	299	6	US-10-449-902-29085	Sequence 29085, A
513	63	5.2	302	6	US-10-953-349-6419	Sequence 6419, Ap
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519	63	5.2	333	7	US-11-056-355B-91716	Sequence 91716, A
520	63	5.2	333	7	US-11-056-355B-95472	Sequence 95472, A
521	63	5.2	333	7	US-11-056-355B-104220	Sequence 104220,
522	63	5.2	333	7	US-11-056-355B-115459	Sequence 115459,
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524	63	5.2	348	7	US-11-056-355B-104219	Sequence 104219,
525	63	5.2	348	7	US-11-056-355B-115458	Sequence 115458,
526	63	5.2	349	7	US-11-056-355B-42183	Sequence 42183, A
527	63	5.2	349	7	US-11-056-355B-104218	Sequence 104218,
528	63	5.2	349	7	US-11-056-355B-115457	Sequence 115457,
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533	63	5.2	418	6	US-10-374-780A-2592	Sequence 2592, Ap
534	63	5.2	517	7	US-11-056-355B-42672	Sequence 42672, A
535	63	5.2	517	7	US-11-056-355B-45760	Sequence 45760, A
536	63	5.2	517	7	US-11-056-355B-49436	Sequence 49436, A
537	63	5.2	517	7	US-11-056-355B-76765	Sequence 76765, A
538	63	5.2	518	7	US-11-056-355B-42671	Sequence 42671, A
539	63	5.2	518	7	US-11-056-355B-45759	Sequence 45759, A
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543	63	5.2	532	6	US-10-374-780A-2290	Sequence 2290, Ap

544	63	5.2	532	7	US-11-056-355B-76763	Sequence 76763, A
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546	63	5.2	533	7	US-11-056-355B-45758	Sequence 45758, A
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549	63	5.2	572	7	US-11-208-544-2	Sequence 2, Appli
550	63	5.2	616	7	US-11-056-355B-86798	Sequence 86798, A
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552	63	5.2	688	7	US-11-056-355B-86797	Sequence 86797, A
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555	63	5.2	746	7	US-11-056-355B-87569	Sequence 87569, A
556	63	5.2	770	6	US-10-449-902-46147	Sequence 46147, A
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558	63	5.2	832	6	US-10-449-902-45254	Sequence 45254, A
559	63	5.2	896	7	US-11-056-355B-86796	Sequence 86796, A
560	63	5.2	919	7	US-11-056-355B-80540	Sequence 80540, A
561	63	5.2	921	7	US-11-056-355B-80539	Sequence 80539, A
562	63	5.2	974	7	US-11-330-403-5381	Sequence 5381, Ap
563	63	5.2	974	7	US-11-330-403-9008	Sequence 9008, Ap
564	63	5.2	1134	6	US-10-833-833-169	Sequence 169, App
565	63	5.2	1233	7	US-11-324-768-7	Sequence 7, Appli
566	63	5.2	1243	7	US-11-324-768-8	Sequence 8, Appli
567	62.5	5.1	128	6	US-10-953-349-37107	Sequence 37107, A
568	62.5	5.1	164	6	US-10-953-349-37106	Sequence 37106, A
569	62.5	5.1	206	7	US-11-489-391-64	Sequence 64, Appl
570	62.5	5.1	233	6	US-10-526-324-2072	Sequence 2072, Ap
571	62.5	5.1	251	7	US-11-330-403-6013	Sequence 6013, Ap
572	62.5	5.1	297	6	US-10-511-937-2997	Sequence 2997, Ap
573	62.5	5.1	297	7	US-11-291-698A-40	Sequence 40, Appl
574	62.5	5.1	297	7	US-11-347-766-40	Sequence 40, Appl
575	62.5	5.1	297	7	US-11-316-370-1	Sequence 1, Appli
576	62.5	5.1	297	7	US-11-323-325-5	Sequence 5, Appli
577	62.5	5.1	305	7	US-11-265-762-104	Sequence 104, App
578	62.5	5.1	305	7	US-11-265-762-120	Sequence 120, App
579	62.5	5.1	306	6	US-10-953-349-21237	Sequence 21237, A
580	62.5	5.1	306	7	US-11-056-355B-52900	Sequence 52900, A
581	62.5	5.1	315	7	US-11-339-733-4	Sequence 4, Appli
582	62.5	5.1	334	7	US-11-056-355B-10038	Sequence 10038, A
583	62.5	5.1	335	6	US-10-953-349-21236	Sequence 21236, A
584	62.5	5.1	335	7	US-11-056-355B-52899	Sequence 52899, A
585	62.5	5.1	354	7	US-11-056-355B-10037	Sequence 10037, A
586	62.5	5.1	355	6	US-10-471-571A-4160	Sequence 4160, Ap
587	62.5	5.1	376	7	US-11-056-355B-10036	Sequence 10036, A
588	62.5	5.1	379	6	US-10-805-394-3656	Sequence 3656, Ap
589	62.5	5.1	386	7	US-11-441-587-6	Sequence 6, Appli
590	62.5	5.1	386	7	US-11-240-891-29	Sequence 29, Appl
591	62.5	5.1	408	7	US-11-330-403-5580	Sequence 5580, Ap
592	62.5	5.1	411	7	US-11-330-403-6515	Sequence 6515, Ap
593	62.5	5.1	413	6	US-10-530-187-262	Sequence 262, App
594	62.5	5.1	426	6	US-10-953-349-21235	Sequence 21235, A
595	62.5	5.1	426	7	US-11-056-355B-52898	Sequence 52898, A
596	62.5	5.1	448	7	US-11-056-355B-81526	Sequence 81526, A
597	62.5	5.1	487	7	US-11-330-403-18566	Sequence 18566, A
598	62.5	5.1	496	7	US-11-056-355B-81525	Sequence 81525, A
599	62.5	5.1	502	7	US-11-056-355B-81524	Sequence 81524, A
600	62.5	5.1	548	7	US-11-056-355B-106604	Sequence 106604,
601	62.5	5.1	548	7	US-11-056-355B-117843	Sequence 117843,
602	62.5	5.1	710	6	US-10-449-902-52297	Sequence 52297, A
603	62.5	5.1	727	7	US-11-330-403-4392	Sequence 4392, Ap
604	62.5	5.1	800	6	US-10-449-902-41601	Sequence 41601, A
605	62.5	5.1	805	7	US-11-386-937-19	Sequence 19, Appl
606	62.5	5.1	862	6	US-10-805-394-3956	Sequence 3956, Ap
607	62.5	5.1	1079	7	US-11-242-079-8	Sequence 8, Appli
608	62	5.1	183	7	US-11-434-137-4894	Sequence 4894, Ap
609	62	5.1	183	7	US-11-434-184-4894	Sequence 4894, Ap
610	62	5.1	183	7	US-11-434-199-4894	Sequence 4894, Ap
611	62	5.1	183	7	US-11-434-203-4894	Sequence 4894, Ap
612	62	5.1	204	7	US-11-056-355B-49059	Sequence 49059, A
613	62	5.1	214	6	US-10-515-429-72	Sequence 72, Appl
614	62	5.1	230	7	US-11-101-316-80	Sequence 80, Appl
615	62	5.1	230	7	US-11-376-673-80	Sequence 80, Appl
616	62	5.1	230	7	US-11-271-357-186	Sequence 186, App
617	62	5.1	230	7	US-11-366-486-840	Sequence 840, App
618	62	5.1	237	6	US-10-449-902-47644	Sequence 47644, A
619	62	5.1	250	6	US-10-449-902-53359	Sequence 53359, A
620	62	5.1	251	6	US-10-449-902-30589	Sequence 30589, A
621	62	5.1	272	7	US-11-056-355B-49058	Sequence 49058, A
622	62	5.1	272	7	US-11-330-403-223	Sequence 223, App
623	62	5.1	279	7	US-11-056-355B-100101	Sequence 100101,
624	62	5.1	279	7	US-11-056-355B-111340	Sequence 111340,
625	62	5.1	346	7	US-11-056-355B-72070	Sequence 72070, A
626	62	5.1	351	7	US-11-330-403-6521	Sequence 6521, Ap
627	62	5.1	353	7	US-11-056-355B-72069	Sequence 72069, A
628	62	5.1	364	7	US-11-056-355B-45410	Sequence 45410, A
629	62	5.1	364	7	US-11-056-355B-72068	Sequence 72068, A
630	62	5.1	365	7	US-11-056-355B-45409	Sequence 45409, A
631	62	5.1	394	7	US-11-056-355B-85623	Sequence 85623, A
632	62	5.1	397	7	US-11-056-355B-45408	Sequence 45408, A
633	62	5.1	404	7	US-11-056-355B-47158	Sequence 47158, A
634	62	5.1	404	7	US-11-056-355B-50102	Sequence 50102, A
635	62	5.1	405	6	US-10-449-902-48026	Sequence 48026, A
636	62	5.1	405	7	US-11-330-403-9230	Sequence 9230, Ap
637	62	5.1	405	7	US-11-330-403-18961	Sequence 18961, A
638	62	5.1	406	6	US-10-953-349-14270	Sequence 14270, A
639	62	5.1	414	7	US-11-330-403-15640	Sequence 15640, A
640	62	5.1	416	7	US-11-330-403-8958	Sequence 8958, Ap
641	62	5.1	419	6	US-10-953-349-14269	Sequence 14269, A
642	62	5.1	427	7	US-11-056-355B-85622	Sequence 85622, A
643	62	5.1	432	7	US-11-056-355B-85621	Sequence 85621, A
644	62	5.1	445	7	US-11-056-355B-87703	Sequence 87703, A
645	62	5.1	477	6	US-10-449-902-48148	Sequence 48148, A
646	62	5.1	492	7	US-11-285-701-23	Sequence 23, Appl
647	62	5.1	492	7	US-11-056-355B-47157	Sequence 47157, A
648	62	5.1	492	7	US-11-056-355B-50101	Sequence 50101, A
649	62	5.1	507	7	US-11-056-355B-47156	Sequence 47156, A
650	62	5.1	507	7	US-11-056-355B-50100	Sequence 50100, A
651	62	5.1	516	7	US-11-330-403-4196	Sequence 4196, Ap
652	62	5.1	546	6	US-10-449-902-42886	Sequence 42886, A
653	62	5.1	583	7	US-11-330-403-6772	Sequence 6772, Ap
654	62	5.1	774	6	US-10-449-902-41096	Sequence 41096, A
655	62	5.1	794	6	US-10-953-349-9558	Sequence 9558, Ap
656	62	5.1	877	7	US-11-056-355B-39835	Sequence 39835, A
657	62	5.1	877	7	US-11-056-355B-44815	Sequence 44815, A
658	62	5.1	885	7	US-11-056-355B-39834	Sequence 39834, A
659	62	5.1	885	7	US-11-056-355B-44814	Sequence 44814, A
660	62	5.1	949	7	US-11-056-355B-39833	Sequence 39833, A
661	62	5.1	949	7	US-11-056-355B-44813	Sequence 44813, A
662	62	5.1	962	6	US-10-805-394-3800	Sequence 3800, Ap
663	62	5.1	1012	6	US-10-669-920-1201	Sequence 1201, Ap
664	61.5	5.1	122	7	US-11-293-697-4395	Sequence 4395, Ap
665	61.5	5.1	157	6	US-10-449-902-39201	Sequence 39201, A
666	61.5	5.1	200	6	US-10-449-902-36578	Sequence 36578, A
667	61.5	5.1	212	6	US-10-449-902-30328	Sequence 30328, A
668	61.5	5.1	246	6	US-10-449-902-44946	Sequence 44946, A
669	61.5	5.1	275	7	US-11-293-697-4717	Sequence 4717, Ap
670	61.5	5.1	291	7	US-11-056-355B-97897	Sequence 97897, A
671	61.5	5.1	291	7	US-11-056-355B-109136	Sequence 109136,
672	61.5	5.1	292	6	US-10-449-902-51341	Sequence 51341, A
673	61.5	5.1	339	7	US-11-056-355B-102977	Sequence 102977,
674	61.5	5.1	339	7	US-11-056-355B-114216	Sequence 114216,
675	61.5	5.1	350	7	US-11-212-506-6	Sequence 6, Appli
676	61.5	5.1	350	7	US-11-212-506-12	Sequence 12, Appl
677	61.5	5.1	441	6	US-10-449-902-54798	Sequence 54798, A
678	61.5	5.1	441	7	US-11-056-355B-102976	Sequence 102976,
679	61.5	5.1	441	7	US-11-056-355B-114215	Sequence 114215,
680	61.5	5.1	448	7	US-11-056-355B-102975	Sequence 102975,
681	61.5	5.1	448	7	US-11-056-355B-114214	Sequence 114214,
682	61.5	5.1	451	7	US-11-330-403-15320	Sequence 15320, A
683	61.5	5.1	459	7	US-11-271-287-6	Sequence 6, Appli
684	61.5	5.1	464	7	US-11-056-355B-86421	Sequence 86421, A
685	61.5	5.1	473	7	US-11-056-355B-86420	Sequence 86420, A
686	61.5	5.1	491	7	US-11-247-138-2	Sequence 2, Appli
687	61.5	5.1	527	6	US-10-449-902-50024	Sequence 50024, A
688	61.5	5.1	533	6	US-10-553-928-253	Sequence 253, App
689	61.5	5.1	538	6	US-10-449-902-52940	Sequence 52940, A

690	61.5	5.1	538	6	US-10-612-783-6648	Sequence 6648, Ap
691	61.5	5.1	542	7	US-11-440-090-4	Sequence 4, Appli
692	61.5	5.1	569	6	US-10-449-902-54432	Sequence 54432, A
693	61.5	5.1	673	7	US-11-251-208-168	Sequence 168, App
694	61.5	5.1	696	6	US-10-449-902-41608	Sequence 41608, A
695	61.5	5.1	879	7	US-11-226-554-136	Sequence 136, App
696	61.5	5.1	879	7	US-11-248-718-136	Sequence 136, App
697	61.5	5.1	889	6	US-10-449-902-55069	Sequence 55069, A
698	61.5	5.1	889	6	US-10-449-902-55493	Sequence 55493, A
699	61.5	5.1	973	6	US-10-449-902-45586	Sequence 45586, A
700	61.5	5.1	1294	6	US-10-612-783-6698	Sequence 6698, Ap
701	61	5.0	108	6	US-10-805-394-3790	Sequence 3790, Ap
702	61	5.0	137	6	US-10-471-571A-5218	Sequence 5218, Ap
703	61	5.0	160	6	US-10-953-349-25835	Sequence 25835, A
704	61	5.0	173	7	US-11-056-355B-8554	Sequence 8554, Ap
705	61	5.0	174	7	US-11-293-697-4760	Sequence 4760, Ap
706	61	5.0	177	7	US-11-056-355B-8553	Sequence 8553, Ap
707	61	5.0	190	6	US-10-953-349-25834	Sequence 25834, A
708	61	5.0	194	7	US-11-056-355B-8552	Sequence 8552, Ap
709	61	5.0	194	7	US-11-366-965-469	Sequence 469, App
710	61	5.0	204	6	US-10-953-349-2522	Sequence 2522, Ap
711	61	5.0	204	7	US-11-056-355B-36397	Sequence 36397, A
712	61	5.0	204	7	US-11-056-355B-102176	Sequence 102176,
713	61	5.0	204	7	US-11-056-355B-113415	Sequence 113415,
714	61	5.0	220	7	US-11-229-770-1129	Sequence 1129, Ap
715	61	5.0	225	6	US-10-953-349-2521	Sequence 2521, Ap
716	61	5.0	225	7	US-11-056-355B-36396	Sequence 36396, A
717	61	5.0	225	7	US-11-056-355B-102175	Sequence 102175,
718	61	5.0	225	7	US-11-056-355B-113414	Sequence 113414,
719	61	5.0	225	7	US-11-330-403-10854	Sequence 10854, A
720	61	5.0	228	7	US-11-330-403-12241	Sequence 12241, A
721	61	5.0	236	6	US-10-953-349-2520	Sequence 2520, Ap
722	61	5.0	236	7	US-11-056-355B-36395	Sequence 36395, A
723	61	5.0	236	7	US-11-056-355B-102174	Sequence 102174,
724	61	5.0	236	7	US-11-056-355B-113413	Sequence 113413,
725	61	5.0	247	7	US-11-434-137-10228	Sequence 10228, A
726	61	5.0	247	7	US-11-434-184-10228	Sequence 10228, A
727	61	5.0	247	7	US-11-434-199-10228	Sequence 10228, A
728	61	5.0	247	7	US-11-434-203-10228	Sequence 10228, A
729	61	5.0	251	6	US-10-471-571A-4658	Sequence 4658, Ap
730	61	5.0	253	7	US-11-434-137-1844	Sequence 1844, Ap
731	61	5.0	253	7	US-11-434-184-1844	Sequence 1844, Ap
732	61	5.0	253	7	US-11-434-199-1844	Sequence 1844, Ap
733	61	5.0	253	7	US-11-434-203-1844	Sequence 1844, Ap
734	61	5.0	269	6	US-10-471-571A-4828	Sequence 4828, Ap
735	61	5.0	274	7	US-11-330-403-17424	Sequence 17424, A
736	61	5.0	292	6	US-10-953-349-18698	Sequence 18698, A
737	61	5.0	312	7	US-11-330-403-3565	Sequence 3565, Ap
738	61	5.0	318	7	US-11-056-355B-91358	Sequence 91358, A
739	61	5.0	318	7	US-11-056-355B-95114	Sequence 95114, A
740	61	5.0	321	6	US-10-953-349-25001	Sequence 25001, A
741	61	5.0	321	7	US-11-056-355B-57855	Sequence 57855, A
742	61	5.0	328	6	US-10-471-571A-4218	Sequence 4218, Ap
743	61	5.0	333	7	US-11-056-355B-91357	Sequence 91357, A
744	61	5.0	333	7	US-11-056-355B-95113	Sequence 95113, A
745	61	5.0	337	7	US-11-056-355B-91356	Sequence 91356, A
746	61	5.0	337	7	US-11-056-355B-95112	Sequence 95112, A
747	61	5.0	344	7	US-11-330-403-9125	Sequence 9125, Ap
748	61	5.0	358	7	US-11-090-997-1892	Sequence 1892, Ap
749	61	5.0	365	6	US-10-612-783-4895	Sequence 4895, Ap
750	61	5.0	390	7	US-11-056-355B-102212	Sequence 102212,
751	61	5.0	390	7	US-11-056-355B-113451	Sequence 113451,
752	61	5.0	402	6	US-10-471-571A-4282	Sequence 4282, Ap
753	61	5.0	418	6	US-10-953-349-8976	Sequence 8976, Ap
754	61	5.0	428	7	US-11-330-403-3134	Sequence 3134, Ap
755	61	5.0	443	7	US-11-317-789A-770	Sequence 770, App
756	61	5.0	445	7	US-11-330-403-15968	Sequence 15968, A
757	61	5.0	460	7	US-11-056-355B-1752	Sequence 1752, Ap
758	61	5.0	465	7	US-11-330-403-16786	Sequence 16786, A
759	61	5.0	467	7	US-11-051-725-129	Sequence 129, App
760	61	5.0	469	6	US-10-953-349-18697	Sequence 18697, A
761	61	5.0	485	7	US-11-051-725-154	Sequence 154, App
762	61	5.0	485	7	US-11-051-725-170	Sequence 170, App
763	61	5.0	502	7	US-11-056-355B-86994	Sequence 86994, A
764	61	5.0	506	7	US-11-056-355B-96895	Sequence 96895, A
765	61	5.0	512	7	US-11-056-355B-1751	Sequence 1751, Ap
766	61	5.0	513	7	US-11-056-355B-1750	Sequence 1750, Ap
767	61	5.0	514	6	US-10-539-228-831	Sequence 831, App
768	61	5.0	532	6	US-10-953-349-5123	Sequence 5123, Ap
769	61	5.0	535	7	US-11-056-355B-96894	Sequence 96894, A
770	61	5.0	555	7	US-11-330-403-6828	Sequence 6828, Ap
771	61	5.0	558	7	US-11-051-725-137	Sequence 137, App
772	61	5.0	564	6	US-10-547-975-4	Sequence 4, Appli
773	61	5.0	569	6	US-10-449-902-36835	Sequence 36835, A
774	61	5.0	569	6	US-10-449-902-48588	Sequence 48588, A
775	61	5.0	569	6	US-10-449-902-50106	Sequence 50106, A
776	61	5.0	569	6	US-10-449-902-50472	Sequence 50472, A
777	61	5.0	574	7	US-11-208-544-4	Sequence 4, Appli
778	61	5.0	574	7	US-11-208-544-6	Sequence 6, Appli
779	61	5.0	581	7	US-11-226-554-153	Sequence 153, App
780	61	5.0	581	7	US-11-248-718-153	Sequence 153, App
781	61	5.0	616	7	US-11-056-355B-100223	Sequence 100223,
782	61	5.0	616	7	US-11-056-355B-111462	Sequence 111462,
783	61	5.0	636	7	US-11-056-355B-86993	Sequence 86993, A
784	61	5.0	639	7	US-11-056-355B-86992	Sequence 86992, A
785	61	5.0	641	7	US-11-056-355B-80823	Sequence 80823, A
786	61	5.0	656	6	US-10-449-902-53611	Sequence 53611, A
787	61	5.0	685	7	US-11-056-355B-100222	Sequence 100222,
788	61	5.0	685	7	US-11-056-355B-111461	Sequence 111461,
789	61	5.0	717	7	US-11-056-355B-100221	Sequence 100221,
790	61	5.0	717	7	US-11-056-355B-111460	Sequence 111460,
791	61	5.0	771	6	US-10-199-229-16	Sequence 16, Appl
792	61	5.0	932	7	US-11-051-725-133	Sequence 133, App
793	61	5.0	989	7	US-11-051-725-4	Sequence 4, Appli
794	61	5.0	1765	7	US-11-324-768-5	Sequence 5, Appli
795	61	5.0	2105	7	US-11-051-725-9	Sequence 9, Appli
796	61	5.0	2123	7	US-11-051-725-180	Sequence 180, App
797	61	5.0	2138	6	US-10-543-503-124	Sequence 124, App
798	61	5.0	2169	7	US-11-051-725-5	Sequence 5, Appli
799	61	5.0	2182	7	US-11-051-725-8	Sequence 8, Appli
800	61	5.0	2192	7	US-11-051-725-147	Sequence 147, App
801	61	5.0	2221	6	US-10-829-000-3	Sequence 3, Appli
802	61	5.0	2221	7	US-11-051-725-162	Sequence 162, App
803	60.5	5.0	167	7	US-11-056-355B-22974	Sequence 22974, A
804	60.5	5.0	167	7	US-11-056-355B-99674	Sequence 99674, A
805	60.5	5.0	167	7	US-11-056-355B-110913	Sequence 110913,
806	60.5	5.0	189	6	US-10-449-902-39228	Sequence 39228, A
807	60.5	5.0	199	6	US-10-449-902-41625	Sequence 41625, A
808	60.5	5.0	211	7	US-11-441-587-18	Sequence 18, Appl
809	60.5	5.0	243	6	US-10-449-902-28973	Sequence 28973, A
810	60.5	5.0	255	6	US-10-953-349-31570	Sequence 31570, A
811	60.5	5.0	255	7	US-11-056-355B-66510	Sequence 66510, A
812	60.5	5.0	302	7	US-11-293-697-2659	Sequence 2659, Ap
813	60.5	5.0	305	6	US-10-471-571A-4220	Sequence 4220, Ap
814	60.5	5.0	305	7	US-11-056-355B-86557	Sequence 86557, A
815	60.5	5.0	311	6	US-10-953-349-21965	Sequence 21965, A
816	60.5	5.0	312	7	US-11-056-355B-86556	Sequence 86556, A
817	60.5	5.0	318	6	US-10-953-349-2122	Sequence 2122, Ap
818	60.5	5.0	319	6	US-10-539-377-2	Sequence 2, Appli
819	60.5	5.0	321	6	US-10-953-349-21964	Sequence 21964, A
820	60.5	5.0	324	7	US-11-056-355B-2880	Sequence 2880, Ap
821	60.5	5.0	334	7	US-11-317-789A-944	Sequence 944, App
822	60.5	5.0	340	7	US-11-056-355B-86555	Sequence 86555, A
823	60.5	5.0	344	7	US-11-056-355B-69786	Sequence 69786, A
824	60.5	5.0	345	7	US-11-056-355B-2879	Sequence 2879, Ap
825	60.5	5.0	352	7	US-11-056-355B-42259	Sequence 42259, A
826	60.5	5.0	352	7	US-11-056-355B-99986	Sequence 99986, A
827	60.5	5.0	352	7	US-11-056-355B-111225	Sequence 111225,
828	60.5	5.0	357	7	US-11-056-355B-42258	Sequence 42258, A
829	60.5	5.0	357	7	US-11-056-355B-99985	Sequence 99985, A
830	60.5	5.0	357	7	US-11-056-355B-111224	Sequence 111224,
831	60.5	5.0	363	6	US-10-953-349-2121	Sequence 2121, Ap
832	60.5	5.0	365	6	US-10-953-349-4614	Sequence 4614, Ap
833	60.5	5.0	365	7	US-11-056-355B-39429	Sequence 39429, A
834	60.5	5.0	371	7	US-11-056-355B-2878	Sequence 2878, Ap
835	60.5	5.0	381	6	US-10-496-164-50	Sequence 50, Appl

836	60.5	5.0	383	6	US-10-953-349-5125	Sequence 5125, Ap
837	60.5	5.0	383	7	US-11-056-355B-42257	Sequence 42257, A
838	60.5	5.0	383	7	US-11-056-355B-99984	Sequence 99984, A
839	60.5	5.0	383	7	US-11-056-355B-111223	Sequence 111223,
840	60.5	5.0	390	6	US-10-953-349-2120	Sequence 2120, Ap
841	60.5	5.0	390	7	US-11-056-355B-97731	Sequence 97731, A
842	60.5	5.0	390	7	US-11-056-355B-108970	Sequence 108970,
843	60.5	5.0	393	7	US-11-056-355B-54432	Sequence 54432, A
844	60.5	5.0	397	6	US-10-449-902-33856	Sequence 33856, A
845	60.5	5.0	397	6	US-10-449-902-44582	Sequence 44582, A
846	60.5	5.0	397	6	US-10-612-783-6786	Sequence 6786, Ap
847	60.5	5.0	398	7	US-11-056-355B-54431	Sequence 54431, A
848	60.5	5.0	401	6	US-10-953-349-31569	Sequence 31569, A
849	60.5	5.0	401	6	US-10-612-783-3761	Sequence 3761, Ap
850	60.5	5.0	401	7	US-11-056-355B-66509	Sequence 66509, A
851	60.5	5.0	401	7	US-11-330-403-19198	Sequence 19198, A
852	60.5	5.0	409	6	US-10-953-349-5124	Sequence 5124, Ap
853	60.5	5.0	416	6	US-10-953-349-4613	Sequence 4613, Ap
854	60.5	5.0	416	7	US-11-056-355B-39428	Sequence 39428, A
855	60.5	5.0	439	6	US-10-953-349-2086	Sequence 2086, Ap
856	60.5	5.0	441	6	US-10-449-902-42651	Sequence 42651, A
857	60.5	5.0	449	7	US-11-174-307B-4758	Sequence 4758, Ap
858	60.5	5.0	451	6	US-10-953-349-4612	Sequence 4612, Ap
859	60.5	5.0	451	7	US-11-056-355B-39427	Sequence 39427, A
860	60.5	5.0	463	6	US-10-953-349-31568	Sequence 31568, A
861	60.5	5.0	463	7	US-11-056-355B-66508	Sequence 66508, A
862	60.5	5.0	531	6	US-10-953-349-2085	Sequence 2085, Ap
863	60.5	5.0	595	6	US-10-553-298-9	Sequence 9, Appli
864	60.5	5.0	678	6	US-10-449-902-52824	Sequence 52824, A
865	60.5	5.0	678	6	US-10-449-902-53058	Sequence 53058, A
866	60.5	5.0	678	7	US-11-056-355B-71572	Sequence 71572, A
867	60.5	5.0	681	7	US-11-485-158-2	Sequence 2, Appli
868	60.5	5.0	719	7	US-11-056-355B-71571	Sequence 71571, A
869	60.5	5.0	805	6	US-10-530-187-241	Sequence 241, App
870	60.5	5.0	928	7	US-11-343-271-8	Sequence 8, Appli
871	60.5	5.0	1199	7	US-11-056-355B-83585	Sequence 83585, A
872	60.5	5.0	1213	7	US-11-056-355B-83584	Sequence 83584, A
873	60.5	5.0	1245	7	US-11-056-355B-83583	Sequence 83583, A
874	60.5	5.0	1693	7	US-11-174-307B-4190	Sequence 4190, Ap
875	60.5	5.0	2307	7	US-11-335-891-33	Sequence 33, Appl
876	60	4.9	134	6	US-10-805-394-3722	Sequence 3722, Ap
877	60	4.9	137	6	US-10-449-902-38787	Sequence 38787, A
878	60	4.9	157	6	US-10-953-349-16183	Sequence 16183, A
879	60	4.9	173	7	US-11-056-355B-7122	Sequence 7122, Ap
880	60	4.9	177	7	US-11-056-355B-7121	Sequence 7121, Ap
881	60	4.9	190	7	US-11-056-355B-3897	Sequence 3897, Ap
882	60	4.9	190	7	US-11-056-355B-10299	Sequence 10299, A
883	60	4.9	190	7	US-11-056-355B-13118	Sequence 13118, A
884	60	4.9	194	7	US-11-056-355B-7120	Sequence 7120, Ap
885	60	4.9	198	7	US-11-330-403-4459	Sequence 4459, Ap
888	60	4.9	211	7	US-11-441-587-4	Sequence 4, Appli
889	60	4.9	214	7	US-11-219-121-27	Sequence 27, Appl
890	60	4.9	223	6	US-10-449-902-39181	Sequence 39181, A
891	60	4.9	227	7	US-11-326-148-6	Sequence 6, Appli
892	60	4.9	227	7	US-11-366-331-6	Sequence 6, Appli
893	60	4.9	227	7	US-11-364-102-10	Sequence 10, Appl
894	60	4.9	228	7	US-11-330-403-11438	Sequence 11438, A
895	60	4.9	234	7	US-11-375-221-12	Sequence 12, Appl
896	60	4.9	234	7	US-11-330-403-19028	Sequence 19028, A
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898	60	4.9	247	7	US-11-337-300-96	Sequence 96, Appl
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902	60	4.9	259	6	US-10-449-902-49775	Sequence 49775, A
903	60	4.9	259	6	US-10-449-902-53081	Sequence 53081, A
904	60	4.9	259	6	US-10-612-783-6830	Sequence 6830, Ap
905	60	4.9	259	7	US-11-330-403-4432	Sequence 4432, Ap
906	60	4.9	259	7	US-11-330-403-10905	Sequence 10905, A
907	60	4.9	277	6	US-10-449-902-41727	Sequence 41727, A
908	60	4.9	279	7	US-11-056-355B-30231	Sequence 30231, A
909	60	4.9	279	7	US-11-056-355B-33821	Sequence 33821, A
910	60	4.9	281	6	US-10-805-394-4971	Sequence 4971, Ap
911	60	4.9	283	6	US-10-570-909-33	Sequence 33, Appl
912	60	4.9	283	6	US-10-570-909-114	Sequence 114, App
913	60	4.9	283	7	US-11-105-233-161	Sequence 161, App
914	60	4.9	283	7	US-11-226-554-124	Sequence 124, App
915	60	4.9	283	7	US-11-248-718-124	Sequence 124, App
916	60	4.9	306	7	US-11-056-355B-5754	Sequence 5754, Ap
917	60	4.9	308	6	US-10-449-902-38607	Sequence 38607, A
918	60	4.9	308	7	US-11-056-355B-30230	Sequence 30230, A
919	60	4.9	308	7	US-11-056-355B-33820	Sequence 33820, A
920	60	4.9	328	6	US-10-449-902-56550	Sequence 56550, A
921	60	4.9	333	6	US-10-805-394-5365	Sequence 5365, Ap
922	60	4.9	344	6	US-10-526-324-460	Sequence 460, App
923	60	4.9	356	7	US-11-330-403-8931	Sequence 8931, Ap
924	60	4.9	377	7	US-11-056-355B-42862	Sequence 42862, A
925	60	4.9	395	7	US-11-056-355B-5753	Sequence 5753, Ap
926	60	4.9	395	7	US-11-330-403-15588	Sequence 15588, A
927	60	4.9	402	6	US-10-530-187-264	Sequence 264, App
928	60	4.9	418	6	US-10-449-902-34462	Sequence 34462, A
929	60	4.9	418	6	US-10-449-902-56242	Sequence 56242, A
930	60	4.9	425	6	US-10-449-902-37011	Sequence 37011, A
931	60	4.9	425	6	US-10-449-902-49196	Sequence 49196, A
932	60	4.9	455	7	US-11-330-403-6849	Sequence 6849, Ap
933	60	4.9	465	7	US-11-330-403-13465	Sequence 13465, A
934	60	4.9	491	7	US-11-174-307B-4448	Sequence 4448, Ap
935	60	4.9	503	6	US-10-612-783-3949	Sequence 3949, Ap
936	60	4.9	505	7	US-11-056-355B-96638	Sequence 96638, A
937	60	4.9	530	6	US-10-449-902-42736	Sequence 42736, A
938	60	4.9	530	6	US-10-612-783-4594	Sequence 4594, Ap
939	60	4.9	530	6	US-10-612-783-6768	Sequence 6768, Ap
940	60	4.9	534	7	US-11-056-355B-96637	Sequence 96637, A
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942	60	4.9	553	6	US-10-953-349-35588	Sequence 35588, A
943	60	4.9	586	7	US-11-056-355B-99113	Sequence 99113, A
944	60	4.9	586	7	US-11-056-355B-110352	Sequence 110352,
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946	60	4.9	590	7	US-11-094-278-14	Sequence 14, Appl
947	60	4.9	599	6	US-10-953-349-34642	Sequence 34642, A
948	60	4.9	601	6	US-10-953-349-35587	Sequence 35587, A
949	60	4.9	617	7	US-11-056-355B-75247	Sequence 75247, A
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951	60	4.9	676	7	US-11-056-355B-81079	Sequence 81079, A
952	60	4.9	680	6	US-10-953-349-4448	Sequence 4448, Ap
953	60	4.9	680	7	US-11-056-355B-39645	Sequence 39645, A
954	60	4.9	680	7	US-11-056-355B-81078	Sequence 81078, A
955	60	4.9	680	7	US-11-056-355B-99511	Sequence 99511, A
956	60	4.9	680	7	US-11-056-355B-110750	Sequence 110750,
957	60	4.9	705	6	US-10-449-902-42328	Sequence 42328, A
958	60	4.9	717	6	US-10-953-349-4447	Sequence 4447, Ap
959	60	4.9	717	7	US-11-056-355B-39644	Sequence 39644, A
960	60	4.9	717	7	US-11-056-355B-99510	Sequence 99510, A
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962	60	4.9	738	6	US-10-953-349-4446	Sequence 4446, Ap
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965	60	4.9	738	7	US-11-056-355B-110748	Sequence 110748,
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967	60	4.9	880	7	US-11-056-355B-106688	Sequence 106688,
968	60	4.9	880	7	US-11-056-355B-117927	Sequence 117927,
969	60	4.9	888	7	US-11-056-355B-106687	Sequence 106687,
970	60	4.9	888	7	US-11-056-355B-117926	Sequence 117926,
971	60	4.9	896	6	US-10-449-902-42268	Sequence 42268, A
972	60	4.9	960	7	US-11-056-355B-106686	Sequence 106686,
973	60	4.9	960	7	US-11-056-355B-117925	Sequence 117925,
974	60	4.9	1012	7	US-11-330-403-14060	Sequence 14060, A
975	60	4.9	1019	6	US-10-805-394-6499	Sequence 6499, Ap
976	60	4.9	1080	7	US-11-056-355B-69790	Sequence 69790, A
977	60	4.9	1097	7	US-11-056-355B-69789	Sequence 69789, A
978	60	4.9	1128	7	US-11-056-355B-69788	Sequence 69788, A
979	60	4.9	1373	7	US-11-056-355B-88967	Sequence 88967, A
980	60	4.9	1373	7	US-11-056-355B-92723	Sequence 92723, A
981	60	4.9	1409	7	US-11-056-355B-88966	Sequence 88966, A
982	60	4.9	1409	7	US-11-056-355B-92722	Sequence 92722, A
983	60	4.9	1487	7	US-11-056-355B-88965	Sequence 88965, A

984	60	4.9	1487	7	US-11-056-355B-92721	Sequence 92721, A
985	60	4.9	2162	6	US-10-669-920-1219	Sequence 1219, Ap
986	59.5	4.9	176	7	US-11-056-355B-91718	Sequence 91718, A
987	59.5	4.9	176	7	US-11-056-355B-95474	Sequence 95474, A
988	59.5	4.9	206	7	US-11-056-355B-13923	Sequence 13923, A
989	59.5	4.9	208	7	US-11-395-249-22	Sequence 22, Appl
990	59.5	4.9	213	6	US-10-515-429-73	Sequence 73, Appl
991	59.5	4.9	235	7	US-11-375-221-32	Sequence 32, Appl
992	59.5	4.9	238	6	US-10-449-902-30619	Sequence 30619, A
993	59.5	4.9	238	6	US-10-449-902-31961	Sequence 31961, A
994	59.5	4.9	238	6	US-10-449-902-48149	Sequence 48149, A
995	59.5	4.9	244	6	US-10-526-324-950	Sequence 950, App
996	59.5	4.9	289	6	US-10-449-902-39555	Sequence 39555, A
997	59.5	4.9	297	7	US-11-056-355B-3542	Sequence 3542, Ap
998	59.5	4.9	314	7	US-11-056-355B-3541	Sequence 3541, Ap
999	59.5	4.9	330	7	US-11-056-355B-41942	Sequence 41942, A
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1001	59.5	4.9	361	7	US-11-056-355B-103244	Sequence 103244,
1002	59.5	4.9	361	7	US-11-056-355B-114483	Sequence 114483,
1003	59.5	4.9	365	7	US-11-056-355B-103243	Sequence 103243,
1004	59.5	4.9	365	7	US-11-056-355B-114482	Sequence 114482,
1005	59.5	4.9	366	7	US-11-330-403-840	Sequence 840, App
1006	59.5	4.9	373	7	US-11-056-355B-41941	Sequence 41941, A
1007	59.5	4.9	382	7	US-11-056-355B-3540	Sequence 3540, Ap
1008	59.5	4.9	387	7	US-11-056-355B-103242	Sequence 103242,
1009	59.5	4.9	387	7	US-11-056-355B-114481	Sequence 114481,
1010	59.5	4.9	387	7	US-11-330-403-19016	Sequence 19016, A
1011	59.5	4.9	398	7	US-11-330-403-17325	Sequence 17325, A
1012	59.5	4.9	401	7	US-11-226-554-113	Sequence 113, App
1013	59.5	4.9	401	7	US-11-248-718-113	Sequence 113, App
1014	59.5	4.9	408	6	US-10-449-902-37978	Sequence 37978, A
1015	59.5	4.9	408	6	US-10-449-902-49113	Sequence 49113, A
1016	59.5	4.9	408	7	US-11-056-355B-85082	Sequence 85082, A
1017	59.5	4.9	408	7	US-11-330-403-3277	Sequence 3277, Ap
1018	59.5	4.9	409	6	US-10-471-571A-4638	Sequence 4638, Ap
1019	59.5	4.9	409	7	US-11-056-355B-76729	Sequence 76729, A
1020	59.5	4.9	423	6	US-10-449-902-45075	Sequence 45075, A
1021	59.5	4.9	441	6	US-10-449-902-54653	Sequence 54653, A
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1023	59.5	4.9	442	7	US-11-056-355B-21114	Sequence 21114, A
1024	59.5	4.9	447	6	US-10-953-349-32130	Sequence 32130, A
1025	59.5	4.9	447	7	US-11-056-355B-67307	Sequence 67307, A
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1027	59.5	4.9	447	7	US-11-434-184-6446	Sequence 6446, Ap
1028	59.5	4.9	447	7	US-11-434-199-6446	Sequence 6446, Ap
1029	59.5	4.9	447	7	US-11-434-203-6446	Sequence 6446, Ap
1030	59.5	4.9	448	6	US-10-953-349-901	Sequence 901, App
1031	59.5	4.9	448	7	US-11-056-355B-21113	Sequence 21113, A
1032	59.5	4.9	449	6	US-10-449-902-53110	Sequence 53110, A
1033	59.5	4.9	461	7	US-11-434-137-2882	Sequence 2882, Ap
1034	59.5	4.9	461	7	US-11-434-184-2882	Sequence 2882, Ap
1035	59.5	4.9	461	7	US-11-434-199-2882	Sequence 2882, Ap
1036	59.5	4.9	461	7	US-11-434-203-2882	Sequence 2882, Ap
1037	59.5	4.9	464	7	US-11-056-355B-85081	Sequence 85081, A
1038	59.5	4.9	465	7	US-11-366-965-233	Sequence 233, App
1039	59.5	4.9	466	6	US-10-449-902-49928	Sequence 49928, A
1040	59.5	4.9	467	6	US-10-449-902-28716	Sequence 28716, A
1041	59.5	4.9	467	6	US-10-449-902-30001	Sequence 30001, A
1042	59.5	4.9	476	7	US-11-056-355B-85080	Sequence 85080, A
1043	59.5	4.9	478	6	US-10-953-349-32129	Sequence 32129, A
1044	59.5	4.9	478	7	US-11-056-355B-67306	Sequence 67306, A
1045	59.5	4.9	479	7	US-11-056-355B-70749	Sequence 70749, A
1046	59.5	4.9	483	7	US-11-289-102-314	Sequence 314, App
1047	59.5	4.9	483	7	US-11-232-404-45	Sequence 45, Appl
1048	59.5	4.9	483	7	US-11-403-580-5	Sequence 5, Appli
1049	59.5	4.9	483	7	US-11-188-417A-63	Sequence 63, Appl
1050	59.5	4.9	490	6	US-10-953-349-4157	Sequence 4157, Ap
1051	59.5	4.9	490	7	US-11-241-596-50	Sequence 50, Appl
1052	59.5	4.9	490	7	US-11-056-355B-39739	Sequence 39739, A
1053	59.5	4.9	503	6	US-10-526-324-407	Sequence 407, App
1054	59.5	4.9	508	6	US-10-953-349-4156	Sequence 4156, Ap
1055	59.5	4.9	508	7	US-11-241-596-49	Sequence 49, Appl
1056	59.5	4.9	508	7	US-11-056-355B-39738	Sequence 39738, A
1057	59.5	4.9	513	7	US-11-056-355B-51185	Sequence 51185, A
1058	59.5	4.9	520	7	US-11-056-355B-51184	Sequence 51184, A
1059	59.5	4.9	532	7	US-11-056-355B-51183	Sequence 51183, A
1060	59.5	4.9	539	6	US-10-620-061-30	Sequence 30, Appl
1061	59.5	4.9	541	6	US-10-449-902-47071	Sequence 47071, A
1062	59.5	4.9	541	6	US-10-449-902-54067	Sequence 54067, A
1063	59.5	4.9	552	6	US-10-953-349-4155	Sequence 4155, Ap
1064	59.5	4.9	552	7	US-11-241-596-48	Sequence 48, Appl
1065	59.5	4.9	552	7	US-11-056-355B-39737	Sequence 39737, A
1066	59.5	4.9	562	6	US-10-953-349-20235	Sequence 20235, A
1067	59.5	4.9	568	6	US-10-953-349-20234	Sequence 20234, A
1068	59.5	4.9	568	6	US-10-449-902-53241	Sequence 53241, A
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1070	59.5	4.9	588	6	US-10-553-298-11	Sequence 11, Appl
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1073	59.5	4.9	595	6	US-10-553-298-4	Sequence 4, Appli
1074	59.5	4.9	595	6	US-10-553-298-5	Sequence 5, Appli
1075	59.5	4.9	595	6	US-10-553-298-6	Sequence 6, Appli
1076	59.5	4.9	595	6	US-10-553-298-7	Sequence 7, Appli
1077	59.5	4.9	595	6	US-10-553-298-8	Sequence 8, Appli
1078	59.5	4.9	595	6	US-10-553-298-10	Sequence 10, Appl
1079	59.5	4.9	595	6	US-10-553-298-12	Sequence 12, Appl
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1081	59.5	4.9	618	7	US-11-320-412-6	Sequence 6, Appli
1082	59.5	4.9	643	6	US-10-449-902-33120	Sequence 33120, A
1083	59.5	4.9	658	7	US-11-056-355B-50747	Sequence 50747, A
1084	59.5	4.9	662	7	US-11-301-764-5	Sequence 5, Appli
1085	59.5	4.9	662	7	US-11-353-451-8	Sequence 8, Appli
1086	59.5	4.9	685	7	US-11-056-355B-50746	Sequence 50746, A
1087	59.5	4.9	732	7	US-11-353-451-6	Sequence 6, Appli
1088	59.5	4.9	852	6	US-10-725-037-7	Sequence 7, Appli
1089	59.5	4.9	852	6	US-10-725-488-7	Sequence 7, Appli
1090	59.5	4.9	915	6	US-10-540-808-2	Sequence 2, Appli
1091	59.5	4.9	915	6	US-10-540-808-3	Sequence 3, Appli
1092	59.5	4.9	1122	7	US-11-330-403-9440	Sequence 9440, Ap
1093	59.5	4.9	1138	7	US-11-241-596-153	Sequence 153, App
1094	59.5	4.9	1690	7	US-11-241-596-154	Sequence 154, App
1095	59.5	4.9	1690	7	US-11-241-596-155	Sequence 155, App
1096	59.5	4.9	1690	7	US-11-241-596-156	Sequence 156, App
1097	59.5	4.9	1690	7	US-11-241-596-157	Sequence 157, App
1098	59.5	4.9	2295	6	US-10-543-503-132	Sequence 132, App
1099	59.5	4.9	2412	6	US-10-527-191-70	Sequence 70, Appl
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1101	59	4.9	87	6	US-10-449-902-33711	Sequence 33711, A
1102	59	4.9	136	7	US-11-375-359-115	Sequence 115, App
1103	59	4.9	174	7	US-11-302-607-154	Sequence 154, App
1104	59	4.9	176	6	US-10-449-902-32493	Sequence 32493, A
1105	59	4.9	189	7	US-11-282-117-2	Sequence 2, Appli
1106	59	4.9	202	7	US-11-056-355B-35425	Sequence 35425, A
1107	59	4.9	202	7	US-11-056-355B-47173	Sequence 47173, A
1108	59	4.9	208	6	US-10-471-571A-2762	Sequence 2762, Ap
1109	59	4.9	209	7	US-11-056-355B-35424	Sequence 35424, A
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1112	59	4.9	220	7	US-11-434-184-932	Sequence 932, App
1113	59	4.9	220	7	US-11-434-199-932	Sequence 932, App
1114	59	4.9	220	7	US-11-434-203-932	Sequence 932, App
1115	59	4.9	223	6	US-10-449-902-49000	Sequence 49000, A
1116	59	4.9	224	6	US-10-449-902-30304	Sequence 30304, A
1117	59	4.9	229	7	US-11-056-355B-96876	Sequence 96876, A
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1119	59	4.9	234	6	US-10-560-723-180	Sequence 180, App
1120	59	4.9	234	7	US-11-211-917-88	Sequence 88, Appl
1121	59	4.9	236	7	US-11-290-687-25	Sequence 25, Appl
1122	59	4.9	236	7	US-11-404-967-25	Sequence 25, Appl
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1125	59	4.9	248	7	US-11-056-355B-32570	Sequence 32570, A
1126	59	4.9	248	7	US-11-056-355B-78330	Sequence 78330, A
1127	59	4.9	248	7	US-11-056-355B-82330	Sequence 82330, A
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1145	59	4.9	323	7	US-11-056-355B-81187	Sequence 81187, A
1146	59	4.9	335	7	US-11-056-355B-24740	Sequence 24740, A
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1154	59	4.9	355	7	US-11-056-355B-24739	Sequence 24739, A
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1166	59	4.9	381	6	US-10-449-902-53664	Sequence 53664, A
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1168	59	4.9	402	6	US-10-471-571A-5294	Sequence 5294, Ap
1169	59	4.9	404	7	US-11-330-403-14913	Sequence 14913, A
1170	59	4.9	405	6	US-10-805-394-4758	Sequence 4758, Ap
1171	59	4.9	409	7	US-11-330-403-6443	Sequence 6443, Ap
1172	59	4.9	413	7	US-11-056-355B-58825	Sequence 58825, A
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1175	59	4.9	429	7	US-11-418-347-4	Sequence 4, Appli
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1178	59	4.9	461	7	US-11-056-355B-38339	Sequence 38339, A
1179	59	4.9	462	6	US-10-560-723-174	Sequence 174, App
1180	59	4.9	464	7	US-11-330-403-9677	Sequence 9677, Ap
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1182	59	4.9	475	6	US-10-449-902-33523	Sequence 33523, A
1183	59	4.9	478	6	US-10-471-571A-3890	Sequence 3890, Ap
1184	59	4.9	480	7	US-11-056-355B-51388	Sequence 51388, A
1185	59	4.9	504	7	US-11-056-355B-51387	Sequence 51387, A
1186	59	4.9	513	7	US-11-330-403-11599	Sequence 11599, A
1189	59	4.9	545	7	US-11-101-316-110	Sequence 110, App
1190	59	4.9	545	7	US-11-293-697-3725	Sequence 3725, Ap
1191	59	4.9	545	7	US-11-376-673-110	Sequence 110, App
1192	59	4.9	550	6	US-10-449-902-49398	Sequence 49398, A
1193	59	4.9	572	7	US-11-208-544-10	Sequence 10, Appl
1194	59	4.9	574	7	US-11-330-403-7965	Sequence 7965, Ap
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1196	59	4.9	577	7	US-11-317-260-3	Sequence 3, Appli
1197	59	4.9	591	6	US-10-449-902-42654	Sequence 42654, A
1198	59	4.9	591	6	US-10-449-902-43740	Sequence 43740, A
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1205	59	4.9	714	7	US-11-056-355B-83304	Sequence 83304, A
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1207	59	4.9	747	7	US-11-330-403-10834	Sequence 10834, A
1208	59	4.9	772	7	US-11-056-355B-96477	Sequence 96477, A
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1214	59	4.9	884	7	US-11-056-355B-94101	Sequence 94101, A
1215	59	4.9	949	7	US-11-056-355B-90344	Sequence 90344, A
1216	59	4.9	949	7	US-11-056-355B-94100	Sequence 94100, A
1217	59	4.9	951	6	US-10-612-783-4169	Sequence 4169, Ap
1218	59	4.9	964	7	US-11-056-355B-90343	Sequence 90343, A
1219	59	4.9	964	7	US-11-056-355B-94099	Sequence 94099, A
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1221	59	4.9	980	7	US-11-397-247A-3	Sequence 3, Appli
1222	59	4.9	980	7	US-11-397-275A-3	Sequence 3, Appli
1223	59	4.9	1002	7	US-11-056-355B-50734	Sequence 50734, A
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1225	59	4.9	1206	7	US-11-056-355B-80505	Sequence 80505, A
1226	59	4.9	1214	7	US-11-056-355B-80504	Sequence 80504, A
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1229	58.5	4.8	148	7	US-11-056-355B-37834	Sequence 37834, A
1230	58.5	4.8	181	7	US-11-056-355B-84301	Sequence 84301, A
1231	58.5	4.8	204	7	US-11-056-355B-58751	Sequence 58751, A
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1233	58.5	4.8	235	7	US-11-375-221-44	Sequence 44, Appl
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1235	58.5	4.8	251	7	US-11-056-355B-10719	Sequence 10719, A
1236	58.5	4.8	251	7	US-11-366-965-579	Sequence 579, App
1237	58.5	4.8	257	6	US-10-953-349-18227	Sequence 18227, A
1238	58.5	4.8	263	6	US-10-953-349-18226	Sequence 18226, A
1239	58.5	4.8	281	6	US-10-526-324-1314	Sequence 1314, Ap
1240	58.5	4.8	296	6	US-10-953-349-35299	Sequence 35299, A
1241	58.5	4.8	299	6	US-10-528-630-27	Sequence 27, Appl
1242	58.5	4.8	302	7	US-11-056-355B-10130	Sequence 10130, A
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1244	58.5	4.8	306	7	US-11-056-355B-10718	Sequence 10718, A
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1246	58.5	4.8	318	6	US-10-612-783-4339	Sequence 4339, Ap
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1248	58.5	4.8	333	6	US-10-953-349-19345	Sequence 19345, A
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1253	58.5	4.8	409	7	US-11-330-403-1311	Sequence 1311, Ap
1254	58.5	4.8	421	6	US-10-449-902-37757	Sequence 37757, A
1255	58.5	4.8	422	6	US-10-449-902-32842	Sequence 32842, A
1256	58.5	4.8	422	6	US-10-449-902-53486	Sequence 53486, A
1257	58.5	4.8	422	6	US-10-449-902-53550	Sequence 53550, A
1258	58.5	4.8	441	7	US-11-330-403-17327	Sequence 17327, A
1259	58.5	4.8	446	6	US-10-471-571A-4476	Sequence 4476, Ap
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1261	58.5	4.8	453	6	US-10-449-902-45426	Sequence 45426, A
1262	58.5	4.8	457	6	US-10-449-902-45580	Sequence 45580, A
1263	58.5	4.8	467	6	US-10-805-394-3974	Sequence 3974, Ap
1264	58.5	4.8	472	6	US-10-953-349-5135	Sequence 5135, Ap
1265	58.5	4.8	485	6	US-10-449-902-48086	Sequence 48086, A
1266	58.5	4.8	513	6	US-10-953-349-34357	Sequence 34357, A
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1271	58.5	4.8	534	7	US-11-330-403-7989	Sequence 7989, Ap
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1275	58.5	4.8	558	7	US-11-056-355B-45229	Sequence 45229, A
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1277	58.5	4.8	573	7	US-11-056-355B-83929	Sequence 83929, A
1278	58.5	4.8	574	6	US-10-449-902-42518	Sequence 42518, A
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1285	58.5	4.8	907	6	US-10-570-909-115	Sequence 115, App
1286	58.5	4.8	907	6	US-10-541-749-141	Sequence 141, App
1287	58.5	4.8	982	6	US-10-449-902-41115	Sequence 41115, A
1288	58.5	4.8	996	6	US-10-449-902-44549	Sequence 44549, A
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1290	58.5	4.8	1785	6	US-10-527-191-90	Sequence 90, Appl
1291	58.5	4.8	2403	6	US-10-527-191-88	Sequence 88, Appl
1292	58.5	4.8	2413	6	US-10-511-937-2616	Sequence 2616, Ap
1293	58.5	4.8	2413	6	US-10-527-191-89	Sequence 89, Appl
1294	58.5	4.8	2413	6	US-10-527-191-106	Sequence 106, App
1295	58.5	4.8	3533	7	US-11-063-439-14	Sequence 14, Appl
1296	58	4.8	130	7	US-11-293-697-4264	Sequence 4264, Ap
1297	58	4.8	189	7	US-11-056-355B-8756	Sequence 8756, Ap
1298	58	4.8	191	7	US-11-056-355B-34748	Sequence 34748, A
1299	58	4.8	195	7	US-11-056-355B-34747	Sequence 34747, A
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1301	58	4.8	198	7	US-11-388-642-86	Sequence 86, Appl
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1308	58	4.8	245	7	US-11-395-249-152	Sequence 152, App
1309	58	4.8	259	7	US-11-056-355B-97093	Sequence 97093, A
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1311	58	4.8	261	7	US-11-056-355B-55071	Sequence 55071, A
1312	58	4.8	262	6	US-10-511-937-2431	Sequence 2431, Ap
1313	58	4.8	270	7	US-11-330-403-8277	Sequence 8277, Ap
1314	58	4.8	273	6	US-10-953-349-35140	Sequence 35140, A
1315	58	4.8	273	7	US-11-056-355B-2104	Sequence 2104, Ap
1316	58	4.8	273	7	US-11-056-355B-7591	Sequence 7591, Ap
1317	58	4.8	276	6	US-10-449-902-46638	Sequence 46638, A
1318	58	4.8	277	7	US-11-330-403-13396	Sequence 13396, A
1319	58	4.8	298	7	US-11-056-355B-60483	Sequence 60483, A
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1322	58	4.8	308	6	US-10-953-349-38123	Sequence 38123, A
1323	58	4.8	312	6	US-10-612-783-5715	Sequence 5715, Ap
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1325	58	4.8	316	7	US-11-056-355B-7590	Sequence 7590, Ap
1326	58	4.8	317	6	US-10-953-349-35139	Sequence 35139, A
1327	58	4.8	317	7	US-11-056-355B-2103	Sequence 2103, Ap
1328	58	4.8	321	7	US-11-330-403-15702	Sequence 15702, A
1329	58	4.8	331	6	US-10-953-349-1501	Sequence 1501, Ap
1330	58	4.8	337	6	US-10-953-349-38122	Sequence 38122, A
1331	58	4.8	343	6	US-10-471-571A-5330	Sequence 5330, Ap
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1333	58	4.8	352	7	US-11-056-355B-54047	Sequence 54047, A
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1336	58	4.8	361	7	US-11-056-355B-67145	Sequence 67145, A
1337	58	4.8	366	7	US-11-056-355B-71231	Sequence 71231, A
1338	58	4.8	370	7	US-11-056-355B-67144	Sequence 67144, A
1339	58	4.8	377	7	US-11-056-355B-67143	Sequence 67143, A
1340	58	4.8	386	6	US-10-953-349-20571	Sequence 20571, A
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1342	58	4.8	391	7	US-11-373-686-16	Sequence 16, Appl
1343	58	4.8	394	7	US-11-056-355B-71230	Sequence 71230, A
1344	58	4.8	397	7	US-11-330-403-2615	Sequence 2615, Ap
1345	58	4.8	397	7	US-11-330-403-15382	Sequence 15382, A
1346	58	4.8	404	6	US-10-449-902-30274	Sequence 30274, A
1347	58	4.8	413	7	US-11-056-355B-20242	Sequence 20242, A
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1349	58	4.8	420	7	US-11-248-718-112	Sequence 112, App
1350	58	4.8	425	6	US-10-527-422-13	Sequence 13, Appl
1351	58	4.8	447	6	US-10-471-571A-4560	Sequence 4560, Ap
1352	58	4.8	447	7	US-11-361-528-1	Sequence 1, Appli
1353	58	4.8	448	6	US-10-975-692-15	Sequence 15, Appl
1354	58	4.8	451	7	US-11-434-137-514	Sequence 514, App
1355	58	4.8	451	7	US-11-434-184-514	Sequence 514, App
1356	58	4.8	451	7	US-11-434-199-514	Sequence 514, App
1357	58	4.8	451	7	US-11-434-203-514	Sequence 514, App
1358	58	4.8	453	6	US-10-471-571A-5512	Sequence 5512, Ap
1359	58	4.8	456	6	US-10-953-349-1500	Sequence 1500, Ap
1362	58	4.8	457	7	US-11-101-316-12	Sequence 12, Appl
1363	58	4.8	457	7	US-11-376-673-12	Sequence 12, Appl
1364	58	4.8	458	6	US-10-449-902-35627	Sequence 35627, A
1365	58	4.8	458	6	US-10-449-902-51682	Sequence 51682, A
1366	58	4.8	458	6	US-10-449-902-54211	Sequence 54211, A
1367	58	4.8	458	7	US-11-317-789A-438	Sequence 438, App
1368	58	4.8	471	6	US-10-953-349-1499	Sequence 1499, Ap
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1379	58	4.8	519	7	US-11-056-355B-20240	Sequence 20240, A
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1381	58	4.8	530	7	US-11-056-355B-78242	Sequence 78242, A
1382	58	4.8	532	7	US-11-056-355B-90219	Sequence 90219, A
1383	58	4.8	532	7	US-11-056-355B-93975	Sequence 93975, A
1384	58	4.8	545	7	US-11-056-355B-75967	Sequence 75967, A
1385	58	4.8	546	7	US-11-056-355B-75966	Sequence 75966, A
1386	58	4.8	547	7	US-11-056-355B-90218	Sequence 90218, A
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1392	58	4.8	565	7	US-11-056-355B-72984	Sequence 72984, A
1393	58	4.8	567	7	US-11-056-355B-72983	Sequence 72983, A
1394	58	4.8	573	6	US-10-612-783-6029	Sequence 6029, Ap
1395	58	4.8	589	7	US-11-056-355B-72982	Sequence 72982, A
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1412	58	4.8	755	7	US-11-056-355B-84922	Sequence 84922, A
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1417	58	4.8	811	6	US-10-805-394-4314	Sequence 4314, Ap
1418	58	4.8	898	7	US-11-056-355B-79052	Sequence 79052, A
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1422	58	4.8	1871	6	US-10-501-834-26	Sequence 26, Appl
1423	57.5	4.7	111	7	US-11-293-697-2685	Sequence 2685, Ap
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1425	57.5	4.7	117	7	US-11-413-563-28	Sequence 28, Appl
1426	57.5	4.7	171	7	US-11-056-355B-87536	Sequence 87536, A
1427	57.5	4.7	175	7	US-11-056-355B-87535	Sequence 87535, A

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1433	57.5	4.7	198	7	US-11-388-642-83	Sequence 83, Appl
1434	57.5	4.7	213	6	US-10-515-429-74	Sequence 74, Appl
1435	57.5	4.7	213	7	US-11-434-137-3730	Sequence 3730, Ap
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1446	57.5	4.7	263	6	US-10-953-349-21739	Sequence 21739, A
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1453	57.5	4.7	266	7	US-11-434-199-3176	Sequence 3176, Ap
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1459	57.5	4.7	291	7	US-11-056-355B-103952	Sequence 103952,
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1461	57.5	4.7	293	7	US-11-318-156-2	Sequence 2, Appli
1462	57.5	4.7	293	7	US-11-345-661-4	Sequence 4, Appli
1463	57.5	4.7	304	6	US-10-953-349-2023	Sequence 2023, Ap
1464	57.5	4.7	304	7	US-11-056-355B-41956	Sequence 41956, A
1465	57.5	4.7	304	7	US-11-056-355B-105456	Sequence 105456,
1466	57.5	4.7	304	7	US-11-056-355B-116695	Sequence 116695,
1467	57.5	4.7	308	6	US-10-449-902-43700	Sequence 43700, A
1468	57.5	4.7	309	7	US-11-393-643-20	Sequence 20, Appl
1469	57.5	4.7	309	7	US-11-479-174-16	Sequence 16, Appl
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1472	57.5	4.7	324	7	US-11-056-355B-57638	Sequence 57638, A
1473	57.5	4.7	325	7	US-11-056-355B-78426	Sequence 78426, A
1474	57.5	4.7	327	7	US-11-056-355B-73702	Sequence 73702, A
1475	57.5	4.7	331	6	US-10-536-606-16	Sequence 16, Appl
1476	57.5	4.7	336	7	US-11-056-355B-91354	Sequence 91354, A
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1480	57.5	4.7	339	7	US-11-366-001-66	Sequence 66, Appl
1481	57.5	4.7	340	7	US-11-366-001-174	Sequence 174, App
1482	57.5	4.7	348	7	US-11-056-355B-91353	Sequence 91353, A
1483	57.5	4.7	348	7	US-11-056-355B-95109	Sequence 95109, A
1484	57.5	4.7	352	7	US-11-056-355B-91352	Sequence 91352, A
1485	57.5	4.7	352	7	US-11-056-355B-95108	Sequence 95108, A
1486	57.5	4.7	359	7	US-11-056-355B-78425	Sequence 78425, A
1487	57.5	4.7	362	7	US-11-197-712-280	Sequence 280, App
1488	57.5	4.7	368	7	US-11-056-355B-54215	Sequence 54215, A
1489	57.5	4.7	371	7	US-11-330-403-5175	Sequence 5175, Ap
1490	57.5	4.7	374	7	US-11-174-307B-3144	Sequence 3144, Ap
1491	57.5	4.7	381	7	US-11-174-307B-2946	Sequence 2946, Ap
1492	57.5	4.7	381	7	US-11-056-355B-54214	Sequence 54214, A
1493	57.5	4.7	393	7	US-11-330-403-4636	Sequence 4636, Ap
1494	57.5	4.7	394	6	US-10-535-928A-41	Sequence 41, Appl
1495	57.5	4.7	396	7	US-11-330-403-1445	Sequence 1445, Ap
1496	57.5	4.7	401	7	US-11-330-403-14879	Sequence 14879, A
1497	57.5	4.7	415	7	US-11-056-355B-54213	Sequence 54213, A
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OM protein - protein search, using sw model

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(without alignments)
515.785 Million cell updates/sec

Title: US-10-063-553-48
Perfect score: 1215
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	170	14.0	202	2	A42926	L6 surface protein
2	166	13.7	197	2	JC6544	tumor-associated a
3	160	13.2	202	2	A53399	L6 antigen - mouse
4	136	11.2	202	2	JC4635	tumor-associated L
5	133	10.9	202	2	JC6205	cell surface antig
6	90.5	7.4	610	2	A85870	probable transport
7	90.5	7.4	610	2	H91025	probable transport
8	90.5	7.4	610	2	B65001	probable transport
9	89.5	7.4	310	2	A81298	formate dehydrogen
10	88.5	7.3	319	2	T33261	hypothetical prote
11	88	7.2	1036	2	A82357	probable multidrug
12	86.5	7.1	891	2	B82495	probable NADH dehy
13	86	7.1	283	2	AC1340	maltodextrin ABC-t
14	86	7.1	438	2	H64713	Na+/H+-exchanging
15	85.5	7.0	271	2	B82295	prolipoprotein dia
16	85.5	7.0	457	2	T46332	hypothetical prote
17	85	7.0	283	2	AI1710	maltodextrin ABC-t
18	85	7.0	379	2	S58057	ubiquinol-cytochro
19	84.5	7.0	281	2	T51961	ATAF1-like protein
20	84	6.9	286	2	AC0848	Iron transport pro
21	84	6.9	438	2	B71805	Na+/H+-exchanging
22	83	6.8	332	2	T33258	hypothetical prote
23	82	6.7	858	2	T08881	prominin - mouse
24	81.5	6.7	494	2	T32644	hypothetical prote
25	81	6.7	254	2	S20741	chitinase (EC 3.2.
26	81	6.7	461	2	T25671	hypothetical prote
27	80	6.6	379	1	S17418	ubiquinol-cytochro
28	80	6.6	721	2	AH3417	lpsA protein [impo
29	79.5	6.5	369	2	T24620	hypothetical prote
30	79.5	6.5	558	2	T47505	hypothetical prote
31	79.5	6.5	608	2	AC0798	probable sodium/su
32	79.5	6.5	1143	2	T10636	hypothetical prote
33	79	6.5	1353	2	JC4279	adenylate cyclase
34	78.5	6.5	363	2	AH2796	hypothetical prote
35	78.5	6.5	363	2	H97575	probable permease
36	78	6.4	309	2	C89831	conserved hypothet
37	78	6.4	1062	2	F83335	RND multidrug effl
38	78	6.4	1062	2	T30830	hypothetical prote
39	78	6.4	1783	2	T37258	probable voltage-d
40	78	6.4	1917	2	C88728	protein C48A7.1 [i
41	77.5	6.4	459	2	T11489	NADH2 dehydrogenas
42	77.5	6.4	459	2	A89785	hexose phosphate t
43	77.5	6.4	500	2	C70175	L-lactate permease
44	77.5	6.4	557	2	JC5487	cellulase (EC 3.2.
45	77	6.3	347	2	T15672	hypothetical prote
46	77	6.3	1032	2	H64100	acriflavine resist
47	77	6.3	1215	2	C84848	hypothetical prote
48	76.5	6.3	379	2	T11505	ubiquinol-cytochro
49	76.5	6.3	451	2	B70792	hypothetical prote
50	76.5	6.3	538	2	T47624	hypothetical prote
51	76.5	6.3	614	2	S78277	dnaK-type molecula
52	76	6.3	346	2	T28718	hypothetical prote
53	76	6.3	431	2	AD1237	arsenic efflux pum
54	76	6.3	447	2	D90012	hypothetical prote
55	76	6.3	532	1	E69821	multidrug resistan
56	76	6.3	561	2	T23564	hypothetical prote
57	76	6.3	604	2	T31042	hypothetical prote
58	76	6.3	751	2	T15230	hypothetical prote
59	76	6.3	1011	2	T13669	neuromusculin - fr
60	75.5	6.2	384	2	T11931	ubiquinol-cytochro
61	75.5	6.2	409	2	AG0362	manganese transpor
62	75.5	6.2	476	2	A84454	hypothetical prote
63	75.5	6.2	788	2	S48191	probable ubiquinol
64	75.5	6.2	824	1	S50767	S-receptor kinase
65	75.5	6.2	1106	2	T19948	hypothetical prote
66	75	6.2	373	2	AI1832	hypothetical prote
67	75	6.2	379	2	I49399	ubiquinol-cytochro
68	75	6.2	385	2	G82789	permease XF0589 [i
69	75	6.2	581	2	I45971	prolactin receptor
70	75	6.2	1015	2	T15830	hypothetical prote
71	75	6.2	2201	2	A32160	tenascin-C - human
72	74.5	6.1	254	2	S19390	probable membrane
73	74.5	6.1	429	1	B41902	arsenical pump mem
74	74.5	6.1	432	2	A97832	hypothetical prote
75	74.5	6.1	458	2	S23743	tetracycline resis
76	74.5	6.1	468	2	H82321	arginine/ornithine
77	74.5	6.1	618	2	F86149	hypothetical prote
78	74	6.1	379	1	S17406	ubiquinol-cytochro
79	74	6.1	379	2	I49400	ubiquinol-cytochro
80	74	6.1	431	2	AI1599	arsenic efflux pum
81	74	6.1	555	2	T47512	probable transport
82	74	6.1	857	2	JC7716	prominin - rat
83	73.5	6.0	380	2	S70594	ubiquinol-cytochro
84	73.5	6.0	387	2	B84721	hypothetical prote
85	73.5	6.0	429	1	C41903	arsenical pump mem
86	73.5	6.0	544	2	C96943	uncharacterized me
87	73	6.0	280	2	D84015	maltose/maltodextr
88	73	6.0	298	2	F87570	hypothetical prote
89	73	6.0	379	1	S17413	ubiquinol-cytochro
90	73	6.0	413	2	S01076	aspartate transami
91	73	6.0	458	1	YTBSRT	tetracycline resis
92	73	6.0	458	1	YTSOG	tetracycline resis
93	73	6.0	458	1	YTBSU6	tetracycline resis
94	73	6.0	458	2	JQ1211	tetracycline resis
95	73	6.0	501	2	H89844	hypothetical prote
96	73	6.0	582	2	T05020	L-ascorbate oxidas
97	73	6.0	718	2	A42163	Na+/myo-inositol c
98	73	6.0	1291	1	A28334	protein-tyrosine-p
99	72.5	6.0	215	2	JU0385	hypothetical 22.6K
100	72.5	6.0	215	2	AH1863	hypothetical prote
101	72.5	6.0	275	2	C89858	conserved hypothet
102	72.5	6.0	290	2	T06856	hypothetical prote

103	72.5	6.0	397	2	S49301	AWJL175 protein -
104	72.5	6.0	575	2	A54861	tenascin - rat (fr
105	72.5	6.0	598	2	T32166	hypothetical prote
106	72.5	6.0	606	2	T27072	hypothetical prote
107	72.5	6.0	616	2	S50998	transporter protei
108	72.5	6.0	904	2	T40072	P Type Copper ATPa
109	72.5	6.0	1267	2	T21340	hypothetical prote
110	72	5.9	344	2	S42648	photosystem II chl
111	72	5.9	344	2	AB2306	photosystem II chl
112	72	5.9	378	2	S39007	ubiquinol-cytochro
113	72	5.9	441	2	D85647	hypothetical prote
114	72	5.9	441	2	D90787	hypothetical prote
115	72	5.9	441	2	D64844	probable gylcosylt
116	72	5.9	447	2	B95369	hypothetical prote
117	72	5.9	475	2	T39486	hypothetical prote
118	72	5.9	607	2	T26845	hypothetical prote
119	72	5.9	617	2	T01227	glutathione-regula
120	72	5.9	982	2	E88465	protein B0244.6 [i
121	72	5.9	1253	2	T21065	hypothetical prote
122	72	5.9	1583	2	S59644	sister chromatid c
123	71.5	5.9	363	2	H71335	probable phospho-N
124	71.5	5.9	366	2	C64449	cationic amino aci
125	71.5	5.9	386	2	AD0218	flagellar biosynth
126	71.5	5.9	398	2	JN0708	thyrotropin-releas
127	71.5	5.9	444	2	G70042	multidrug-efflux t
128	71.5	5.9	495	2	T12401	NADH2 dehydrogenas
129	71.5	5.9	581	2	S03540	gene frizzled prot
130	71.5	5.9	784	2	A86676	carbon starvation
131	71.5	5.9	880	2	AI1179	cation (calcium) t
132	71.5	5.9	1029	2	C97665	multidrug efflux t
133	71.5	5.9	1029	2	AF2889	acriflavin resista
134	71.5	5.9	1043	2	AB0370	multidrug efflux p
135	71	5.8	344	2	A69507	conserved hypothet
136	71	5.8	345	2	B90600	hypothetical prote
137	71	5.8	430	2	G89962	hypothetical prote
138	71	5.8	487	2	B72755	probable antibioti
139	71	5.8	614	2	T29937	hypothetical prote
140	71	5.8	708	2	T19969	hypothetical prote
141	71	5.8	712	2	AG1888	Na+/H+ antiporter
142	71	5.8	1246	2	C36806	hypothetical prote
143	70.5	5.8	129	2	S40363	Ig kappa chain - h
144	70.5	5.8	141	2	T11270	NADH2 dehydrogenas
145	70.5	5.8	229	1	LCBO	prolactin precurso
146	70.5	5.8	230	2	A95034	conserved hypothet
147	70.5	5.8	236	2	A97905	conserved hypothet
148	70.5	5.8	239	2	T48120	hypothetical prote
149	70.5	5.8	282	1	SAVL64	middle surface ant
150	70.5	5.8	352	2	I50047	rhodopsin - Mexica
151	70.5	5.8	374	2	C83078	still frameshift t
152	70.5	5.8	379	2	A53077	ubiquinol-cytochro
153	70.5	5.8	420	2	T47998	pectinacetylestera
154	70.5	5.8	446	2	T35005	probable integral
155	70.5	5.8	477	2	A87285	phosphate ABC tran
156	70.5	5.8	506	2	F83369	hypothetical prote
157	70.5	5.8	522	2	B81584	conserved hypothet
158	70.5	5.8	591	2	C86538	hypothetical prote
159	70.5	5.8	591	2	B72086	hypothetical prote
160	70.5	5.8	594	2	G84441	probable sucrose-p
161	70.5	5.8	760	2	S19374	probable membrane
162	70.5	5.8	1056	2	A53767	mucin MUC5B, trach
163	70.5	5.8	1583	2	F86366	protein F26F24.8 [
164	70.5	5.8	2051	2	T13164	plexin B - fruit f
165	70	5.8	185	2	A70075	hypothetical prote
166	70	5.8	253	2	B89779	hypothetical prote
167	70	5.8	255	2	E81197	hypothetical prote
168	70	5.8	283	2	E81895	probable prolipopr
169	70	5.8	379	1	S17419	ubiquinol-cytochro
170	70	5.8	379	2	I48180	ubiquinol-cytochro
171	70	5.8	379	2	S58460	ubiquinol-cytochro
172	70	5.8	437	2	E84619	probable serine ca
173	70	5.8	490	2	S52830	HMS1 protein - yea
174	70	5.8	510	2	C64883	membrane protein y
175	70	5.8	512	2	E81794	probable inner mem
176	70	5.8	520	2	E86200	protein F12K11.18
177	70	5.8	544	2	T27444	hypothetical prote
178	70	5.8	557	2	T47506	hypothetical prote
179	70	5.8	710	2	B71417	hypothetical prote
180	70	5.8	795	2	T21487	hypothetical prote
181	70	5.8	1083	2	S54293	regulator protein
182	70	5.8	1748	1	JQ1555	genome polyprotein
183	70	5.8	2049	2	T43161	sodium channel pro
184	69.5	5.7	158	2	H71902	phosphatidylglycer
185	69.5	5.7	231	2	AE2537	two-component resp
186	69.5	5.7	283	2	B86902	permease [imported
187	69.5	5.7	347	2	AD3513	channel protein vi
188	69.5	5.7	356	2	T22882	hypothetical prote
189	69.5	5.7	474	2	AI1821	protein-export mem
190	69.5	5.7	551	2	A87019	probable cytochrom
191	69.5	5.7	638	2	B34285	NADH2 dehydrogenas
192	69.5	5.7	669	2	T08827	hypothetical prote
193	69.5	5.7	675	2	D85065	receptor protein k
194	69.5	5.7	702	2	E64250	cell division prot
195	69.5	5.7	724	2	A42953	nitrous oxide redu
196	69.5	5.7	822	2	S56823	probable membrane
197	69.5	5.7	1018	2	E83099	probable RND efflu
198	69.5	5.7	1817	2	T34249	hypothetical prote
199	69.5	5.7	2019	1	JQ1322	tenascin precursor
200	69	5.7	202	2	T26214	hypothetical prote
201	69	5.7	216	2	A54305	KRAG protein - mou
202	69	5.7	231	2	C64826	aquaporin Z - Esch
203	69	5.7	231	2	A99749	transmembrane wate
204	69	5.7	231	2	E85599	transmembrane wate
205	69	5.7	283	2	C81124	prolipoprotein dia
206	69	5.7	285	2	AI0633	probable membrane
207	69	5.7	300	2	B69072	hypothetical prote
208	69	5.7	303	2	T31909	hypothetical prote
209	69	5.7	309	2	T34080	hypothetical prote
210	69	5.7	355	2	D71429	hypothetical prote
211	69	5.7	371	2	B86489	protein T32E20.25
212	69	5.7	377	2	T11361	ubiquinol-cytochro
213	69	5.7	397	2	F83385	probable MFS trans
214	69	5.7	426	2	T20253	hypothetical prote
215	69	5.7	475	2	T46745	arginine/ornithine
216	69	5.7	494	2	A82294	probable carbon st
217	69	5.7	513	2	B81217	virulence factor M
218	69	5.7	549	2	E70784	cytochrome b homol
219	69	5.7	617	2	T02668	probable receptor
220	69	5.7	622	2	AI1453	bacteriophage mino
221	69	5.7	678	2	B71308	hypothetical prote
222	69	5.7	692	2	H71494	probable thiol-dis
223	69	5.7	709	2	S75212	comE protein - Syn
224	69	5.7	814	2	T05537	probable serine/th
225	69	5.7	829	2	B86467	hypothetical prote
226	69	5.7	882	2	AH1536	cation (calcium) t
227	69	5.7	971	2	S50912	probable membrane
228	69	5.7	1852	2	A37860	calcium channel pr
229	68.5	5.6	176	2	I53630	cell surface glyco
230	68.5	5.6	269	2	I54432	MHC class II histo
231	68.5	5.6	306	2	D90670	hypothetical prote
232	68.5	5.6	306	2	G85520	hypothetical prote
233	68.5	5.6	361	2	T45918	hypothetical prote
234	68.5	5.6	369	2	I64234	competence locus E
235	68.5	5.6	374	2	T09771	phosphatidate cyti
236	68.5	5.6	379	1	S43262	ubiquinol-cytochro
237	68.5	5.6	426	1	SAVLC	large surface anti
238	68.5	5.6	443	2	C70818	probable ABC trans
239	68.5	5.6	452	1	D69810	phosphotransferase
240	68.5	5.6	454	2	AC1413	PTS system, cellob
241	68.5	5.6	454	2	AB1789	PTS system, cellob
242	68.5	5.6	469	2	C90446	permease, multidru
243	68.5	5.6	511	2	G64902	extreme acid resis
244	68.5	5.6	511	2	A90891	acid sensitivity p
245	68.5	5.6	511	2	H85726	acid sensitivity p
246	68.5	5.6	627	2	T11125	NADH2 dehydrogenas
247	68.5	5.6	643	2	C90035	hypothetical prote
248	68.5	5.6	646	2	JQ2150	B west mating prot

249	68.5	5.6	1016	2	F82159	transporter, AcrB/
250	68.5	5.6	1091	2	G59435	DLC-1 (deleted in
251	68.5	5.6	1500	2	T03824	probable immediate
252	68	5.6	206	2	S08632	nodulin-21 - soybe
253	68	5.6	228	2	C82400	TonB system transp
254	68	5.6	312	2	G69423	branched-chain ami
255	68	5.6	379	1	S17405	ubiquinol-cytochro
256	68	5.6	379	1	S17409	ubiquinol-cytochro
257	68	5.6	379	2	I48133	ubiquinol-cytochro
258	68	5.6	379	2	S58451	ubiquinol-cytochro
259	68	5.6	379	2	S58447	ubiquinol-cytochro
260	68	5.6	405	2	T44249	transport protein
261	68	5.6	423	2	S74046	probable sugar tra
262	68	5.6	425	2	G91082	probable transport
263	68	5.6	425	2	H85927	probable transport
264	68	5.6	425	2	C65059	probable transport
265	68	5.6	443	2	E65008	hypothetical prote
266	68	5.6	448	2	B82171	probable sodium-de
267	68	5.6	465	2	B71716	transhydrogenase c
268	68	5.6	498	2	A48203	interleukin-14 pre
269	68	5.6	504	2	S00390	Ig gamma chain (cl
270	68	5.6	510	2	E97307	probable cardiolip
271	68	5.6	516	2	F82070	2-isopropylmalate
272	68	5.6	527	2	H85135	hypothetical prote
273	68	5.6	610	2	H83165	probable sodium/su
274	68	5.6	641	2	S44253	raffinose carrier
275	68	5.6	689	2	D85013	hypothetical prote
276	68	5.6	725	2	B82425	conserved hypothet
277	68	5.6	799	2	A48716	glycine transporte
278	68	5.6	865	2	B96558	probable protein k
279	68	5.6	926	2	T16184	hypothetical prote
280	68	5.6	1008	1	GNVUUK	glycoprotein precu
281	68	5.6	1247	2	C89583	protein K07E3.1 [i
282	68	5.6	1810	1	A32230	tenascin precursor
283	68	5.6	3176	2	CGHU3A	collagen alpha 3(V
284	67.5	5.6	120	2	AI1727	hypothetical prote
285	67.5	5.6	197	2	B69447	hypothetical prote
286	67.5	5.6	208	2	E97899	hypothetical prote
287	67.5	5.6	228	2	T16678	hypothetical prote
288	67.5	5.6	229	1	LCSH	prolactin precurso
289	67.5	5.6	261	2	I68718	MHC class II histo
290	67.5	5.6	328	1	S25993	NADH2 dehydrogenas
291	67.5	5.6	337	2	B88957	protein ZK697.7 [i
292	67.5	5.6	379	2	S58458	ubiquinol-cytochro
293	67.5	5.6	386	2	G84386	oligopeptide trans
294	67.5	5.6	415	2	B84858	hypothetical prote
295	67.5	5.6	431	1	SAVL59	large surface anti
296	67.5	5.6	431	2	F90316	dsrP protein, prob
297	67.5	5.6	452	2	G95306	putrescine/ornithi
298	67.5	5.6	456	2	H96902	membrane protein,
299	67.5	5.6	472	2	T29313	hypothetical prote
300	67.5	5.6	491	2	G90689	regulates beta-lac
301	67.5	5.6	491	2	C85540	regulates beta-lac
302	67.5	5.6	491	2	S37391	signal transducer
303	67.5	5.6	509	2	S45413	probable membrane
304	67.5	5.6	548	2	T25401	hypothetical prote
305	67.5	5.6	553	2	T38541	probable sucrose c
306	67.5	5.6	656	2	T31884	hypothetical prote
307	67.5	5.6	907	2	JG0193	G protein-coupled
308	67.5	5.6	955	2	T21612	hypothetical prote
309	67.5	5.6	968	2	F70746	probable mmpL2 pro
310	67.5	5.6	1041	2	AC0423	multidrug efflux p
311	67.5	5.6	1610	2	A46227	voltage-dependent
312	67.5	5.6	2161	2	JH0564	calcium channel al
313	67.5	5.6	2181	2	A38198	calcium channel al
314	67	5.5	252	2	A86449	hypothetical prote
315	67	5.5	296	2	AH1173	conserved hypothet
316	67	5.5	314	2	T15519	hypothetical prote
317	67	5.5	360	2	T06786	6a-hydroxymaackiai
318	67	5.5	379	1	S17420	ubiquinol-cytochro
319	67	5.5	379	2	S58085	ubiquinol-cytochro
320	67	5.5	393	2	A39251	thyrotropin-releas
321	67	5.5	407	2	S37550	triose phosphate/3
322	67	5.5	408	2	S37553	triose phosphate/3
323	67	5.5	411	2	I56444	thyrotrophin-relea
324	67	5.5	411	2	T17653	hypothetical prote
325	67	5.5	412	2	S23436	thyroliberin recep
326	67	5.5	428	2	S61186	glutamate 5-kinase
327	67	5.5	448	2	C96542	hypothetical prote
328	67	5.5	454	2	E85826	probable amino aci
329	67	5.5	454	2	H90980	probable amino aci
330	67	5.5	454	2	E64966	probable amino aci
331	67	5.5	462	2	S42372	hypothetical prote
332	67	5.5	486	2	T42254	amino acid permeas
333	67	5.5	518	2	S61920	B-alpha pheromone-
334	67	5.5	526	2	T23779	hypothetical prote
335	67	5.5	536	2	A71491	probable integral
336	67	5.5	537	2	H88087	protein B0454.4 [i
337	67	5.5	554	2	G96598	protein F20N2.6 [i
338	67	5.5	602	2	G97784	hypothetical prote
339	67	5.5	630	2	S46740	hypothetical prote
340	67	5.5	637	2	S01509	NADH2 dehydrogenas
341	67	5.5	685	2	S67146	probable membrane
342	67	5.5	792	2	G84830	probable potassium
343	67	5.5	992	2	S49835	hypothetical prote
344	67	5.5	2958	2	S64921	probable membrane
345	66.5	5.5	229	1	LCPG	prolactin precurso
346	66.5	5.5	234	2	T11914	cox1 intron protei
347	66.5	5.5	268	2	C71872	hypothetical prote
348	66.5	5.5	319	2	AF0489	probable iron tran
349	66.5	5.5	407	2	A69188	ammonium transport
350	66.5	5.5	410	2	C64618	conserved hypothet
351	66.5	5.5	482	2	T02538	hypothetical prote
352	66.5	5.5	489	2	B69833	metabolite permeas
353	66.5	5.5	489	2	T24971	hypothetical prote
354	66.5	5.5	705	2	S23352	gene unc-93 protei
355	66.5	5.5	719	2	T00266	hypothetical prote
356	66.5	5.5	937	2	A56517	nucleoporin Nup98
357	66.5	5.5	1078	2	A56715	calcium receptor (
358	66.5	5.5	1088	2	B56715	calcium receptor (
359	66.5	5.5	3391	1	GNWV16	genome polyprotein
360	66.5	5.5	4981	2	T18489	hypothetical prote
361	66	5.4	218	1	A43522	23K integral membr
362	66	5.4	222	2	F64563	hypothetical prote
363	66	5.4	238	2	A45544	BoLA-DQ beta-1 - b
364	66	5.4	239	2	S64327	probable membrane
365	66	5.4	255	2	F81833	conserved hypothet
366	66	5.4	271	2	AC1692	hypothetical prote
367	66	5.4	295	2	C70166	hypothetical prote
368	66	5.4	339	2	T22195	hypothetical prote
369	66	5.4	342	2	A40191	platelet-activatin
370	66	5.4	348	2	E82896	hemin permease UU3
371	66	5.4	352	2	JE0296	thyrotropin releas
372	66	5.4	373	2	S54545	hypothetical prote
373	66	5.4	379	1	CBBO	ubiquinol-cytochro
374	66	5.4	379	2	T11259	ubiquinol-cytochro
375	66	5.4	381	1	CBMS	ubiquinol-cytochro
376	66	5.4	383	2	S54213	flagellar biosynth
377	66	5.4	402	2	T29703	hypothetical prote
378	66	5.4	413	2	H82270	hypothetical prote
379	66	5.4	414	2	S34829	triose phosphate/3
380	66	5.4	414	2	S23224	triose phosphate/3
381	66	5.4	422	2	D72302	hypothetical prote
382	66	5.4	422	2	E82904	hypothetical prote
383	66	5.4	444	2	S62414	probable ubiquitin
384	66	5.4	447	2	AI0701	probable amino aci
385	66	5.4	482	2	A39285	calcitonin recepto
386	66	5.4	498	2	I47130	calcitonin recepto
387	66	5.4	505	2	F90427	amino acid transpo
388	66	5.4	581	2	S17150	potassium channel
389	66	5.4	583	2	A25096	NADH2 dehydrogenas
390	66	5.4	598	2	B70036	capsular polysacch
391	66	5.4	609	2	T11310	NADH2 dehydrogenas
392	66	5.4	611	2	S09142	ND5 intron 1 prote
393	66	5.4	650	2	S23217	beta-fructofuranos
394	66	5.4	674	2	T21217	hypothetical prote

395	66	5.4	689	2	T11917	NADH2 dehydrogenas
396	66	5.4	718	2	A56851	Na+/myo-inositol c
397	66	5.4	754	2	AI1627	protein-export mem
398	66	5.4	770	2	S60676	cellobiose oxidase
399	66	5.4	877	2	C46356	env polyprotein -
400	66	5.4	893	2	S64926	probable membrane
401	66	5.4	1034	2	D65119	acriflavin resista
402	66	5.4	1217	2	T00270	hypothetical prote
403	66	5.4	1218	2	T30293	ABC transport prot
404	66	5.4	1615	2	JE0372	low density lipopr
405	65.5	5.4	83	2	AG3378	hypothetical membr
406	65.5	5.4	139	2	G32536	T-cell receptor al
407	65.5	5.4	226	1	JX0221	CD9 antigen - bovi
408	65.5	5.4	229	2	A61133	prolactin precurso
409	65.5	5.4	233	2	H82944	thymidylate kinase
410	65.5	5.4	258	2	A29088	Smh class II histo
411	65.5	5.4	259	2	S64423	probable membrane
412	65.5	5.4	261	1	HLHUDB	MHC class II histo
413	65.5	5.4	277	2	D42400	membrane protein M
414	65.5	5.4	279	2	AB1745	conserved hypothet
415	65.5	5.4	279	2	AD1375	conserved hypothet
416	65.5	5.4	293	1	QQCVBV	BL1 protein - squa
417	65.5	5.4	342	2	AD2367	hypothetical prote
418	65.5	5.4	361	2	T21529	hypothetical prote
419	65.5	5.4	379	1	S43261	ubiquinol-cytochro
420	65.5	5.4	379	1	S43265	ubiquinol-cytochro
421	65.5	5.4	379	1	S43269	ubiquinol-cytochro
422	65.5	5.4	379	2	S58459	ubiquinol-cytochro
423	65.5	5.4	380	1	S73751	high affinity tran
424	65.5	5.4	405	2	C71462	hypothetical prote
425	65.5	5.4	435	2	AC0104	probable sugar tra
426	65.5	5.4	529	2	T22398	hypothetical prote
427	65.5	5.4	530	1	A56841	glucose-6-phosphat
428	65.5	5.4	534	2	A37483	F protein - Muraya
429	65.5	5.4	587	2	D84426	hypothetical prote
430	65.5	5.4	620	2	T49067	transcription fact
431	65.5	5.4	656	2	B49423	semaphorin I - fru
432	65.5	5.4	806	2	C86445	hypothetical prote
433	65.5	5.4	856	1	A44963	env polyprotein pr
434	65.5	5.4	868	2	T31527	hypothetical prote
435	65.5	5.4	897	2	S67283	hypothetical prote
436	65.5	5.4	910	2	C69069	cation-transportin
437	65.5	5.4	928	2	S50578	hypothetical prote
438	65.5	5.4	1029	2	D83120	probable RND efflu
439	65.5	5.4	1085	2	S40476	Ca(2+)-sensing rec
440	65.5	5.4	1246	2	T00826	hypothetical prote
441	65.5	5.4	1623	2	T01369	ABC transporter At
442	65.5	5.4	1737	2	T17101	probable voltage-a
443	65.5	5.4	1816	2	A84845	probable ABC trans
444	65.5	5.4	2163	2	T15276	hypothetical prote
445	65	5.3	136	2	S05628	NADH2 dehydrogenas
446	65	5.3	172	2	E82464	probable acetyltra
447	65	5.3	203	2	F91006	hypothetical prote
448	65	5.3	212	2	AI2032	hypothetical prote
449	65	5.3	271	2	AH0161	probable membrane
450	65	5.3	301	2	C69143	hypothetical prote
451	65	5.3	336	2	E64717	methicillin resist
452	65	5.3	338	2	S50339	NADH2 dehydrogenas
453	65	5.3	365	2	AE2782	transcription regu
454	65	5.3	365	2	F97561	hypothetical prote
455	65	5.3	373	2	G85355	nodulin-like prote
456	65	5.3	379	1	S41832	ubiquinol-cytochro
457	65	5.3	379	1	S43263	ubiquinol-cytochro
458	65	5.3	379	2	S58452	ubiquinol-cytochro
459	65	5.3	379	2	E58851	ubiquinol-cytochro
460	65	5.3	379	2	S58448	ubiquinol-cytochro
461	65	5.3	379	2	I48134	ubiquinol-cytochro
462	65	5.3	389	2	B96522	hypothetical prote
463	65	5.3	400	2	E82367	probable multidrug
464	65	5.3	410	2	C84176	oxalate/formate an
465	65	5.3	423	2	AG2394	hypothetical prote
466	65	5.3	455	2	T16070	hypothetical prote
467	65	5.3	473	2	S51256	probable membrane
468	65	5.3	487	2	C82215	probable transport
469	65	5.3	509	2	A33801	muscle-fat glucose
470	65	5.3	563	2	T44214	probable phosphotr
471	65	5.3	563	2	T44029	ganciclovir kinase
472	65	5.3	580	2	A56382	purine permease, b
473	65	5.3	616	2	T03027	receptor-like prot
474	65	5.3	652	2	H96924	probable phosphohy
475	65	5.3	667	2	S51763	sulfate transport
476	65	5.3	728	2	C75601	cation-transportin
477	65	5.3	754	2	AG1265	protein-export mem
478	65	5.3	826	2	E81706	conserved hypothet
479	65	5.3	1018	1	GNWXG7	genome polyprotein
480	65	5.3	1042	2	I50099	H,K-ATPase - giant
481	65	5.3	1106	2	T25065	hypothetical prote
482	65	5.3	1219	2	T06608	disease resistance
483	65	5.3	1231	2	E90182	hypothetical prote
484	65	5.3	2195	2	T34264	hypothetical prote
485	64.5	5.3	125	2	JH0184	hydrophobin Sc3 pr
486	64.5	5.3	154	2	T18204	mnxB protein - Bac
487	64.5	5.3	163	2	B84731	hypothetical prote
488	64.5	5.3	191	2	AD2040	hypothetical prote
489	64.5	5.3	197	2	B81720	conserved hypothet
490	64.5	5.3	218	2	G71260	probable ribulose-
491	64.5	5.3	218	2	F81111	nickel-dependent h
492	64.5	5.3	220	2	D71946	hypothetical prote
493	64.5	5.3	229	2	I83982	prolactin - goat
494	64.5	5.3	247	2	I45942	MHC class II - bov
495	64.5	5.3	253	2	B34801	pathogenesis-relat
496	64.5	5.3	261	2	I45928	MHC class II - bov
497	64.5	5.3	305	2	S29711	olfactory factor O
498	64.5	5.3	321	2	AI0007	lipopolysaccharide
499	64.5	5.3	322	2	C83562	hypothetical prote
500	64.5	5.3	326	2	G84748	hypothetical prote
501	64.5	5.3	330	2	T43061	hypothetical prote
502	64.5	5.3	331	1	DNOBU1	NADH2 dehydrogenas
503	64.5	5.3	331	2	F89771	lipoprotein [impor
504	64.5	5.3	340	2	E83126	ferric enterobacti
505	64.5	5.3	346	2	AH3563	ribose transport s
506	64.5	5.3	372	2	AG1834	NADH dehydrogenase
507	64.5	5.3	379	1	S43266	ubiquinol-cytochro
508	64.5	5.3	379	1	S43268	ubiquinol-cytochro
509	64.5	5.3	379	2	S58466	ubiquinol-cytochro
510	64.5	5.3	385	2	I84455	dopamine transport
511	64.5	5.3	393	2	A64036	hypothetical prote
512	64.5	5.3	402	2	A84581	probable disease r
513	64.5	5.3	431	1	SAVL7	large surface anti
514	64.5	5.3	431	1	SAVLW8	large surface anti
515	64.5	5.3	435	2	G69779	arsenical pump mem
516	64.5	5.3	441	2	C96759	protein serine car
517	64.5	5.3	443	2	T20292	hypothetical prote
518	64.5	5.3	454	2	AG0763	probable amino aci
519	64.5	5.3	464	2	T50785	nucleoid DNA-bindi
520	64.5	5.3	503	2	T38303	SWI/SNF complex tr
521	64.5	5.3	512	2	G90399	amino acid transpo
522	64.5	5.3	561	2	AI1409	potassium-transpor
523	64.5	5.3	574	2	T41068	hypothetical prote
524	64.5	5.3	620	2	I57937	dopamine transport
525	64.5	5.3	620	2	A48980	dopamine transport
526	64.5	5.3	634	2	T22351	hypothetical prote
527	64.5	5.3	659	2	H96693	hypothetical prote
528	64.5	5.3	683	2	T03146	probable glycoprot
529	64.5	5.3	689	1	E70408	ferrous iron trans
530	64.5	5.3	724	2	D84377	protein export [im
531	64.5	5.3	803	2	S45916	hypothetical prote
532	64.5	5.3	879	2	D96902	MDR-type permease
533	64.5	5.3	958	2	A70634	probable mmpL1 pro
534	64.5	5.3	1028	2	AD0052	probable multi-dru
535	64.5	5.3	1135	1	JQ1928	G2-G1 polyprotein
536	64.5	5.3	1150	2	AB0064	probable membrane
537	64.5	5.3	1165	1	S45879	chitin synthase (E
538	64.5	5.3	1447	1	VGIHE3	E2 glycoprotein pr
539	64.5	5.3	1447	1	VGIHE2	E2 glycoprotein pr
540	64.5	5.3	1487	2	S62048	probable membrane

541	64.5	5.3	1495	2	E86428	probable ABC trans
542	64.5	5.3	1646	2	JH0422	voltage-dependent
543	64.5	5.3	1687	2	T30244	phosphodiesterase
544	64.5	5.3	1719	2	T30174	exoribonuclease, v
545	64.5	5.3	1748	1	JN0786	integrin beta-4 ch
546	64.5	5.3	2203	2	T42742	voltage-dependent
547	64.5	5.3	2262	2	T30890	calcium channel al
548	64	5.3	159	2	G75555	conserved hypothet
549	64	5.3	167	2	I58352	p16INK4a - mouse
550	64	5.3	227	2	F96777	germin-like protei
551	64	5.3	232	2	S32398	serine proteinase
552	64	5.3	253	2	AE2797	cytochrome c-type
553	64	5.3	254	2	A64728	probable membrane
554	64	5.3	261	2	T11486	cytochrome-c oxida
555	64	5.3	267	2	E97576	cytochrome c-type
556	64	5.3	318	2	AH0499	probable phosphate
557	64	5.3	333	2	T02614	hypothetical prote
558	64	5.3	335	2	B71801	probable undecapre
559	64	5.3	350	2	E81303	probable branched-
560	64	5.3	355	1	A46191	iodopsin homolog -
561	64	5.3	357	2	C69223	anion permease - M
562	64	5.3	378	2	D64181	probable cytochrom
563	64	5.3	379	1	S17407	ubiquinol-cytochro
564	64	5.3	379	2	S58461	ubiquinol-cytochro
565	64	5.3	379	2	T11349	ubiquinol-cytochro
566	64	5.3	382	2	A72373	conserved hypothet
567	64	5.3	396	2	F96545	hypothetical prote
568	64	5.3	405	2	A57479	amino acid transpo
569	64	5.3	426	2	E71675	hypothetical prote
570	64	5.3	428	2	T33775	hypothetical prote
571	64	5.3	444	2	JC1141	metacyclic-form-sp
572	64	5.3	445	2	A70732	hypothetical prote
573	64	5.3	447	2	T13204	hypothetical prote
574	64	5.3	457	2	T39751	major facilitator
575	64	5.3	461	2	T11800	NADH2 dehydrogenas
576	64	5.3	466	2	G71542	probable amino aci
577	64	5.3	470	2	AD1430	transmembrane effl
578	64	5.3	492	2	S59107	NADH2 dehydrogenas
579	64	5.3	565	2	T16408	hypothetical prote
580	64	5.3	692	2	E90113	hypothetical prote
581	64	5.3	768	2	T22758	hypothetical prote
582	64	5.3	798	2	T23539	hypothetical prote
583	64	5.3	810	2	T33323	hypothetical prote
584	64	5.3	953	2	T01093	luminidependens pr
585	64	5.3	970	2	F64230	spore germination
586	64	5.3	992	2	A42318	glycogen phosphory
587	64	5.3	996	2	A95228	bacteriocin format
588	64	5.3	996	2	E98092	cylM protein, cyto
589	64	5.3	1174	2	A39927	RNA-directed RNA p
590	64	5.3	1182	2	T13952	membrane protein p
591	64	5.3	1280	2	A39117	170K lectin precur
592	64	5.3	1297	2	T39287	hypothetical prote
593	64	5.3	1689	2	S72467	sodium channel pro
594	64	5.3	2787	2	S45416	TEL1 protein - yea
595	63.5	5.2	115	2	AB2223	hypothetical prote
596	63.5	5.2	145	2	T42280	hypothetical prote
597	63.5	5.2	158	2	I61900	eosinophil-derived
598	63.5	5.2	171	2	I48085	integral membrane
599	63.5	5.2	219	2	I45937	MHC cell surface g
600	63.5	5.2	253	2	S20737	chitinase (EC 3.2.
601	63.5	5.2	253	2	S20738	chitinase (EC 3.2.
602	63.5	5.2	261	1	HLHU1C	MHC class II histo
603	63.5	5.2	261	2	I55996	MHC HLA-DQ-beta ce
604	63.5	5.2	261	2	B37044	MHC class II histo
605	63.5	5.2	261	2	I68732	MHC class II histo
606	63.5	5.2	261	2	I54480	HLA DQ-beta - huma
607	63.5	5.2	261	2	I45943	MHC class II - bov
608	63.5	5.2	263	2	T46093	hypothetical prote
609	63.5	5.2	273	2	T49007	hypothetical prote
610	63.5	5.2	275	2	D65100	hypothetical L-ser
611	63.5	5.2	286	2	AI3105	hypothetical prote
612	63.5	5.2	288	2	A90135	SAM-dependent meth
613	63.5	5.2	301	2	C98181	sitC protein (AF12
614	63.5	5.2	308	2	T24453	hypothetical prote
615	63.5	5.2	350	2	C88987	protein C50H11.2 [
616	63.5	5.2	351	2	T23990	hypothetical prote
617	63.5	5.2	367	2	C82943	ferrichrome ABC tr
618	63.5	5.2	379	1	S17415	ubiquinol-cytochro
619	63.5	5.2	379	2	T11492	ubiquinol-cytochro
620	63.5	5.2	379	2	T10998	ubiquinol-cytochro
621	63.5	5.2	385	2	H71960	hypothetical prote
622	63.5	5.2	387	2	F82692	conserved hypothet
623	63.5	5.2	389	2	H86266	hypothetical prote
624	63.5	5.2	442	2	H81402	probable integral
625	63.5	5.2	446	2	H90094	hypothetical prote
626	63.5	5.2	454	2	H91127	L-serine deaminase
627	63.5	5.2	456	2	G85972	probable L-serine
628	63.5	5.2	458	1	YTBSY8	tetracycline resis
629	63.5	5.2	463	2	D69792	amino acid permeas
630	63.5	5.2	508	2	T21866	hypothetical prote
631	63.5	5.2	521	2	C86678	hypothetical prote
632	63.5	5.2	522	2	T29705	hypothetical prote
633	63.5	5.2	531	2	T19232	hypothetical prote
634	63.5	5.2	532	2	T52442	hypothetical prote
635	63.5	5.2	561	2	AH1785	potassium-transpor
636	63.5	5.2	568	2	T31692	hypothetical prote
637	63.5	5.2	596	2	T17333	hypothetical prote
638	63.5	5.2	608	2	AG0846	formate hydrogenly
639	63.5	5.2	610	2	F82192	ABC transporter, A
640	63.5	5.2	621	2	AF3016	Na+/H+ antiporter
641	63.5	5.2	642	2	B98268	probable sodium/hy
642	63.5	5.2	696	2	T48432	maturase-like prot
643	63.5	5.2	698	2	T10541	cyclic nucleotide
644	63.5	5.2	741	2	S73827	hypothetical prote
645	63.5	5.2	771	2	T50299	hypothetical serin
646	63.5	5.2	776	2	T20896	hypothetical prote
647	63.5	5.2	845	2	D97163	cation transport P
648	63.5	5.2	936	2	T26521	hypothetical prote
649	63.5	5.2	1050	2	AE0380	multidrug efflux p
650	63.5	5.2	1103	2	T42022	probable chitin sy
651	63.5	5.2	1142	2	S59359	GIN4 protein - yea
652	63.5	5.2	1220	2	S64916	probable membrane
653	63.5	5.2	1604	2	B86287	F9L1.23 protein -
654	63.5	5.2	1612	2	S51243	probable ATPase (E
655	63.5	5.2	2143	2	JH0427	voltage-dependent
656	63.5	5.2	3388	1	GNWVDP	genome polyprotein
657	63	5.2	115	2	G97022	probable membrane
658	63	5.2	134	2	S40376	Ig kappa chain - h
659	63	5.2	217	2	F83840	stage II sporulati
660	63	5.2	218	1	A40181	23K integral membr
661	63	5.2	232	2	B90129	26S proteasome SU
662	63	5.2	239	2	S66341	ribonuclease I (EC
663	63	5.2	239	2	F64382	hypothetical prote
664	63	5.2	251	2	H90568	conserved hypothet
665	63	5.2	254	2	E90637	hypothetical prote
666	63	5.2	254	2	E85488	hypothetical prote
667	63	5.2	257	2	A32283	MHC class II histo
668	63	5.2	260	2	A34178	bacteriorhodopsin
669	63	5.2	271	2	AC1320	hypothetical prote
670	63	5.2	276	2	F72342	conserved hypothet
671	63	5.2	292	2	T19669	hypothetical prote
672	63	5.2	292	2	G88783	protein C33A12.16
673	63	5.2	295	2	A41241	ubiquitin-conjugat
674	63	5.2	309	2	AC0489	probable membrane
675	63	5.2	313	2	S66962	probable membrane
676	63	5.2	314	2	T33862	hypothetical prote
677	63	5.2	320	2	T26259	hypothetical prote
678	63	5.2	339	2	A81288	probable sugar kin
679	63	5.2	341	2	S63666	platelet activatin
680	63	5.2	341	2	AE1824	permease protein o
681	63	5.2	353	2	A88987	protein C50H11.4 [
682	63	5.2	354	2	T20169	hypothetical prote
683	63	5.2	356	2	G82938	hemin transport sy
684	63	5.2	360	2	F70819	probable ionictran
685	63	5.2	376	2	S33654	zinc transport pro
686	63	5.2	379	2	S58464	ubiquinol-cytochro

687	63	5.2	391	2	H88955	protein K04F1.2 [i
688	63	5.2	394	2	AC1554	DltB protein for D
689	63	5.2	400	2	F86887	hypothetical prote
690	63	5.2	418	2	E86395	hypothetical prote
691	63	5.2	429	2	AC0801	probable amino aci
692	63	5.2	430	2	A90313	transport protein
693	63	5.2	433	2	AF1739	PTS system, cellob
694	63	5.2	434	2	T19205	hypothetical prote
695	63	5.2	437	2	H81041	citrate transporte
696	63	5.2	438	2	A64147	hypothetical prote
697	63	5.2	440	2	T24837	hypothetical prote
698	63	5.2	458	2	JS0616	serotonin receptor
699	63	5.2	470	2	AF0771	probable transport
700	63	5.2	493	2	C97853	NADH2 dehydrogenas
701	63	5.2	494	2	B33531	cytochrome P450 2A
702	63	5.2	521	2	T15322	hypothetical prote
703	63	5.2	526	2	C71315	probable virulence
704	63	5.2	532	2	T23481	hypothetical prote
705	63	5.2	533	2	H86282	protein F10B6.34 [
706	63	5.2	556	2	S51892	probable membrane
707	63	5.2	567	2	S58750	NADH2 dehydrogenas
708	63	5.2	600	2	T11889	NADH2 dehydrogenas
709	63	5.2	619	1	KSNCLO	laccase (EC 1.10.3
710	63	5.2	619	1	KSNCLT	laccase (EC 1.10.3
711	63	5.2	651	2	AG0448	probable membrane
712	63	5.2	653	2	T03102	semaphorin homolog
713	63	5.2	662	2	S51764	sulfate transport
714	63	5.2	681	2	S33316	structural protein
715	63	5.2	745	1	S75354	probable copper-tr
716	63	5.2	763	2	S17998	gene COX1 intron 4
717	63	5.2	835	1	WZBE51	gene 51 protein -
718	63	5.2	870	2	T25338	hypothetical prote
719	63	5.2	921	2	T51804	respiratory burst
720	63	5.2	956	2	T40953	hypothetical prote
721	63	5.2	974	2	S15038	cell division cont
722	63	5.2	994	2	H96510	probable disease r
723	63	5.2	1030	2	T18669	hypothetical prote
724	63	5.2	1043	2	F97302	hypothetical prote
725	63	5.2	1125	1	OYURCP	speract receptor p
726	63	5.2	1194	2	E96624	hypothetical prote
727	63	5.2	1294	2	S77690	probable membrane
728	63	5.2	1430	2	T27924	hypothetical prote
729	63	5.2	1776	1	RRWPYM	genome polyprotein
730	63	5.2	1998	2	T13009	hypothetical prote
731	63	5.2	2809	2	T30213	G-cadherin + sea u
732	62.5	5.1	144	2	S21349	hypothetical 16.3K
733	62.5	5.1	174	1	RDSPTA	ferredoxin-thiored
734	62.5	5.1	206	2	D83317	conserved hypothet
735	62.5	5.1	207	2	AG2553	hypothetical prote
736	62.5	5.1	237	2	T05249	hypothetical prote
737	62.5	5.1	249	2	E90048	hypothetical prote
738	62.5	5.1	261	1	HLHU2C	MHC class II histo
739	62.5	5.1	261	2	B32527	class II histocomp
740	62.5	5.1	276	2	H96985	probable hydrolase
741	62.5	5.1	296	2	AI1530	conserved hypothet
742	62.5	5.1	297	1	A30586	B-cell surface ant
743	62.5	5.1	301	2	H70584	phosphate specific
744	62.5	5.1	301	2	C85049	hypothetical prote
745	62.5	5.1	311	2	S66600	cytochrome-c oxida
746	62.5	5.1	326	2	G89835	conserved hypothet
747	62.5	5.1	327	2	T25780	hypothetical prote
748	62.5	5.1	350	1	KIBEFC	thymidine kinase (
749	62.5	5.1	350	2	D97298	uncharacterized co
750	62.5	5.1	351	2	S29152	rhodopsin - chicke
751	62.5	5.1	394	2	S39739	efflux protein hom
752	62.5	5.1	396	1	G64313	protein-export mem
753	62.5	5.1	397	2	C83470	hypothetical prote
754	62.5	5.1	413	2	S29027	aspartate transami
755	62.5	5.1	416	2	E83590	cytosine permease
756	62.5	5.1	435	2	AI2082	hypothetical prote
757	62.5	5.1	446	2	G72287	hypothetical prote
758	62.5	5.1	450	2	B81730	conserved hypothet
759	62.5	5.1	465	2	H97712	hypothetical prote
760	62.5	5.1	466	2	T32204	hypothetical prote
761	62.5	5.1	470	2	G97263	PTS system enzyme
762	62.5	5.1	473	2	G90401	flagella-related p
763	62.5	5.1	481	2	T23131	hypothetical prote
764	62.5	5.1	497	2	F86712	di-/tripeptide tra
765	62.5	5.1	502	2	T05135	hypothetical prote
766	62.5	5.1	505	2	AD0511	probable carnitine
767	62.5	5.1	516	2	A84081	hypothetical prote
768	62.5	5.1	522	2	T18504	hypothetical prote
769	62.5	5.1	546	2	D83408	hypothetical prote
770	62.5	5.1	548	2	T47510	probable transport
771	62.5	5.1	617	2	T51917	related to transfo
772	62.5	5.1	638	2	S36546	E1 protein - human
773	62.5	5.1	657	2	A54011	cationic amino aci
774	62.5	5.1	661	2	S37592	beta-fructofuranos
775	62.5	5.1	698	2	T12161	NADH2 dehydrogenas
776	62.5	5.1	700	2	T12162	NADH2 dehydrogenas
777	62.5	5.1	711	2	D86296	hypothetical prote
778	62.5	5.1	715	2	B83222	regulatory protein
779	62.5	5.1	718	2	A99195	hypothetical prote
780	62.5	5.1	849	2	T01286	probable RNA-bindi
781	62.5	5.1	855	1	JQ2003	env polyprotein -
782	62.5	5.1	1021	2	A28199	Na+/K+-exchanging
783	62.5	5.1	1070	2	F90106	IAP100 protein [im
784	62.5	5.1	1079	2	I59362	calcium/polyvalent
785	62.5	5.1	1083	2	S76111	acriflavin resista
786	62.5	5.1	1242	2	G88480	protein C16A3.7 [i
787	62.5	5.1	1289	2	S69689	hypothetical prote
788	62.5	5.1	1523	2	T13953	MEGF5 protein - ra
789	62.5	5.1	1560	2	T00080	hypothetical prote
790	62.5	5.1	1811	2	T00035	nonstructural poly
791	62	5.1	165	2	AG1903	hypothetical prote
792	62	5.1	167	2	T15114	hypothetical prote
793	62	5.1	261	2	G58888	cytochrome-c oxida
794	62	5.1	265	2	B97272	acyl-CoA thioester
795	62	5.1	318	2	JC6115	gamma-glutamyl hyd
796	62	5.1	319	1	BVECPW	phosphate transpor
797	62	5.1	319	2	AC0956	phosphate transpor
798	62	5.1	319	2	G86057	phosphate transpor
799	62	5.1	319	2	G91211	phosphate transpor
800	62	5.1	320	2	S17177	probable G protein
801	62	5.1	324	1	C69861	toxic anion resist
802	62	5.1	335	2	T32657	hypothetical prote
803	62	5.1	358	2	I38429	connexin40 - human
804	62	5.1	365	2	F85018	hypothetical prote
805	62	5.1	365	2	H71268	conserved hypothet
806	62	5.1	369	2	A72453	hypothetical prote
807	62	5.1	379	1	S17411	ubiquinol-cytochro
808	62	5.1	382	1	S33573	ubiquinol-cytochro
809	62	5.1	388	1	D70006	conserved hypothet
810	62	5.1	402	2	B75297	dipeptidyl peptida
811	62	5.1	414	2	AI0156	probable tryptopha
812	62	5.1	421	2	T27311	hypothetical prote
813	62	5.1	427	2	F97790	putrescine-ornithi
814	62	5.1	429	2	AG3150	hypothetical prote
815	62	5.1	432	2	A84798	hypothetical prote
816	62	5.1	433	2	S77340	hypothetical prote
817	62	5.1	439	2	B40839	putrescine/ornithi
818	62	5.1	439	2	H90718	putrescine transpo
819	62	5.1	439	2	H85568	putrescine transpo
820	62	5.1	444	2	T32648	hypothetical prote
821	62	5.1	445	2	T05887	hypothetical prote
822	62	5.1	447	2	F75016	hypothetical prote
823	62	5.1	448	2	F95036	PTS system, IIC co
824	62	5.1	448	2	B97907	phosphotransferase
825	62	5.1	448	2	JN0118	glucan 1,3-beta-gl
826	62	5.1	450	2	AI2324	hypothetical prote
827	62	5.1	452	2	C71391	NADH2 dehydrogenas
828	62	5.1	473	2	T04965	amino acid transpo
829	62	5.1	488	1	QXASM4	NADH2 dehydrogenas
830	62	5.1	492	2	E96731	endo-1,4-beta-gluc
831	62	5.1	520	2	H97274	uncharacterized me
832	62	5.1	598	2	T05130	hypothetical prote

833	62	5.1	609	2	T32456	hypothetical prote
834	62	5.1	610	2	T11544	NADH2 dehydrogenas
835	62	5.1	628	2	B91146	probable integral
836	62	5.1	628	2	F85991	probable integral
837	62	5.1	631	2	B98137	hypothetical 46.1K
838	62	5.1	640	2	D70850	probable oxidoredu
839	62	5.1	646	2	JN0473	P-selectin precurs
840	62	5.1	659	2	AF3489	cytochrome o ubiqu
841	62	5.1	662	2	T01857	hypothetical prote
842	62	5.1	771	2	S45048	capsid protein - h
843	62	5.1	826	2	T15751	hypothetical prote
844	62	5.1	949	1	PXMUP1	H+-exporting ATPas
845	62	5.1	972	2	E97421	NADH dehydrogenase
846	62	5.1	994	2	AD2639	pH adaption potass
847	62	5.1	1083	2	T05689	hypothetical prote
848	62	5.1	1166	2	T13958	synGAP-b1 protein
849	62	5.1	1249	2	T14270	Ras-GTPase activat
850	62	5.1	1293	2	T14259	ras GTPase-activat
851	62	5.1	2139	2	A44467	voltage-dependent
852	62	5.1	3119	2	I49729	HD protein - mouse
853	61.5	5.1	115	2	A23329	Ly-5-8 glycoprotei
854	61.5	5.1	161	2	I37034	eosinophil-derived
855	61.5	5.1	222	2	T27916	hypothetical prote
856	61.5	5.1	238	2	T23352	hypothetical prote
857	61.5	5.1	248	2	S76774	thiol-disulfide in
858	61.5	5.1	257	2	AC1290	hypothetical prote
859	61.5	5.1	260	2	I45938	MHC cell surface g
860	61.5	5.1	268	2	D29312	MHC class II histo
861	61.5	5.1	272	2	T09132	26S proteasome bet
862	61.5	5.1	281	2	C69504	probable heme A fa
863	61.5	5.1	301	1	S10456	cytochrome c-type
864	61.5	5.1	325	1	B40358	NADH2 dehydrogenas
865	61.5	5.1	325	1	DNWTU1	NADH2 dehydrogenas
866	61.5	5.1	325	1	S49576	NADH2 dehydrogenas
867	61.5	5.1	325	2	T32282	hypothetical prote
868	61.5	5.1	336	2	S75437	hypothetical prote
869	61.5	5.1	355	2	S41686	geranylgeranyltran
870	61.5	5.1	362	2	A39714	G protein-coupled
871	61.5	5.1	371	1	A75033	probable hexosyltr
872	61.5	5.1	377	2	G90737	hypothetical prote
873	61.5	5.1	377	2	H85587	hypothetical prote
874	61.5	5.1	377	2	A64816	ybhS protein - Esc
875	61.5	5.1	385	2	I51307	basolateral Na(+)-
876	61.5	5.1	391	2	AB1285	transmembrane tran
877	61.5	5.1	394	2	S23481	benE protein - Aci
878	61.5	5.1	397	2	AF3285	membrane protein m
879	61.5	5.1	417	2	AG1934	folylpolyglutamate
880	61.5	5.1	444	2	D97142	surface-layer rela
881	61.5	5.1	461	2	T11819	glycerol-3-phospha
882	61.5	5.1	462	2	D26488	tubulin alpha-4 ch
883	61.5	5.1	468	2	T41294	hypothetical prote
884	61.5	5.1	472	2	E81784	glutamate-ammonia
885	61.5	5.1	481	2	T27435	hypothetical prote
886	61.5	5.1	487	2	T49424	hypothetical prote
887	61.5	5.1	491	2	B86096	xylose-proton symp
888	61.5	5.1	491	2	F91255	xylose-proton symp
889	61.5	5.1	491	2	A26430	xylose transport p
890	61.5	5.1	497	1	WMBELM	membrane protein L
891	61.5	5.1	504	2	A83901	hypothetical prote
892	61.5	5.1	510	1	DERZN2	NADH2 dehydrogenas
893	61.5	5.1	510	2	S65075	NADH2 dehydrogenas
894	61.5	5.1	512	2	E96024	conserved hypothet
895	61.5	5.1	516	2	T47509	probable transport
896	61.5	5.1	524	2	S28902	glutamate transpor
897	61.5	5.1	530	2	T04871	hypothetical prote
898	61.5	5.1	533	2	E64626	ABC transporter, A
899	61.5	5.1	533	2	H71886	probable ABC trans
900	61.5	5.1	537	2	T02982	probable sucrose t
901	61.5	5.1	538	2	E72752	hypothetical prote
902	61.5	5.1	543	2	S65462	glucose transport
903	61.5	5.1	547	2	D95337	probable manganese
904	61.5	5.1	575	2	D71642	glutathione-regula
905	61.5	5.1	611	2	T21747	hypothetical prote
906	61.5	5.1	647	2	JQ2149	B west mating prot
907	61.5	5.1	651	2	F82124	cytochrome c-type
908	61.5	5.1	661	2	S37591	beta-fructofuranos
909	61.5	5.1	661	2	S37590	beta-fructofuranos
910	61.5	5.1	670	1	DNOBU5	NADH2 dehydrogenas
911	61.5	5.1	673	2	S59263	probable membrane
912	61.5	5.1	677	1	A45264	system b(0,+) amin
913	61.5	5.1	698	2	T12559	NADH2 dehydrogenas
914	61.5	5.1	699	2	T12167	NADH2 dehydrogenas
915	61.5	5.1	699	2	T12172	NADH2 dehydrogenas
916	61.5	5.1	787	2	S09411	DNA translocase sp
917	61.5	5.1	799	2	T48451	myotubularin-like
918	61.5	5.1	889	2	JC6015	chitin synthase (E
919	61.5	5.1	898	2	D86122	Mg2+ transport ATP
920	61.5	5.1	898	2	E65236	Mg(2+) transport A
921	61.5	5.1	898	2	C91281	Mg2+ transport ATP
922	61.5	5.1	929	2	C90531	cation-transportin
923	61.5	5.1	972	2	S67048	MTR10 protein - ye
924	61.5	5.1	1029	2	AG3363	acriflavin resista
925	61.5	5.1	1034	2	S49947	SMT4 protein - yea
926	61.5	5.1	1344	2	S47412	gene P2 protein -
927	61.5	5.1	1449	2	S47423	E2 glycoprotein pr
928	61.5	5.1	1488	2	F86428	probable ABC trans
929	61.5	5.1	2179	1	GNNYH4	genome polyprotein
930	61	5.0	155	2	G90043	hypothetical prote
931	61	5.0	189	2	A71569	hypothetical prote
932	61	5.0	193	2	B91170	hypothetical membr
933	61	5.0	193	2	B86016	hypothetical prote
934	61	5.0	200	2	S43593	M04D8.6 protein -
935	61	5.0	213	2	A34633	H+-exporting ATPas
936	61	5.0	216	2	C87037	probable secreted
937	61	5.0	226	2	I49589	antigen - mouse
938	61	5.0	251	2	T44070	conserved hypothet
939	61	5.0	255	2	E64604	conserved hypothet
940	61	5.0	257	2	I54285	MHC class II histo
941	61	5.0	274	2	C47700	glycerol uptake fa
942	61	5.0	282	2	T03906	cytochrome B561 ho
943	61	5.0	287	2	C82158	ROK family protein
944	61	5.0	297	2	D83438	probable transport
945	61	5.0	302	2	T03109	probable membrane
946	61	5.0	302	2	C64311	Na+/Ca2+-exchangin
947	61	5.0	316	2	E83768	D-3-phosphoglycera
948	61	5.0	322	2	D96921	oligopeptide trans
949	61	5.0	326	2	S70596	NADH2 dehydrogenas
950	61	5.0	348	2	T04923	hypothetical prote
951	61	5.0	369	2	S74017	hypothetical prote
952	61	5.0	375	2	C97217	gGDEF domain conta
953	61	5.0	379	1	S17417	ubiquinol-cytochro
954	61	5.0	379	1	S41833	ubiquinol-cytochro
955	61	5.0	379	2	I48135	ubiquinol-cytochro
956	61	5.0	379	2	T11401	ubiquinol-cytochro
957	61	5.0	380	2	T11803	ubiquinol-cytochro
958	61	5.0	382	2	S73256	hypothetical prote
959	61	5.0	392	2	E91290	probable transport
960	61	5.0	392	2	H86131	probable transport
961	61	5.0	401	2	H69833	conserved hypothet
962	61	5.0	402	2	G89911	conserved hypothet
963	61	5.0	412	2	S13035	aspartate transami
964	61	5.0	413	2	S29028	aspartate transami
965	61	5.0	413	2	JT0439	aspartate transami
966	61	5.0	429	2	AH2409	hypothetical prote
967	61	5.0	430	2	B83633	hypothetical prote
968	61	5.0	445	2	AI2724	potassium uptake p
969	61	5.0	445	2	B83931	hypothetical prote
970	61	5.0	448	2	S40439	tubulin alpha-2 ch
971	61	5.0	460	1	S48489	allantoinase (EC 3
972	61	5.0	463	2	G85781	part of a kinase [
973	61	5.0	463	2	C90933	part of a kinase [
974	61	5.0	466	2	S36577	L2 protein - human
975	61	5.0	467	2	S33181	glutamate-ammonia
976	61	5.0	475	2	T33943	hypothetical prote
977	61	5.0	480	2	S50525	hypothetical prote
978	61	5.0	485	2	E97506	potassium uptake p

979	61	5.0	494	2	S16068	testosterone 15alp
980	61	5.0	494	2	A32030	coumarin 7-monooxy
981	61	5.0	503	2	F71038	probable pyrimidin
982	61	5.0	532	2	H96840	hypothetical prote
983	61	5.0	535	2	T47629	phosphate transpor
984	61	5.0	545	2	S59143	NADH2 dehydrogenas
985	61	5.0	555	2	T38108	high-affinity gluc
986	61	5.0	574	2	AC1414	ABC transporter re
987	61	5.0	576	2	S14834	lysine-tRNA ligase
988	61	5.0	583	2	T32266	hypothetical prote
989	61	5.0	585	2	B49596	genome polyprotein
990	61	5.0	598	2	S66954	probable membrane
991	61	5.0	602	2	T11438	NADH2 dehydrogenas
992	61	5.0	602	2	AB0024	probable potassium
993	61	5.0	610	2	T26761	hypothetical prote
994	61	5.0	648	2	T47988	serine/threonine-p
995	61	5.0	659	2	D72083	transport ATP bind
996	61	5.0	659	2	C86542	Transport ATP Bind
997	61	5.0	668	2	T05257	probable disease r
998	61	5.0	700	2	E69146	sensory transducti
999	61	5.0	715	2	AF1829	two-component hybr
1000	61	5.0	770	2	T23999	hypothetical prote
1001	61	5.0	970	2	AI3605	potassium efflux s
1002	61	5.0	1036	2	A42895	H+/K+-exchanging A
1003	61	5.0	1037	2	S37879	nuclear pore prote
1004	61	5.0	1041	2	C87645	AcrB/AcrD/AcrF fam
1005	61	5.0	1043	2	T13172	gag-like protein p
1006	61	5.0	1065	2	H95321	NolG efflux transp
1007	61	5.0	1198	2	T49726	hypothetical prote
1008	61	5.0	1441	2	A88355	protein Y48E1A.1 [
1009	61	5.0	1545	1	S71841	multidrug resistan
1010	61	5.0	1737	2	T19606	hypothetical prote
1011	61	5.0	1821	2	AG2335	hypothetical prote
1012	61	5.0	1869	2	A59290	class V chitin syn
1013	61	5.0	2220	2	A45290	calcium channel pr
1014	61	5.0	2539	2	B71619	hypothetical prote
1015	60.5	5.0	113	2	B87205	probable membrane
1016	60.5	5.0	119	2	S41816	Ig kappa chain V r
1017	60.5	5.0	151	2	T34640	probable integral
1018	60.5	5.0	165	2	B72727	hypothetical prote
1019	60.5	5.0	167	2	F84867	hypothetical prote
1020	60.5	5.0	212	2	T26887	hypothetical prote
1021	60.5	5.0	232	2	I47094	MHC class II OLA-D
1022	60.5	5.0	243	2	E70986	hypothetical prote
1023	60.5	5.0	264	2	A75076	membrane protein P
1024	60.5	5.0	267	2	E89870	hypothetical prote
1025	60.5	5.0	269	2	S65034	cytochrome-c oxida
1026	60.5	5.0	276	2	E65072	hypothetical prote
1027	60.5	5.0	277	2	D98085	hypothetical prote
1028	60.5	5.0	278	2	E95221	sugar ABC transpor
1029	60.5	5.0	283	2	T22776	hypothetical prote
1030	60.5	5.0	283	2	AE2081	hypothetical prote
1031	60.5	5.0	289	2	B43747	hypothetical prote
1032	60.5	5.0	289	2	B43748	hypothetical prote
1033	60.5	5.0	293	1	QQCVPY	BL1 protein - pota
1034	60.5	5.0	300	2	S15786	glucose transport
1035	60.5	5.0	304	2	A97768	probable protease
1036	60.5	5.0	305	2	C89915	hypothetical prote
1037	60.5	5.0	314	2	T21003	hypothetical prote
1038	60.5	5.0	315	2	D64458	branched-chain ami
1039	60.5	5.0	323	2	T15808	hypothetical prote
1040	60.5	5.0	328	2	D45774	odorant receptor 3
1041	60.5	5.0	332	2	AE2438	thiamin monophosph
1042	60.5	5.0	344	2	T04924	hypothetical prote
1043	60.5	5.0	349	2	S59648	hypothetical prote
1044	60.5	5.0	363	2	T24809	hypothetical prote
1045	60.5	5.0	363	2	S42386	hypothetical prote
1046	60.5	5.0	379	1	S17414	ubiquinol-cytochro
1047	60.5	5.0	379	2	S58462	ubiquinol-cytochro
1048	60.5	5.0	382	1	A39802	gap junction prote
1049	60.5	5.0	382	1	S00532	gap junction prote
1050	60.5	5.0	383	1	A36623	gap junction prote
1051	60.5	5.0	384	2	A86521	hypothetical prote
1052	60.5	5.0	384	2	E72100	hypothetical prote
1053	60.5	5.0	390	2	B96793	unknown protein F1
1054	60.5	5.0	398	2	A97686	probable transport
1055	60.5	5.0	398	2	AC2911	MFS permease [impo
1056	60.5	5.0	401	2	E82951	probable MFS trans
1057	60.5	5.0	416	2	T02194	probable pectinace
1058	60.5	5.0	417	2	T13759	NADH2 dehydrogenas
1059	60.5	5.0	418	2	T40913	probable integral
1060	60.5	5.0	432	2	A83616	dicarboxylic acid
1061	60.5	5.0	433	2	S74922	hypothetical prote
1062	60.5	5.0	445	2	S77010	nickel resistance
1063	60.5	5.0	452	2	S58994	NADH2 dehydrogenas
1064	60.5	5.0	454	2	F71313	probable V-type AT
1065	60.5	5.0	455	2	E91098	probable oxidoredu
1066	60.5	5.0	455	2	A85944	hypothetical prote
1067	60.5	5.0	458	2	S50919	hypothetical prote
1068	60.5	5.0	459	2	B69580	amino acid permeas
1069	60.5	5.0	467	2	D86583	ubiquinone oxidore
1070	60.5	5.0	467	2	E72040	probable sodium-tr
1071	60.5	5.0	472	2	AI3367	multidrug resistan
1072	60.5	5.0	480	2	S63390	BIO3 protein - yea
1073	60.5	5.0	484	2	T07782	cytochrome-c oxida
1074	60.5	5.0	487	2	AF2692	MFS permease [impo
1075	60.5	5.0	492	2	A34272	testosterone 7alph
1076	60.5	5.0	501	1	DELVN2	NADH2 dehydrogenas
1077	60.5	5.0	528	2	B97474	hypothetical prote
1078	60.5	5.0	529	2	T23190	hypothetical prote
1079	60.5	5.0	546	2	T33745	hypothetical prote
1080	60.5	5.0	554	2	T08976	2-amino-4-hydroxy-
1081	60.5	5.0	586	2	S24966	sucrose synthase (
1082	60.5	5.0	603	2	T11284	NADH2 dehydrogenas
1083	60.5	5.0	623	2	B81037	lipopolysaccharide
1084	60.5	5.0	627	2	A38538	lactose permease -
1085	60.5	5.0	635	1	A64162	cytochrome c-type
1086	60.5	5.0	638	2	T26490	hypothetical prote
1087	60.5	5.0	653	2	A54366	sodium/phosphate c
1088	60.5	5.0	667	2	T41306	probable sulfate t
1089	60.5	5.0	681	2	A45705	type I transmembra
1090	60.5	5.0	682	2	B86336	hypothetical prote
1091	60.5	5.0	694	2	T13573	NADH2 dehydrogenas
1092	60.5	5.0	699	2	T12163	NADH2 dehydrogenas
1093	60.5	5.0	699	2	T12169	NADH2 dehydrogenas
1094	60.5	5.0	699	2	T12164	NADH2 dehydrogenas
1095	60.5	5.0	699	2	T12168	NADH2 dehydrogenas
1096	60.5	5.0	706	2	S53035	probable lysophosp
1097	60.5	5.0	714	2	S56208	hypothetical prote
1098	60.5	5.0	719	2	F96577	hypothetical prote
1099	60.5	5.0	720	2	T02361	hypothetical prote
1100	60.5	5.0	804	2	T14762	hypothetical prote
1101	60.5	5.0	807	2	S29242	sucrose synthase (
1102	60.5	5.0	809	2	T16448	hypothetical prote
1103	60.5	5.0	883	2	T51221	hypothetical prote
1104	60.5	5.0	945	2	S77052	cation-transportin
1105	60.5	5.0	1244	2	C96584	hypothetical prote
1106	60.5	5.0	1245	2	G86404	probable P-glycopr
1107	60.5	5.0	1249	2	F86909	probable DNA gyras
1108	60.5	5.0	1273	2	T10006	DNA topoisomerase
1109	60.5	5.0	1449	1	A43573	E2 glycoprotein pr
1110	60.5	5.0	1449	1	VGIHFS	E2 glycoprotein pr
1111	60.5	5.0	1483	2	S42839	T16G12.5 protein -
1112	60.5	5.0	1657	2	T15838	hypothetical prote
1113	60.5	5.0	1720	2	T07258	cell division prot
1114	60.5	5.0	2718	2	A23475	G surface protein
1115	60.5	5.0	3449	2	T01083	hypothetical prote
1116	60.5	5.0	4845	2	T31067	BIR repeat contain
1117	60	4.9	120	2	AI1357	hypothetical prote
1118	60	4.9	126	2	D96653	hypothetical prote
1119	60	4.9	136	2	B72105	disulfide bond oxi
1120	60	4.9	136	2	C86519	disulfide bond oxi
1121	60	4.9	160	2	G69955	hypothetical prote
1122	60	4.9	202	2	A61379	22K antigen - Rick
1123	60	4.9	205	2	C90491	hypothetical prote
1124	60	4.9	215	2	S16564	nolH protein - Rhi

1125	60	4.9	228	1	A40402	CD9 antigen [valid
1126	60	4.9	228	1	A42929	CD9 antigen - gree
1127	60	4.9	228	2	B90369	hypothetical prote
1128	60	4.9	234	2	AG1220	glycerol uptake fa
1129	60	4.9	251	2	H69441	carboxylesterase (
1130	60	4.9	257	2	AI1661	hypothetical prote
1131	60	4.9	258	2	I54458	MHC class II histo
1132	60	4.9	265	2	A83969	hypothetical prote
1133	60	4.9	268	2	T24795	hypothetical prote
1134	60	4.9	287	2	T18735	hypothetical prote
1135	60	4.9	291	2	E91089	prolipoprotein dia
1136	60	4.9	291	2	G85934	prolipoprotein dia
1137	60	4.9	291	2	A56149	prolipoprotein dia
1138	60	4.9	293	2	AF2904	ABC transporter, m
1139	60	4.9	293	2	H97679	probable ABC trans
1140	60	4.9	301	2	S76574	hypothetical prote
1141	60	4.9	303	2	AE3129	conserved hypothet
1142	60	4.9	303	2	D98158	hypothetical prote
1143	60	4.9	307	2	G84962	hypothetical prote
1144	60	4.9	309	2	T40759	syntaxin, vesicula
1145	60	4.9	338	2	G70584	phosphate transpor
1146	60	4.9	348	2	E86818	dehydrogenase [imp
1147	60	4.9	350	2	B82281	ferric vibriobacti
1148	60	4.9	355	2	I51319	RH2 opsin - green
1149	60	4.9	357	2	T33237	hypothetical prote
1150	60	4.9	365	2	I38748	protaglandin recep
1151	60	4.9	365	2	S51315	prostaglandin E re
1152	60	4.9	370	2	H90559	hypothetical prote
1153	60	4.9	374	2	I38747	protaglandin recep
1154	60	4.9	374	2	S51317	prostaglandin E re
1155	60	4.9	374	2	T26200	hypothetical prote
1156	60	4.9	379	1	S41834	ubiquinol-cytochro
1157	60	4.9	379	1	S43267	ubiquinol-cytochro
1158	60	4.9	379	2	S58450	ubiquinol-cytochro
1159	60	4.9	379	2	AE3225	ABC transporter, m
1160	60	4.9	380	2	JL0053	UDPglucose-hexose-
1161	60	4.9	380	2	E81302	probable type I re
1162	60	4.9	381	2	T11440	ubiquinol-cytochro
1163	60	4.9	381	2	T23250	hypothetical prote
1164	60	4.9	382	2	G90751	probable transport
1165	60	4.9	382	2	E85615	probable transport
1166	60	4.9	382	2	A64829	membrane protein y
1167	60	4.9	388	2	S51316	prostaglandin E re
1168	60	4.9	388	2	I38750	protaglandin recep
1169	60	4.9	390	2	S43375	prostaglandin E re
1170	60	4.9	390	2	S51313	prostaglandin E re
1171	60	4.9	393	2	AC2782	diaminopimelate de
1172	60	4.9	393	2	S51318	prostaglandin E re
1173	60	4.9	393	2	E96954	Na/H antiporter (n
1174	60	4.9	394	2	AE1196	DltB protein for D
1175	60	4.9	400	2	AG0068	cell division prot
1176	60	4.9	403	2	G64427	hypothetical prote
1177	60	4.9	405	2	AE1474	probable permeases
1178	60	4.9	412	2	S72579	hypothetical prote
1179	60	4.9	417	2	A45794	tubulin alpha chai
1180	60	4.9	422	2	AB3635	probable O-antigen
1181	60	4.9	425	2	S51319	prostaglandin E re
1182	60	4.9	436	2	AC1021	proton glutamate s
1183	60	4.9	437	2	JC5459	inulin fructotrans
1184	60	4.9	440	2	D97561	btrK (AB033991) [i
1185	60	4.9	449	2	C75053	DNA damage-inducib
1186	60	4.9	452	2	F64730	UDP-N-acetylmuramo
1187	60	4.9	455	2	T37517	hypothetical prote
1188	60	4.9	458	2	B81409	probable transmemb
1189	60	4.9	462	2	D81251	NADH2 dehydrogenas
1190	60	4.9	463	2	S59968	secY protein - Sul
1191	60	4.9	465	2	H87627	response regulator
1192	60	4.9	469	2	AE3374	glutamate-ammonia
1193	60	4.9	474	2	T34193	G protein-coupled
1194	60	4.9	476	2	H82085	sodium/alanine sym
1195	60	4.9	478	2	A37430	calcitonin recepto
1196	60	4.9	479	2	S33746	calcitonin recepto
1197	60	4.9	491	2	G84498	hypothetical prote
1198	60	4.9	502	2	E87596	tryptophan halogen
1199	60	4.9	508	2	T19350	hypothetical prote
1200	60	4.9	509	2	A32101	glucose transport
1201	60	4.9	534	2	C84811	phosphate transpor
1202	60	4.9	556	2	H82287	malate synthase A
1203	60	4.9	557	2	AE0204	methyl-accepting c
1204	60	4.9	557	2	T46520	probable transmemb
1205	60	4.9	557	2	S58688	probable transport
1206	60	4.9	577	2	T32336	hypothetical prote
1207	60	4.9	578	2	T35537	cytochrome-c oxida
1208	60	4.9	603	2	H69121	hypothetical prote
1209	60	4.9	608	2	T25572	hypothetical prote
1210	60	4.9	616	2	A30304	prolactin receptor
1211	60	4.9	623	2	C86184	hypothetical prote
1212	60	4.9	633	2	S45877	uracil transport p
1213	60	4.9	635	2	S30018	allantoin transpor
1214	60	4.9	638	2	T11801	NADH2 dehydrogenas
1215	60	4.9	640	2	S23008	insulin-like growt
1216	60	4.9	679	2	A83488	hypothetical prote
1217	60	4.9	703	2	T13074	NADH2 dehydrogenas
1218	60	4.9	746	1	HYHUMA	meprin A (EC 3.4.2
1219	60	4.9	795	2	T31180	hypothetical prote
1220	60	4.9	795	2	H70934	hypothetical prote
1221	60	4.9	860	2	T49910	hypothetical prote
1222	60	4.9	933	2	C83514	probable NADH dehy
1223	60	4.9	960	2	T06688	H+-exporting ATPas
1224	60	4.9	975	2	T16073	hypothetical prote
1225	60	4.9	1033	2	T49179	Ca2+-transporting
1226	60	4.9	1095	2	A54145	sodium-potassium-c
1227	60	4.9	1128	2	T04922	hypothetical prote
1228	60	4.9	1307	2	T25106	hypothetical prote
1229	60	4.9	1402	2	T24664	hypothetical prote
1230	60	4.9	1487	2	G96827	protein F20B17.10
1231	60	4.9	1492	2	T18560	DNA-directed DNA p
1232	60	4.9	1592	2	S48933	probable transport
1233	60	4.9	1945	2	T13937	plexin A - fruit f
1234	60	4.9	2090	2	T30075	hypothetical prote
1235	60	4.9	2153	2	T30074	hypothetical prote
1236	60	4.9	2201	2	AH0095	probable sideropho
1237	60	4.9	2476	2	T34022	zonadhesin - pig
1238	60	4.9	3144	2	A46068	Huntington disease
1239	59.5	4.9	88	2	G82754	hypothetical prote
1240	59.5	4.9	92	2	D43674	US5 protein - huma
1241	59.5	4.9	112	2	A46717	colipase precursor
1242	59.5	4.9	128	2	S40379	Ig kappa chain V-J
1243	59.5	4.9	150	2	C86876	hypothetical prote
1244	59.5	4.9	155	2	D72761	hypothetical prote
1245	59.5	4.9	161	2	A33922	eosinophil-derived
1246	59.5	4.9	198	1	A60620	prolactin - green
1247	59.5	4.9	204	2	AI0059	probable LysE type
1248	59.5	4.9	227	2	H90109	27.2K hypothetical
1249	59.5	4.9	234	2	AB1574	glycerol uptake fa
1250	59.5	4.9	234	2	T30473	late expression fa
1251	59.5	4.9	235	2	AD2904	RhtB family transp
1252	59.5	4.9	235	2	F97679	hypothetical prote
1253	59.5	4.9	239	2	G64810	pnuC protein - Esc
1254	59.5	4.9	242	2	A69026	conserved hypothet
1255	59.5	4.9	244	2	B83142	hypothetical prote
1256	59.5	4.9	255	2	D71910	hypothetical prote
1257	59.5	4.9	261	2	S68134	cytochrome-c oxida
1258	59.5	4.9	263	2	S72528	chitinase (EC 3.2.
1259	59.5	4.9	270	2	AF2008	permease protein o
1260	59.5	4.9	287	2	A25877	cytochrome-c oxida
1261	59.5	4.9	289	2	H86880	transporter yvdD [
1262	59.5	4.9	291	2	S73242	hypothetical prote
1263	59.5	4.9	293	1	QQBEG1	HVLF1 protein - hu
1264	59.5	4.9	307	2	B82394	hypothetical prote
1265	59.5	4.9	309	2	T31908	hypothetical prote
1266	59.5	4.9	310	2	S64619	probable membrane
1267	59.5	4.9	318	2	AB0350	probable membrane
1268	59.5	4.9	321	2	T45986	hypothetical prote
1269	59.5	4.9	324	2	H86533	integral membrane
1270	59.5	4.9	324	2	H72088	ABC transporter, p

1271	59.5	4.9	327	2	G88976	protein F54E2.6 [i
1272	59.5	4.9	328	2	T11938	NADH2 dehydrogenas
1273	59.5	4.9	329	2	H83907	cytochrome aa3 qui
1274	59.5	4.9	336	2	AC2413	hypothetical prote
1275	59.5	4.9	337	2	A53041	effector cell prot
1276	59.5	4.9	341	2	F82301	peptide ABC transp
1277	59.5	4.9	343	2	D83282	probable permease
1278	59.5	4.9	343	2	G89795	hypothetical prote
1279	59.5	4.9	345	2	AD2998	transporter Atu359
1280	59.5	4.9	345	2	E98285	yfkh (AJ010131) [i
1281	59.5	4.9	353	1	D65025	probable permease
1282	59.5	4.9	353	2	G85892	probable permease
1283	59.5	4.9	353	2	C91048	probable permease
1284	59.5	4.9	355	2	T32723	hypothetical prote
1285	59.5	4.9	366	2	T50468	probable maturase
1286	59.5	4.9	376	2	A86382	43.4K hypothetical
1287	59.5	4.9	379	1	S41847	ubiquinol-cytochro
1288	59.5	4.9	379	2	S58454	ubiquinol-cytochro
1289	59.5	4.9	379	2	H82284	queuine tRNA-ribos
1290	59.5	4.9	387	2	T31748	hypothetical prote
1291	59.5	4.9	396	2	S01660	glycerol-3-phospha
1292	59.5	4.9	396	2	T39337	hypothetical prote
1293	59.5	4.9	402	2	AG0638	probable membrane
1294	59.5	4.9	410	2	E75048	multidrug resistan
1295	59.5	4.9	410	2	D71897	hypothetical prote
1296	59.5	4.9	418	2	G70864	probable transmemb
1297	59.5	4.9	428	2	T25950	hypothetical prote
1298	59.5	4.9	430	2	T12541	hypothetical prote
1299	59.5	4.9	431	1	SAVLC2	large surface anti
1300	59.5	4.9	433	2	T17654	hypothetical prote
1301	59.5	4.9	433	2	T27731	hypothetical prote
1302	59.5	4.9	437	2	A36372	membrane transport
1303	59.5	4.9	440	2	T11319	NADH2 dehydrogenas
1304	59.5	4.9	441	2	S47049	1-aminocyclopropan
1305	59.5	4.9	445	2	T42366	L-aminoadipate-sem
1306	59.5	4.9	449	2	A48466	tubulin alpha chai
1307	59.5	4.9	457	2	T15271	hypothetical prote
1308	59.5	4.9	465	2	S03325	transforming prote
1309	59.5	4.9	466	2	T41125	glucose-triggered
1310	59.5	4.9	469	2	AC3584	methylenomycin a r
1311	59.5	4.9	476	2	H96802	probable amino aci
1312	59.5	4.9	479	2	T47415	transporter-like p
1313	59.5	4.9	483	2	H97246	UDP-N-acetylmuramy
1314	59.5	4.9	483	2	I55598	diabetes-associate
1315	59.5	4.9	485	1	KIBYHA	hexokinase (EC 2.7
1316	59.5	4.9	497	2	T41015	proline rich prote
1317	59.5	4.9	499	1	S30007	probable UTP-gluco
1318	59.5	4.9	513	2	A81850	probable integral
1319	59.5	4.9	514	2	E86738	multidrug resistan
1320	59.5	4.9	520	1	A42209	D-stereospecific a
1321	59.5	4.9	520	2	T20007	hypothetical prote
1322	59.5	4.9	525	2	T24647	hypothetical prote
1323	59.5	4.9	530	2	AG3622	rtn protein [impor
1324	59.5	4.9	535	2	G95155	hypothetical prote
1325	59.5	4.9	535	2	B98022	hypothetical prote
1326	59.5	4.9	541	2	T31554	hypothetical prote
1327	59.5	4.9	541	2	D97930	conserved hypothet
1328	59.5	4.9	546	2	T23920	hypothetical prote
1329	59.5	4.9	552	2	T51439	oligopeptide trans
1330	59.5	4.9	557	1	S76051	hypothetical prote
1331	59.5	4.9	567	2	H87370	major facilitator
1332	59.5	4.9	567	2	A33974	membrane transport
1333	59.5	4.9	574	2	T14162	hABC transport pro
1334	59.5	4.9	576	2	T41407	membrane transport
1335	59.5	4.9	577	1	G46328	hemagglutinin-neur
1336	59.5	4.9	577	1	D46328	hemagglutinin-neur
1337	59.5	4.9	577	1	HNNZNC	hemagglutinin-neur
1338	59.5	4.9	577	2	H81355	probable integral
1339	59.5	4.9	586	2	A95167	ABC transporter, A
1340	59.5	4.9	601	2	T48539	probable potassium
1341	59.5	4.9	605	2	T11111	NADH2 dehydrogenas
1342	59.5	4.9	607	1	QXMS5M	NADH2 dehydrogenas
1343	59.5	4.9	612	2	A97935	hypothetical prote
1344	59.5	4.9	615	2	H82635	hypothetical prote
1345	59.5	4.9	622	2	B71326	probable V-type AT
1346	59.5	4.9	626	2	H82133	conserved hypothet
1347	59.5	4.9	633	2	T33306	hypothetical prote
1348	59.5	4.9	646	2	T48902	sulfate transporte
1349	59.5	4.9	658	2	T49069	sulfate transporte
1350	59.5	4.9	658	2	T48901	sulfate transporte
1351	59.5	4.9	660	2	H87590	cytochrome c-type
1352	59.5	4.9	682	2	T18847	hypothetical prote
1353	59.5	4.9	686	2	A45483	chloride channel,
1354	59.5	4.9	699	2	T12170	NADH2 dehydrogenas
1355	59.5	4.9	699	2	T12173	NADH2 dehydrogenas
1356	59.5	4.9	703	2	T51161	hypothetical prote
1357	59.5	4.9	710	2	S62575	hypothetical prote
1358	59.5	4.9	714	2	S76082	hypothetical prote
1359	59.5	4.9	726	2	S22258	probable protein k
1360	59.5	4.9	778	2	T05341	S-receptor kinase
1361	59.5	4.9	800	2	G89831	hypothetical prote
1362	59.5	4.9	821	2	T41364	hypothetical prote
1363	59.5	4.9	828	2	E71417	hypothetical prote
1364	59.5	4.9	914	1	JN0550	iodide peroxidase
1365	59.5	4.9	953	2	S19427	probable membrane
1366	59.5	4.9	1027	2	T43024	ceoB protein - Bur
1367	59.5	4.9	1088	2	T41671	hypothetical prote
1368	59.5	4.9	1129	2	D84022	ATP-dependent nucl
1369	59.5	4.9	1161	2	B70172	DNA polymerase III
1370	59.5	4.9	1187	2	T20544	hypothetical prote
1371	59.5	4.9	1217	2	T13996	pol protein - frui
1372	59.5	4.9	1220	2	T18291	patched protein -
1373	59.5	4.9	1237	2	A54080	protein-tyrosine-p
1374	59.5	4.9	1247	2	T18671	hypothetical prote
1375	59.5	4.9	1268	2	G85154	hypothetical prote
1376	59.5	4.9	1289	1	GUBPT4	proximal tail fibe
1377	59.5	4.9	1429	2	T19422	hypothetical prote
1378	59.5	4.9	1584	2	T18276	protein-tyrosine k
1379	59.5	4.9	1758	2	F88559	protein C48B4.4b [
1380	59.5	4.9	1807	2	JC6319	integrin beta-4 ch
1381	59.5	4.9	1964	2	T09059	notch4 - mouse
1382	59.5	4.9	2514	2	T37320	ataxia telangiecta
1383	59.5	4.9	2619	2	T24588	hypothetical prote
1384	59.5	4.9	3766	2	T29165	hypothetical prote
1385	59.5	4.9	3944	2	T19997	hypothetical prote
1386	59	4.9	125	2	T49512	hypothetical prote
1387	59	4.9	158	2	AI1184	hypothetical prote
1388	59	4.9	208	2	T05859	hypothetical prote
1389	59	4.9	208	2	A89773	hypothetical prote
1390	59	4.9	219	2	D90448	conserved hypothet
1391	59	4.9	226	2	S57521	probable arsenical
1392	59	4.9	242	2	S60143	cellulase (EC 3.2.
1393	59	4.9	248	2	T01080	hypothetical prote
1394	59	4.9	249	2	T25643	hypothetical prote
1395	59	4.9	250	2	B64417	hypothetical prote
1396	59	4.9	254	2	B90421	hypothetical prote
1397	59	4.9	258	2	I59621	HLA-DPB1 - human
1398	59	4.9	265	2	H90868	probable pump prot
1399	59	4.9	265	2	A85750	probable pump prot
1400	59	4.9	277	2	AE1831	hypothetical prote
1401	59	4.9	281	2	AI0461	sn-glycerol-3-phos
1402	59	4.9	284	2	T06129	zinc finger protei
1403	59	4.9	289	2	G83029	hypothetical prote
1404	59	4.9	292	2	C95147	licB protein [impo
1405	59	4.9	296	2	A98015	hypothetical prote
1406	59	4.9	305	2	E83890	sugar transport sy
1407	59	4.9	307	2	H71160	hypothetical prote
1408	59	4.9	310	2	A29884	prolactin receptor
1409	59	4.9	311	2	T32776	hypothetical prote
1410	59	4.9	313	2	S06214	NADH2 dehydrogenas
1411	59	4.9	322	2	H96994	cobalamin biosynth
1412	59	4.9	325	2	AH0796	NADH2 dehydrogenas
1413	59	4.9	326	2	S59101	NADH2 dehydrogenas
1414	59	4.9	329	2	AC1718	ferrichrome ABC tr
1415	59	4.9	336	2	AF1378	B. subtilis ferric
1416	59	4.9	336	2	AG1747	B. subtilis ferric

1417	59	4.9	343	2	A43577	regulatory protein
1418	59	4.9	345	2	C45456	NADH2 dehydrogenas
1419	59	4.9	346	2	T46914	hypothetical prote
1420	59	4.9	346	2	S49959	probable membrane
1421	59	4.9	348	1	OOBO	rhodopsin - bovine
1422	59	4.9	349	2	AG3010	hypothetical prote
1423	59	4.9	349	2	G98273	iron(III) dicitrat
1424	59	4.9	353	2	S14203	NADH2 dehydrogenas
1425	59	4.9	353	2	C72479	hypothetical prote
1426	59	4.9	356	2	AE2729	cytochrome oxidase
1427	59	4.9	360	2	D84646	hypothetical prote
1428	59	4.9	361	2	T34159	hypothetical prote
1429	59	4.9	363	2	B86229	hypothetical prote
1430	59	4.9	366	2	G95376	conserved hypothet
1431	59	4.9	372	2	F97510	BA483f11.2.1 (cox1
1432	59	4.9	378	2	T15816	hypothetical prote
1433	59	4.9	379	2	T11453	ubiquinol-cytochro
1434	59	4.9	379	2	T11869	ubiquinol-cytochro
1435	59	4.9	382	2	D58930	ubiquinol-cytochro
1436	59	4.9	385	2	G72638	hypothetical prote
1437	59	4.9	386	2	A26017	patatin T5 precurs
1438	59	4.9	387	2	E83679	multidrug-efflux t
1439	59	4.9	388	2	AC2011	hypothetical prote
1440	59	4.9	394	2	AB3073	tetracycline resis
1441	59	4.9	394	2	G98213	drug efflux protei
1442	59	4.9	395	2	E90896	probable transport
1443	59	4.9	395	2	B85721	probable transport
1444	59	4.9	395	2	E90047	hypothetical prote
1445	59	4.9	401	2	S42583	phosphate transloc
1446	59	4.9	403	2	F83092	probable cytochrom
1447	59	4.9	404	2	S03638	triose phosphate/3
1448	59	4.9	408	2	G69819	Na+/H+ antiporter
1449	59	4.9	412	2	A26341	aspartate transami
1450	59	4.9	412	2	T34138	hypothetical prote
1451	59	4.9	412	2	A41070	prolactin receptor
1452	59	4.9	414	2	D82487	multidrug resistan
1453	59	4.9	414	2	S39530	poly(3-hydroxybuty
1454	59	4.9	415	2	D96759	probable serine ca
1455	59	4.9	418	2	E71848	probable nucleosid
1456	59	4.9	419	2	B69819	conserved hypothet
1457	59	4.9	420	2	F69144	O-antigen transpor
1458	59	4.9	428	2	AE1611	probable proteinas
1459	59	4.9	432	2	C85087	hypothetical prote
1460	59	4.9	433	2	S31436	Ig upsilon chain -
1461	59	4.9	433	2	B84566	hypothetical prote
1462	59	4.9	437	2	S11497	branched-chain ami
1463	59	4.9	438	2	AF3215	ABC transporter, m
1464	59	4.9	444	2	T27866	hypothetical prote
1465	59	4.9	444	2	C75428	probable permease
1466	59	4.9	445	2	C69596	branched-chain ami
1467	59	4.9	448	2	T22194	hypothetical prote
1468	59	4.9	449	2	S55911	tubulin alpha-1 ch
1469	59	4.9	449	2	T21415	hypothetical prote
1470	59	4.9	457	2	T12399	NADH2 dehydrogenas
1471	59	4.9	457	2	S18239	glycerol-3-phospha
1472	59	4.9	457	2	H64136	neurotransmitter t
1473	59	4.9	458	2	H82200	sodium/alanine sym
1474	59	4.9	461	2	T00621	hypothetical prote
1475	59	4.9	464	2	H83271	soluble pyridine n
1476	59	4.9	470	2	AB1804	transmembrane effl
1477	59	4.9	471	2	D64974	hypothetical prote
1478	59	4.9	471	2	H85834	probable transport
1479	59	4.9	471	2	E90989	probable transport
1480	59	4.9	473	2	T44709	acetyl/propionyl C
1481	59	4.9	476	2	A44170	membrane-bound rib
1482	59	4.9	487	1	QQECRS	ygjE protein - Esc
1483	59	4.9	487	2	T19237	hypothetical prote
1484	59	4.9	493	2	I39541	cytolytic enteroto
1485	59	4.9	507	2	H75175	thymidine phosphor
1486	59	4.9	508	2	E90594	amino acid permeas
1487	59	4.9	517	2	S77255	hypothetical prote
1488	59	4.9	523	2	S55677	glutamate transpor
1489	59	4.9	529	2	AF3059	cytochrome d oxida
1490	59	4.9	529	2	B98227	cytochrome d oxida
1491	59	4.9	534	1	S75101	hypothetical prote
1492	59	4.9	551	2	B64005	hypothetical prote
1493	59	4.9	552	2	B90476	hypothetical prote
1494	59	4.9	562	2	C71604	RNA helicase PFB08
1495	59	4.9	564	2	S73405	hexosephosphate tr
1496	59	4.9	581	2	B90539	hypothetical prote
1497	59	4.9	597	2	T23961	hypothetical prote
1498	59	4.9	598	2	T28238	ORF MSV077 hypothe
1499	59	4.9	603	2	S53301	H+-exporting ATPas
1500	59	4.9	610	2	A34631	lactogen receptor

ALIGNMENTS

RESULT 1
A42926
L6 surface protein - human
C;Species: Homo sapiens (man)
C;Date: 01-Oct-1992 #sequence_revision 01-Oct-1992 #text_change 09-Jul-2004
C;Accession: A42926
R;Marken, J.S.; Schieven, G.L.; Hellstroem, I.; Hellstroem, K.E.; Aruffo, A.
Proc. Natl. Acad. Sci. U.S.A. 89, 3503-3507, 1992
A;Title: Cloning and expression of the tumor-associated antigen L6.
A;Reference number: A42926; MUID:92228814; PMID:1565644
A;Accession: A42926
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-202 <MAR>
A;Cross-references: UNIPROT:P30408; UNIPARC:UPI0000044E0A; GB:M90657; NID:g186803; PIDN:A
C;Keywords: transmembrane protein

Query Match 14.0%; Score 170; DB 2; Length 202;
Best Local Similarity 27.4%; Pred. No. 3.1e-08;
Matches 62; Conservative 29; Mismatches 77; Indels 58; Gaps 8;

```
Qy         10 CNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAG-LMAIPATTM 68
              | | ||: | || :  | | |      |    |:| :| | |:| ||:| | || :||
Db          9 CIGHSLVGLALLCIAAN-ILLYFPNGETKYASENHLSRFVWFFSGIVGGGLLMLLPAFVF 67

Qy         69 SLTARKRAC-------CNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPSN 121
                 :   |       |  |  |  |   ::| : |: ||::::   | :|||  :|
Db         68 IGLEQDDCCGCCGHENCGKRCAMLSSVLAALIGIAGSGYCVIVAALGLAEGPLCLDSLG- 126

Qy        122 SNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSE- 180
                                  ||                | | ||      :  |:
Db        127 ----------------------QW----------------NYTFAS--TEGQYLLDTST 145

Qy        181 -----ENKHRL-IHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCG 220
                  | || :  : |:|  || :| :| :  | |:: | || :||
Db        146 WSECTEPKHIVEWNVSLFSILLALGGIEFILCLIQVINGVLGGICG 191
```

RESULT 2
JC6544
tumor-associated antigen TM4SF5 - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C;Accession: JC6544
R;Mueller-Pillasch, F.; Wallrapp, C.; Lacher, U.; Friess, H.; Buechler, M.; Adler, G.; Gr
Gene 208, 25-30, 1998
A;Title: Identification of a new tumour-associated antigen TM4SF5 and its expression in h
A;Reference number: JC6544; MUID:98148000; PMID:9479038
A;Accession: JC6544
A;Molecule type: mRNA
A;Residues: 1-197 <MUE>
A;Cross-references: UNIPROT:O14894; UNIPARC:UPI000013683E
C;Comment: This protein plays a role in cell proliferation.
C;Genetics:
A;Gene: tm4sf5
A;Map position: 17p13.3
C;Keywords: glycoprotein; transmembrane protein

```
F;10-30/Domain: transmembrane #status predicted <TM1>
F;43-68/Domain: transmembrane #status predicted <TM2>
F;91-112/Domain: transmembrane #status predicted <TM3>
F;158-187/Domain: transmembrane #status predicted <TM4>
F;138,155/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             13.7%;  Score 166;  DB 2;  Length 197;
  Best Local Similarity   26.1%;  Pred. No. 7e-08;
  Matches   60;  Conservative   32;  Mismatches   92;  Indels   46;  Gaps    7;

Qy          3 CCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA 62
              |       | | ||: |  : :| ||: |:|   |    : | :|   |   | || |||
Db          2 CTGKCARCVGLSLITLCFVCIVANAL-LLVPNGETSWTNTNHLSLQVWLMGGFIGGGLMV 60

Qy         63 IPATTMSLTARKR-----ACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCN 117
              :     :: | :      || ||  |  | | |   |:||:||: :|   |  ||
Db         61 LCPGIAAVRAGGKGCCGAGCCGNRCRMLRSVFSSAFGVLGAIYCLSVSGAGLRNGP---- 116

Qy        118 SPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHF 177
                          | :| ::              || |  :  :   :
Db        117 -------RC-------------LMNGEWGYH-------------FEDT-AGAYLLNRTLW 142

Qy        178 DSEENKHRLIHFSVFLGLLLV--GILEVLFGLSQIVIGFLGCLCGVSKRR 225
              |  |   |:: ::| |  |||    ||::    |:|   :|  ||  :::
Db        143 DRCEAPPRVVPWNVTLFSLLVAASCLEIVLCGIQLVNATIGVFCGDCRKK 192


RESULT 3
A53399
L6 antigen - mouse
C;Species: Mus musculus (house mouse)
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 09-Jul-2004
C;Accession: A53399
R;Marken, J.S.; Bajorath, J.; Edwards, C.P.; Farr, A.G.; Schieven, G.L.; Hellstroem, I.;
J. Biol. Chem. 269, 7397-7401, 1994
A;Title: Membrane topology of the L6 antigen and identification of the protein epitope r
A;Reference number: A53399; MUID:94171760; PMID:7510285
A;Accession: A53399
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-202 <MAR>
A;Cross-references: UNIPROT:Q64302; UNIPARC:UPI0000004117; GB:L15429; NID:g468909; PIDN:

  Query Match             13.2%;  Score 160;  DB 2;  Length 202;
  Best Local Similarity   23.6%;  Pred. No. 2.5e-07;
  Matches   53;  Conservative   34;  Mismatches   92;  Indels   46;  Gaps    4;

Qy         12 GFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPATTMSLT 71
              |:||:   :  :| ||: |      |    ::: :| | |:| ||:| ||: :    : :
Db         11 GYSLVWAAVFCIVANAL-LYFPNGETKYATEDHLSRFVWYFAGIVGGGLLMLLPAFVFIG 69

Qy         72 ARKRACC--------NNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPSNSN 123
                 :  ||         |  | |   ::| ::|: ||::::   | :||
Db         70 MDEEDCCGCCGYENYGKRCSMLSSVLAALIGIVGSAYCVIVASLGLAEGP---------- 119

Qy        124 ANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENK 183
                                  |:  |   |   |         ||      | |
Db        120 -------------------------KCSDAHGVWNYTFASTEGQYLLNSSMWSKCYEPK 153

Qy        184 HRL-IHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQ 227
              | :  | ::|  ||    :| :  | |:: | || |||    | |
Db        154 HIVEWHVTLFSILLAFAAVEFILCLIQVINGMLGGLCGYCCSRQQ 198


RESULT 4
JC4635
tumor-associated L6 antigen homolog - hamster
N;Alternate names: MM3 protein
C;Species: Cricetinae gen. sp. (hamster)
C;Date: 10-Apr-1996 #sequence_revision 24-May-1996 #text_change 07-Dec-1999
C;Accession: JC4635
R;Maruyama, M.; Kozuka-Hata, H.; Sakaguchi-Sanai, A.; Shioda, S.; Yamaguchi, N.; Maruyam
Gene 168, 273-274, 1996
A;Title: The cDNA cloning of the hamster homologue of the human L6 gene.
A;Reference number: JC4635; MUID:96194912; PMID:8654959
A;Accession: JC4635
A;Molecule type: mRNA
A;Residues: 1-202 <MAR>
A;Cross-references: UNIPARC:UPI000000057D; GB:U34276; NID:g1049220; PIDN:AAA80343.1; PID:
A;Experimental source: GHE-L cells
C;Genetics:
A;Gene: mm3
C;Keywords: glycoprotein; surface antigen; transmembrane protein; tumor
F;11-30/Domain: transmembrane #status predicted <TM1>
F;45-70/Domain: transmembrane #status predicted <TM2>
F;90-116/Domain: transmembrane #status predicted <TM3>
F;157-193/Domain: transmembrane #status predicted <TM4>
F;129,159/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             11.2%;  Score 136;  DB 2;  Length 202;
  Best Local Similarity   23.6%;  Pred. No. 4e-05;
  Matches   53;  Conservative   36;  Mismatches   92;  Indels   44;  Gaps    8;

Qy          3 CCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA 62
              |     |   | ||:|  :| :| | | |     |     :: :| | |:| ||:| ||:
Db          2 CSSKCTRYIGHSLVVFAVLCIVAN-ILLYFPNGETKYAYEDHLSRFVWFFAGIVGGGLLI 60

Qy         63 IPATTMSLTARKRACC--------NNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPL 114
              :    : |       ||          |  |  |   ::| : |: ||::::   | :||
Db         61 LLPAFVFLGLEGEDCCGCWSCENYGKRCTMLSSIMAALIGIAGSGYCVIVAALGLAEGP- 119

Qy        115 MCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASS 174
              |    :|:    ::  |           |:  :     || ::|    : :   |  :
Db        120 KC---GDSHGMWNYTFANTDG--------QYLLD-----PTTWSKCHEPNNIVE-WNVTL 162

Qy        175 FHFDSEENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLC 219
              |                   || :| || :  | |:: | |  :|
Db        163 FSI----------------LLALGGLEFILCLIQVINGVLEGMC 190


RESULT 5
JC6205
cell surface antigen MM3 protein - hamster
C;Species: Cricetinae gen. sp. (hamster)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 02-Jun-2000
C;Accession: JC6205
R;Kurihara, T.; Kataoka, K.; Hong, D.; Shioda, S.; Sugano, S.; Mitamura, K.; Maruyama, K.
Gene 185, 277-283, 1997
A;Title: Genomic structure and promoter analysis of the gene encoding MM3, a member of t
A;Reference number: JC6205; MUID:97208885; PMID:9055827
A;Accession: JC6205
A;Molecule type: mRNA
A;Residues: 1-202 <KUR>
A;Cross-references: UNIPARC:UPI00000E7DDF; DDBJ:D86465
C;Genetics:
A;Gene: mm3
A;Introns: 59/3; 89/3; 138/2; 198/3
C;Keywords: surface antigen; transmembrane protein

  Query Match             10.9%;  Score 133;  DB 2;  Length 202;
  Best Local Similarity   24.2%;  Pred. No. 7.5e-05;
  Matches   55;  Conservative   37;  Mismatches   87;  Indels   48;  Gaps    9;

Qy          3 CCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA 62
              |     |   | ||:|  :| :| | | |     |     :: :| | |:| ||:| ||:
Db          2 CSSKCTRYIGHSLVVFAVLCIVAN-ILLYFPNGETKYAYEDHLSRFVWFFAGIVGGGLLI 60

Qy         63 IPATTMSLTARKRACC--------NNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPL 114
              :    : |       ||          |  |  |   ::| : |: ||::::   | :||
Db         61 LLPAFVFLGLEGEDCCGCWSCENYGKRCTMLSSIMAALIGIAGSGYCVIVAALGLAEGP- 119

Qy        115 MCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASS 174
              |    :|:    ::  |           |:  :     || ::|
Db        120 KC---GDSHGMWNYTFANTDG--------QYLLD-----PTTWSK--------------- 148

Qy        175 FHFDSEENKHRLIHFSV--FLGLLLVGILEVLFGLSQIVIGFLGCLC 219
```

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                    | |: :: ::|  |  ||  | || :  | |:: | |  :|
Db        149 ----CHEPKN-IVEWNVTLFSTLLAFGGLEFILCLIQVINGVLEGMC 190
```

RESULT 6
A85870
probable transport protein yfbS [imported] - Escherichia coli (strain O157:H7, substrain
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: A85870
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85870
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-610 <STO>
A;Cross-references: UNIPARC:UPI000016588C; GB:AE005174; NID:g12516645; PIDN:AAG57421.1;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: yfbS

 Query Match 7.4%; Score 90.5; DB 2; Length 610;
 Best Local Similarity 30.8%; Pred. No. 1.8;
 Matches 37; Conservative 20; Mismatches 30; Indels 33; Gaps 7;

```
Qy         15 LLVLLLL------------GVVLNAIPLIVSLVEEDQFSQN----PISCFEWWFPGIIGA 58
              :||||:|             |||   ||:::|:    | | :    |:|     | |:| :
Db         94 MLVLLMLTVAGLGAFMSSTGVVAIFIPVVLSVAMRMQTSPSRLMMPLS-----FAGLI-S 147

Qy         59 GLMAIPATTMSLTARKRACCNNRTGMFLSSFFS------VITVIGALYCMLISIQALLKG 112
              |:| : ||  :|          | |    ||||      |: |:| ||  :: :: :|||
Db        148 GMMTLVATPPNLVVNSELL---REGYHGFSFFSVTPIGLVVLVLGILY--MLVMRFMLKG 202
```

RESULT 7
H91025
probable transport protein ECs3176 [imported] - Escherichia coli (strain O157:H7, substr
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: H91025
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: H91025
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-610 <HAY>
A;Cross-references: UNIPROT:P77741; UNIPARC:UPI000013ADE9; GB:BA000007; PIDN:BAB36599.1;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs3176

 Query Match 7.4%; Score 90.5; DB 2; Length 610;
 Best Local Similarity 30.8%; Pred. No. 1.8;
 Matches 37; Conservative 20; Mismatches 30; Indels 33; Gaps 7;

```
Qy         15 LLVLLLL------------GVVLNAIPLIVSLVEEDQFSQN----PISCFEWWFPGIIGA 58
              :||||:|             |||   ||:::|:    | | :    |:|     | |:| :
Db         94 MLVLLMLTVAGLGAFMSSTGVVAIFIPVVLSVAMRMQTSPSRLMMPLS-----FAGLI-S 147

Qy         59 GLMAIPATTMSLTARKRACCNNRTGMFLSSFFS------VITVIGALYCMLISIQALLKG 112
              |:| : ||  :|          | |    ||||      |: |:| ||  :: :: :|||
Db        148 GMMTLVATPPNLVVNSELL---REGYHGFSFFSVTPIGLVVLVLGILY--MLVMRFMLKG 202
```

RESULT 8
B65001
probable transport protein b2292 [similarity] - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: B65001
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: B65001
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-610 <BLAT>
A;Cross-references: UNIPROT:P77741; UNIPARC:UPI000013ADE9; GB:AE000318; GB:U00096; NID:g1
A;Experimental source: strain K-12, substrain MG1655

 Query Match 7.4%; Score 90.5; DB 2; Length 610;
 Best Local Similarity 30.8%; Pred. No. 1.8;
 Matches 37; Conservative 20; Mismatches 30; Indels 33; Gaps 7;

```
Qy         15 LLVLLLL------------GVVLNAIPLIVSLVEEDQFSQN----PISCFEWWFPGIIGA 58
              :||||:|             |||   ||:::|:    | | :    |:|     | |:| :
Db         94 MLVLLMLTVAGLGAFMSSTGVVAIFIPVVLSVAMRMQTSPSRLMMPLS-----FAGLI-S 147

Qy         59 GLMAIPATTMSLTARKRACCNNRTGMFLSSFFS------VITVIGALYCMLISIQALLKG 112
              |:| : ||  :|          | |    ||||      |: |:| ||  :: :: :|||
Db        148 GMMTLVATPPNLVVNSELL---REGYHGFSFFSVTPIGLVVLVLGILY--MLVMRFMLKG 202
```

RESULT 9
A81298
formate dehydrogenase (EC 1.2.1.2) cytochrome B chain Cj1509c [imported] - Campylobacter
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: A81298
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: A81298
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-310 <PAR>
A;Cross-references: UNIPROT:Q9PMF4; UNIPARC:UPI00000C1F50; GB:AL139078; GB:AL111168; NID:
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: fdhC; Cj1509c
C;Superfamily: formate dehydrogenase chain C
C;Keywords: oxidoreductase

 Query Match 7.4%; Score 89.5; DB 2; Length 310;
 Best Local Similarity 18.1%; Pred. No. 1.1;
 Matches 49; Conservative 35; Mismatches 64; Indels 123; Gaps 11;

```
Qy          7 WTSCNGFSLLVLLLLGV--VLNAIPLIVSLVEEDQFSQNP--------------ISCFE 49
              ||:  |  :  : |: |  ||:|  |    ::  ||| :                |:
Db         48 WTTLQGEYIATIALIAVIAVLSAFALHYMVIGPKQFSHDGKKIYAFTLFERLFHFIAAIS 107

Qy         50 W----------WFPGIIGAGLMAIPATTMSLTARKRACCNNRTGMFLSSFFSVITVIGAL 99
              |          |  : | |:              | | |      | :| ::: :|  :
Db        108 WVILVPTGFVMMFGEVFGGGVFV-----------RVCKN------LHAFATILFIISII 149

Qy        100 YCMLISIQALLKGPLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNK 159
                |  |: :|                                | |::::|
Db        150 PMFLCWIKRML--------------------------PASYDIRWMM------------ 170

Qy        160 PTSNDTMASGW--------RASSFHFDSEENKHRLIHFSVFLGLLLV------------- 198
                :  |:          |  |:|  :       : :|| | |::
Db        171 ------IVGGYLSKIKRPVPAGKFNFGQKS----WYYIAVFGGFLMIITGGFMYFLDFNS 220

Qy        199 GILEVLFGLSQ--------IVIGFLGCLCGV 221
              :: ||||:|         ||  ||| :| |
Db        221 TAIQGLFGLTQIELLRISAIVHNFLGIVCAV 251
```

```
RESULT 10
T33261
hypothetical protein C24B9.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33261
R;Murray, J.; Wohldmann, P.; Langston, Y.; O'Neal, D.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid C24B9.
A;Reference number: Z21310
A;Accession: T33261
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-319 <MUR>
A;Cross-references: UNIPROT:O76434; UNIPARC:UPI000007D80C; EMBL:AF068709; PIDN:AAC19249.
A;Experimental source: strain Bristol N2; clone C24B9
C;Genetics:
A;Gene: CESP:C24B9.6
A;Map position: 5
A;Introns: 19/2; 49/3; 195/3; 239/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C16D9.7

  Query Match             7.3%;  Score 88.5;  DB 2;  Length 319;
  Best Local Similarity   19.6%;  Pred. No. 1.4;
  Matches   42;  Conservative   29;  Mismatches   50;  Indels   93;  Gaps   11;

Qy          5 EGWTSCNGFSL----LVLLLLGVVLNA--IPLIVSLVEEDQFSQNPISCFE-WWFPGIIG 57
              | |:  ||:      :: :  |:::|   ||::  ::||: |    :|||:   | ||:
Db         24 EEWSELNGYKRPIAGIIDMTYGILMNIVYIPILAVMLEEEHFK---MSCFKVMTFLGIV- 79

Qy         58 AGLMAIPATTMSLTARKRACCNNRTGMFLSSFFS-VITVIGALYCM---LISIQALLKGP 113
                                :   ::::|  :  :   ||:||    || |  :
Db         80 ----------------------DMLALWVNSIITGFLAYQGAVYCSYPNLIYISGMAGFG 117

Qy        114 LMCNSPSNSNANC----EFSLKNISDIHPESF--------------------------- 141
              | |        :|       :  | |:  ||
Db        118 LWC-------CSCIIAMSLVINRILDLSKESLCKLIFDGAKTYGVLTLPVIYGMYFVIFT 170

Qy        142 --------NLQWFFNDSCAP---------PTGFN 158
                    :| ||||    |          | |||
Db        171 TPIAFSSKHLTWFFNPLIFPNMTHEYTNLPHGFN 204


RESULT 11
A82357
probable multidrug resistance protein VC0164 [imported] - Vibrio cholerae (strain N16961
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: A82357
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: A82357
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1036 <HEI>
A;Cross-references: UNIPROT:Q9KVI2; UNIPARC:UPI00000C2BFE; GB:AE004106; GB:AE003852; NID
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC0164
A;Map position: 1
C;Superfamily: acriflavin resistance protein

  Query Match             7.2%;  Score 88;  DB 2;  Length 1036;
  Best Local Similarity   31.5%;  Pred. No. 5.4;
  Matches   41;  Conservative   18;  Mismatches   53;  Indels   18;  Gaps    7;

Qy         12 GFSLLVLLLLGVVLNAIPLIVS-----LVEEDQFSQNPISCFEWWFPGIIGAGLMAIPAT 66
                |||  :: || :|| || |:|      |   |:  :   | |      |||   :|||
Db        380 GFSWNLMTLLAMVL-AIGLVVDDAIVVLENVDRHIKEGESPFR---AAIIGTREIAIPVI 435

Qy         67 TMSLTA----RKRACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPSNS 122
               |:||       |     ||     |   :|: |:::  :  | ||   |:||:    :
Db        436 AMTLTLGAVYAPIALMGGITGSLFKEF--ALTLAGSVF--VSGIVALTLSPMMCSKMLKA 491

Qy        123 N-ANCEFSLK 131
              | |  :| ||
Db        492 NEAPNKFELK 501


RESULT 12
B82495
probable NADH dehydrogenase VCA0157 [imported] - Vibrio cholerae (strain N16961 serogrou
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82495
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: B82495
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-891 <HEI>
A;Cross-references: UNIPROT:Q9KN09; UNIPARC:UPI00000C344D; GB:AE004356; GB:AE003853; NID:
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VCA0157
A;Map position: 2

  Query Match             7.1%;  Score 86.5;  DB 2;  Length 891;
  Best Local Similarity   22.6%;  Pred. No. 6.3;
  Matches   30;  Conservative   28;  Mismatches   34;  Indels   41;  Gaps    6;

Qy          8 TSCNGFSLLV-LLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPAT 66
              |   | :||  |:|||:: |:  : | :   |  :|:|     |: | :|   |: : |
Db        154 TGAGGLALLAGLILLGLMANSYQISVIIEHADHIAQHP-----WFMPSLI---LVLLGAF 205

Qy         67 TMS-----------------LTARKRACCNNRTGMFLSS----------FFSVITVIG 97
              | |                   ::|   :    : |::| :          :|  :|::|
Db        206 TKSAQFPFHFWLPNAMAAPTPVSAYLHSATMVKAGIYLLARLSPIYASSDFWFYCLTIVG 265

Qy         98 ---ALYCMLISIQ 107
                 ||:| |:: :
Db        266 AVTALWCALLAFK 278


RESULT 13
AC1340
maltodextrin ABC-transport system (permease) homolog lmo2123 [imported] - Listeria monocy
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC1340
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1340
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-283 <GLA>
A;Cross-references: UNIPROT:Q8Y5E1; UNIPARC:UPI0000054F68; GB:NC_003210; PIDN:CAD00201.1;
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo2123
```

```
C;Superfamily: maltose transport protein malG

  Query Match             7.1%;  Score 86;  DB 2;  Length 283;
  Best Local Similarity   24.7%;  Pred. No. 2.1;
  Matches   39;  Conservative   28;  Mismatches   57;  Indels   34;  Gaps    7;

Qy         79 NNRTGMFLSSFF-----SVITVIGALYCMLISIQALLKGPLMCNSPSNSNA-----NCEF 128
              : ||  ||: ||      :|:|:|  || :||:  :  |       | |  |     :  :
Db          7 DQRTTKFLTQFFTYLFLTVLTII-ILYPILITASSAFK-------PGNIAAFTLEWSDSW 58

Qy        129 SLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRLIH 188
              :| | : :  |:  | |: |             :  |:| |:  | : |   :|   ||
Db         59 TLNNFTRLFNETLYLDWYKNTLIIAVVTMIMQVTIVTLA-GYTYSRYRFKGRKNS--LIF 115

Qy        189 FSV-------------FLGLLLVGILEVLFGLSQIVIG 213
              | :             ::  :|:| |:  : |: | ||
Db        116 FLIIQMVPTMAALTAFYVLAMLLGALDQYWFLTLIYIG 153


RESULT 14
H64713
Na+/H+-exchanging protein - Helicobacter pylori (strain 26695)
N;Alternate names: Na+/H+ antiporter
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 31-Dec-2004
C;Accession: H64713
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: H64713
A;Status: preliminary; nucleic acid sequence not shown; translation not shown.
A;Molecule type: DNA
A;Residues: 1-438 <TOM>
A;Cross-references: UNIPROT:O26076; UNIPARC:UPI00000D3083; GB:AE000653; GB:AE000511; NID
C;Superfamily: Na(+)/H(+) antiporter, NhaA type

  Query Match             7.1%;  Score 86;  DB 2;  Length 438;
  Best Local Similarity   31.5%;  Pred. No. 3.3;
  Matches   34;  Conservative   15;  Mismatches   39;  Indels   20;  Gaps    5;

Qy         19 LLLGVVLN-------AIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPATTMSL- 70
              :||||:|         | ||  : |: : :  |     ||   |:||||:|    :||:
Db        335 VLLGVILGLCLGKPLGIFLITFISEKLKITARP-KGISWWH--ILGAGLLAGIGFTMSMF 391

Qy         71 -------TARKRACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLK 111
                    :  | |    :  : | |  |   :|||||  :  :| ||
Db        392 ISNLAFTSEHKDAMEVAKIAILLGSLIS--GIIGALYLFALDKRAALK 437


RESULT 15
B82295
prolipoprotein diacylglyceryl transferase VC0674 [imported] - Vibrio cholerae (strain N1
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82295
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: B82295
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-271 <HEI>
A;Cross-references: UNIPROT:O87077; UNIPARC:UPI0000031D92; GB:AE004153; GB:AE003852; NID
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC0674
A;Map position: 1
C;Superfamily: prolipoprotein diacylglyceryl transferase

  Query Match             7.0%;  Score 85.5;  DB 2;  Length 271;
  Best Local Similarity   23.1%;  Pred. No. 2.2;
  Matches   53;  Conservative   31;  Mismatches  100;  Indels   45;  Gaps   10;

Qy          6 GWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGI-IGAGLMAIP 64
              |||      ||    ||||:      |    | |  :|:  |: |  |:    ||: :
Db         51 GWTREQVSDLLFAGFLGVVIGGRVGYVIFYNFDLFLADPLYLFKVWTGGMSFHGGLLGV- 109

Qy         65 ATTMSLTARKRACCNNRTGMFLSSFFSVITVIG-----------ALYCMLISIQALL-- 110
              | |   |||    | ||   :: | : :   |              |:  :  :
Db        110 ITAMFWYARK----NQRTFFGVADFVAPLVPFGLGMGRIGNFMNSELWGRVTDVPWAFVF 165

Qy        111 --KGPLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMAS 168
                |||    | : :   ||:|: :       | | ||           ||    :::
Db        166 PNGGPL----PRHPSQLYEFALEGVVLF----FILNWF----------IGKPRPLGSVSG 207

Qy        169 GWRA--SSFHFDSEENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFL 215
              : |   :| |  |  :       :| | : :|    :  |  ::|| |
Db        208 LFLAGYGTFRFLVEYVREPDAQLGLFGGFISMG---QILSLPMVIIGIL 253


Search completed: November 21, 2006, 20:09:03
Job time : 64.7187 secs
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2006, 19:59:24 ; Search time 335.446 Seconds
(without alignments)
631.482 Million cell updates/sec

Title: US-10-063-553-48
Perfect score: 1215
Sequence: 1 MTCCEGWTSCNGFSLLVLLL.....IVIGFLGCLCGVSKRRSQIV 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1215	100.0	229	2	Q6UWS1_HUMAN	Q6uws1 homo sapien
2	1211	99.7	229	2	Q5U609_HUMAN	Q5u609 homo sapien
3	1209	99.5	229	2	Q53R12_HUMAN	Q53r12 homo sapien
4	1205	99.2	229	2	Q9H5X9_HUMAN	Q9h5x9 homo sapien
5	931.5	76.7	230	2	Q3T0Z4_BOVIN	Q3t0z4 bos taurus
6	924.5	76.1	226	2	Q9CQY8_MOUSE	Q9cqy8 m 11 days p
7	918.5	75.6	226	2	Q9D3Q0_MOUSE	Q9d3q0 mus musculu
8	912.5	75.1	226	2	Q9D3R0_MOUSE	Q9d3r0 mus musculu
9	528	43.5	242	2	Q4KL96_XENLA	Q4kl96 xenopus lae
10	217.5	17.9	205	2	Q4KLD0_XENLA	Q4kld0 xenopus lae
11	195.5	16.1	203	2	Q66KQ0_XENLA	Q66kq0 xenopus lae
12	193	15.9	199	2	Q4T901_TETNG	Q4t901 tetraodon n
13	190.5	15.7	203	2	Q5U519_XENLA	Q5u519 xenopus lae
14	183.5	15.1	142	2	Q4S8Y9_TETNG	Q4s8y9 tetraodon n
15	182	15.0	197	2	Q7SYW6_XENLA	Q7syw6 xenopus lae
16	175	14.4	202	1	T4S1_PONPY	Q5re43 pongo pygma
17	173	14.2	197	2	Q6FHF6_HUMAN	Q6fhf6 homo sapien
18	170	14.0	197	1	T4S5_HUMAN	O14894 homo sapien
19	170	14.0	202	1	T4S1_HUMAN	P30408 homo sapien
20	170	14.0	232	2	Q8NE91_HUMAN	Q8ne91 homo sapien
21	169	13.9	201	2	Q6DHT3_BRARE	Q6dht3 brachydanio
22	168	13.8	203	2	Q3ZBI0_BOVIN	Q3zbi0 bos taurus
23	166.5	13.7	202	1	T4S4_HUMAN	P48230 homo sapien
24	166.5	13.7	202	1	T4S4_PONPY	Q5r6z4 pongo pygma
25	163.5	13.5	198	2	Q6DBQ4_BRARE	Q6dbq4 brachydanio
26	160.5	13.2	202	1	T4S4_RAT	Q9eql5 rattus norv
27	160	13.2	202	1	T4S1_MOUSE	Q64302 mus musculu
28	160	13.2	202	2	Q3TP49_MOUSE	Q3tp49 mus musculu
29	157.5	13.0	202	1	T4S4_MOUSE	Q91xd3 mus musculu
30	157.5	13.0	202	2	Q3TMT3_MOUSE	Q3tmt3 m adult mal
31	155.5	12.8	202	2	Q4KLC1_XENLA	Q4klc1 xenopus lae
32	154.5	12.7	196	2	Q2KIG8_BOVIN	Q2kig8 bos taurus
33	153	12.6	202	2	Q3UZY2_MOUSE	Q3uzy2 mus musculu
34	151.5	12.5	196	2	Q91XF2_MOUSE	Q91xf2 mus musculu
35	151.5	12.5	196	2	Q9D8G1_MOUSE	Q9d8g1 mus musculu
36	141.5	11.6	202	2	Q6P8F0_XENTR	Q6p8f0 xenopus tro
37	140	11.5	124	2	Q9DFD3_ONCMY	Q9dfd3 oncorhynchu
38	136	11.2	202	1	T4S1_MESAU	P49111 mesocricetu
39	136	11.2	202	2	Q53WX2_MESAU	Q53wx2 mesocricetu
40	133	10.9	202	2	Q60548_MESAU	Q60548 mesocricetu
41	127.5	10.5	143	2	Q4S441_TETNG	Q4s441 tetraodon n
42	126	10.4	201	1	T4S18_HUMAN	Q96ce8 homo sapien
43	124.5	10.2	201	2	Q3T110_BOVIN	Q3t110 bos taurus
44	124	10.2	164	2	Q4T900_TETNG	Q4t900 tetraodon n
45	111.5	9.2	209	1	T4S19_HUMAN	Q96dz7 homo sapien
46	111.5	9.2	209	2	Q336K7_HUMAN	Q336k7 homo sapien
47	103	8.5	1448	2	Q8T683_DICDI	Q8t683 dictyosteli
48	101	8.3	450	1	PEVR2_MOUSE	Q9d8f3 mus musculu
49	100.5	8.3	242	2	Q8TNE9_METAC	Q8tne9 methanosarc
50	100	8.2	505	2	Q89HF9_BRAJA	Q89hf9 bradyrhizob
51	99	8.1	506	2	Q35FR2_9BRAD	Q35fr2 bradyrhizob
52	98.5	8.1	213	2	Q6AZS4_XENLA	Q6azs4 xenopus lae
53	96	7.9	1023	2	Q3QL35_9GAMM	Q3ql35 shewanella
54	95.5	7.9	335	2	Q4Q948_LEIMA	Q4q948 leishmania
55	95.5	7.9	587	2	Q86JT5_DICDI	Q86jt5 dictyosteli
56	94.5	7.8	416	2	Q6CTF7_KLULA	Q6ctf7 kluyveromyc
57	94.5	7.8	503	2	Q36Y03_RHOPA	Q36y03 rhodopseudo
58	94.5	7.8	750	2	Q8H4T2_ORYSA	Q8h4t2 oryza sativ
59	93.5	7.7	422	2	Q2ZS17_SHEPU	Q2zs17 shewanella
60	92.5	7.6	510	2	Q37P22_RHOPA	Q37p22 rhodopseudo
61	92.5	7.6	746	2	Q3NNH6_SHEFR	Q3nnh6 shewanella
62	92.5	7.6	1053	2	Q3NMC7_SHEFR	Q3nmc7 shewanella
63	92	7.6	337	2	Q9U2L6_CAEEL	Q9u2l6 caenorhabdi
64	91	7.5	365	2	Q73LB7_TREDE	Q73lb7 treponema d
65	91	7.5	382	2	Q8EBM5_SHEON	Q8ebm5 shewanella
66	91	7.5	499	2	Q34DR5_RHOPA	Q34dr5 rhodopseudo
67	90.5	7.4	610	1	YFBS_ECO57	P0afu3 escherichia
68	90.5	7.4	610	1	YFBS_ECOLI	P0afu2 escherichia
69	90.5	7.4	610	2	Q31YH0_SHIBS	Q31yh0 shigella bo
70	90.5	7.4	610	2	Q32DP7_SHIDS	Q32dp7 shigella dy
71	90.5	7.4	610	2	Q3YZR8_SHISS	Q3yzr8 shigella so
72	90.5	7.4	610	2	Q8FFJ4_ECOL6	Q8ffj4 escherichia
73	90.5	7.4	1036	2	Q7VLE5_HAEDU	Q7vle5 haemophilus
74	90.5	7.4	1044	2	Q6LGT2_PHOPR	Q6lgt2 photobacter
75	90	7.4	364	2	Q2RT41_RHORU	Q2rt41 rhodospiril
76	90	7.4	501	2	Q4RSY5_TETNG	Q4rsy5 tetraodon n
77	90	7.4	1058	2	Q3CN66_ALTAT	Q3cn66 pseudoalter
78	89.5	7.4	310	2	Q5HSS2_CAMJR	Q5hss2 campylobact
79	89.5	7.4	310	2	Q9PMF4_CAMJE	Q9pmf4 campylobact
80	89.5	7.4	415	2	Q2X5Z2_9GAMM	Q2x5z2 shewanella
81	89.5	7.4	510	2	Q2IUI4_RHOPA	Q2iui4 rhodopseudo
82	89	7.3	275	2	O81655_HEMSP	O81655 hemerocalli
83	89	7.3	318	2	Q86UG8_HUMAN	Q86ug8 homo sapien
84	89	7.3	599	2	Q644K7_9SALA	Q644k7 desmognathu
85	88.5	7.3	278	2	Q3M6J6_ANAVT	Q3m6j6 anabaena va
86	88.5	7.3	319	2	O76434_CAEEL	O76434 caenorhabdi
87	88.5	7.3	361	2	Q2K8H0_RHIET	Q2k8h0 rhizobium e
88	88.5	7.3	568	2	Q9YLE7_9HIV1	Q9yle7 human immun
89	88	7.2	142	2	Q695C3_PICMA	Q695c3 picea maria
90	88	7.2	148	2	O65095_PICMA	O65095 picea maria
91	88	7.2	309	2	Q6GJ51_STAAR	Q6gj51 staphylococ
92	88	7.2	521	2	Q3ZVM2_SPICI	Q3zvm2 spiroplasma
93	88	7.2	521	2	Q3ZVP3_SPICI	Q3zvp3 spiroplasma
94	88	7.2	548	2	Q4DWP3_TRYCR	Q4dwp3 trypanosoma
95	88	7.2	1036	2	Q9KVI2_VIBCH	Q9kvi2 vibrio chol
96	87.5	7.2	225	2	Q3AGW6_SYNSC	Q3agw6 synechococc
97	87.5	7.2	310	2	Q4HEF2_CAMCO	Q4hef2 campylobact
98	87.5	7.2	442	2	Q61H24_CAEBR	Q61h24 caenorhabdi
99	87.5	7.2	836	2	Q37NK2_RHOPA	Q37nk2 rhodopseudo
100	87	7.2	470	2	Q76BF8_ORYLA	Q76bf8 oryzias lat
101	87	7.2	553	2	Q2RBJ0_ORYSA	Q2rbj0 oryza sativ
102	87	7.2	663	2	Q2KEJ3_MAGGR	Q2kej3 magnaporthe
103	86.5	7.1	453	2	Q5R419_PONPY	Q5r419 pongo pygma
104	86.5	7.1	453	2	Q5R4G3_PONPY	Q5r4g3 pongo pygma

105	86.5	7.1	596	2	Q3RRH3_RALME	Q3rrh3 ralstonia m
106	86.5	7.1	891	2	Q9KN09_VIBCH	Q9kn09 vibrio chol
107	86	7.1	283	2	Q4EL77_LISMO	Q4el77 listeria mo
108	86	7.1	283	2	Q4ESM9_LISMO	Q4esm9 listeria mo
109	86	7.1	283	2	Q8Y5E1_LISMO	Q8y5e1 listeria mo
110	86	7.1	283	2	Q71XP0_LISMF	Q71xp0 listeria mo
111	86	7.1	395	2	Q2Z5Q7_9GAMM	Q2z5q7 shewanella
112	86	7.1	438	2	O26076_HELPY	O26076 helicobacte
113	86	7.1	501	2	Q5ZTG4_LEGPH	Q5ztg4 legionella
114	86	7.1	521	2	Q3ZVN4_SPICI	Q3zvn4 spiroplasma
115	86	7.1	521	2	Q3ZVP8_SPICI	Q3zvp8 spiroplasma
116	86	7.1	751	2	Q8MN62_DICDI	Q8mn62 dictyosteli
117	86	7.1	1108	2	Q54ZJ9_DICDI	Q54zj9 dictyosteli
118	85.5	7.0	239	2	Q9NB10_MANSE	Q9nb10 manduca sex
119	85.5	7.0	271	1	LGT_VIBCH	O87077 vibrio chol
120	85.5	7.0	453	1	SERC1_HUMAN	Q9nrx5 homo sapien
121	85.5	7.0	589	2	Q4A7Z2_MYCH7	Q4a7z2 mycoplasma
122	85.5	7.0	589	2	Q4A9W1_MYCHJ	Q4a9w1 mycoplasma
123	85.5	7.0	589	2	Q600R6_MYCH2	Q600r6 mycoplasma
124	85	7.0	283	2	Q929P6_LISIN	Q929p6 listeria in
125	85	7.0	328	2	Q6PHE1_BRARE	Q6phe1 brachydanio
126	85	7.0	375	2	Q4J7M5_SULAC	Q4j7m5 sulfolobus
127	85	7.0	379	1	CYB_PHAAF	Q8m706 phacochoeru
128	85	7.0	379	2	Q36471_PHAAF	Q36471 phacochoeru
129	85	7.0	379	2	Q5BQG8_9CETA	Q5bqg8 sus cebifro
130	85	7.0	463	2	Q30XE9_DESDG	Q30xe9 desulfovibr
131	85	7.0	557	2	Q7XRI7_ORYSA	Q7xri7 oryza sativ
132	85	7.0	1023	2	Q5E1S7_VIBF1	Q5e1s7 vibrio fisc
133	84.5	7.0	149	2	Q695B7_PICMA	Q695b7 picea maria
134	84.5	7.0	156	2	O65096_PICMA	O65096 picea maria
135	84.5	7.0	171	2	Q50HP2_PENJP	Q50hp2 penaeus jap
136	84.5	7.0	281	2	O65061_PICMA	O65061 picea maria
137	84.5	7.0	380	1	CXA1_BRARE	O57474 brachydanio
138	84.5	7.0	382	2	O73863_DANAE	O73863 danio aequi
139	84.5	7.0	610	2	Q83QS3_SHIFL	Q83qs3 shigella fl
140	84	6.9	286	2	Q8Z4A9_SALTI	Q8z4a9 salmonella
141	84	6.9	352	1	OPSD_ZOSOP	Q9ygy9 zosterisess
142	84	6.9	438	2	Q9ZJ68_HELPJ	Q9zj68 helicobacte
143	84	6.9	521	2	Q4VYD7_SPICI	Q4vyd7 spiroplasma
144	84	6.9	798	2	Q2IV13_RHOPA	Q2iv13 rhodopseudo
145	84	6.9	3056	2	Q8I639_PLAF7	Q8i639 plasmodium
146	83.5	6.9	142	2	Q8HII9_9HYME	Q8hii9 halterapis
147	83.5	6.9	277	2	Q66S52_9UROC	Q66s52 oikopleura
148	83.5	6.9	331	2	Q8KKE7_VIBCH	Q8kke7 vibrio chol
149	83.5	6.9	347	2	Q3YPE0_CALDR	Q3ype0 callisaurus
150	83.5	6.9	389	2	Q2ZPR1_SHEPU	Q2zpr1 shewanella
151	83.5	6.9	442	2	Q5CFX3_CRYHO	Q5cfx3 cryptospori
152	83.5	6.9	469	2	Q5NHH4_FRATT	Q5nhh4 francisella
153	83.5	6.9	560	2	Q83DX2_COXBU	Q83dx2 coxiella bu
154	83.5	6.9	752	2	Q6LRB1_PHOPR	Q6lrb1 photobacter
155	83.5	6.9	1052	2	Q3Q420_9GAMM	Q3q420 shewanella
156	83	6.8	237	2	Q38UJ4_LACSS	Q38uj4 lactobacill
157	83	6.8	271	1	LGT_VIBVU	Q8der8 vibrio vuln
158	83	6.8	271	1	LGT_VIBVY	Q7mnn7 vibrio vuln
159	83	6.8	332	2	O76431_CAEEL	O76431 caenorhabdi
160	83	6.8	342	2	Q9PT67_XENLA	Q9pt67 xenopus lae
161	83	6.8	353	2	Q3HGG3_TRIER	Q3hgg3 trichodesmi
162	83	6.8	451	2	Q6BPX5_DEBHA	Q6bpx5 debaryomyce
163	83	6.8	490	2	Q3FUI3_9BURK	Q3fui3 rhodoferax
164	83	6.8	512	2	Q65SY2_MANSM	Q65sy2 mannheimia
165	82.5	6.8	138	2	Q6X9S5_9HYME	Q6x9s5 allodapula
166	82.5	6.8	149	2	Q695B5_PICGL	Q695b5 picea glauc
167	82.5	6.8	149	2	Q695B8_PICAB	Q695b8 picea abies
168	82.5	6.8	154	2	Q9SPX7_PICAB	Q9spx7 picea abies
169	82.5	6.8	180	1	PTTG_HUMAN	P53801 homo sapien
170	82.5	6.8	180	1	PTTG_PONPY	Q5nvi6 pongo pygma
171	82.5	6.8	239	2	Q5MGP8_LONON	Q5mgp8 lonomia obl
172	82.5	6.8	289	2	Q9DSD5_HHV8	Q9dsd5 human herpe
173	82.5	6.8	442	2	Q5CPH5_CRYPV	Q5cph5 cryptospori
174	82.5	6.8	1627	2	Q8GU51_ORYSA	Q8gu51 oryza sativ
175	82.5	6.8	1628	2	Q7XTT6_ORYSA	Q7xtt6 oryza sativ
176	82	6.7	239	2	Q5WCK1_BACSK	Q5wck1 bacillus cl
177	82	6.7	280	2	Q5WAQ1_BACSK	Q5waq1 bacillus cl
178	82	6.7	286	2	Q57KR0_SALCH	Q57kr0 salmonella
179	82	6.7	286	2	Q9XCS0_SALTY	Q9xcs0 salmonella
180	82	6.7	318	2	Q86UG9_HUMAN	Q86ug9 homo sapien
181	82	6.7	379	2	Q5MG50_PIG	Q5mg50 sus scrofa
182	82	6.7	379	2	Q85C79_PIG	Q85c79 sus scrofa
183	82	6.7	393	2	Q41R22_FERAC	Q41r22 ferroplasma
184	82	6.7	445	2	Q5NEU1_FRATT	Q5neu1 francisella
185	82	6.7	453	2	Q5RCN8_PONPY	Q5rcn8 pongo pygma
186	82	6.7	572	2	Q7XUE5_ORYSA	Q7xue5 oryza sativ
187	82	6.7	804	2	Q80XB3_MOUSE	Q80xb3 mus musculu
188	82	6.7	808	2	Q70W02_CIOIN	Q70w02 ciona intes
189	82	6.7	809	2	Q80XB2_MOUSE	Q80xb2 mus musculu
190	82	6.7	823	2	Q80XB6_MOUSE	Q80xb6 mus musculu
191	82	6.7	827	2	Q8CDK8_MOUSE	Q8cdk8 mus musculu
192	82	6.7	834	2	Q8BH12_MOUSE	Q8bh12 mus musculu
193	82	6.7	842	2	Q8R056_MOUSE	Q8r056 mus musculu
194	82	6.7	867	1	PROM1_MOUSE	O54990 mus musculu
195	82	6.7	976	2	Q6FKX5_CANGA	Q6fkx5 candida gla
196	82	6.7	1029	2	Q36CA4_9GAMM	Q36ca4 shewanella
197	81.5	6.7	151	2	Q695B3_PICMA	Q695b3 picea maria
198	81.5	6.7	156	2	O65097_PICMA	O65097 picea maria
199	81.5	6.7	266	2	Q3A9C0_CARHZ	Q3a9c0 carboxydoth
200	81.5	6.7	289	2	P88902_HHV8	P88902 human herpe
201	81.5	6.7	343	2	Q9B4H2_COPTE	Q9b4h2 cophosaurus
202	81.5	6.7	347	2	Q6YIV0_COPTE	Q6yiv0 cophosaurus
203	81.5	6.7	379	2	Q66M71_PIG	Q66m71 sus scrofa
204	81.5	6.7	453	2	Q7TNK0_RAT	Q7tnk0 rattus norv
205	81.5	6.7	454	2	Q8AAS4_BACTN	Q8aas4 bacteroides
206	81.5	6.7	468	2	O44515_CAEEL	O44515 caenorhabdi
207	81.5	6.7	474	2	Q8EP39_OCEIH	Q8ep39 oceanobacil
208	81.5	6.7	510	2	Q4T2X4_TETNG	Q4t2x4 tetraodon n
209	81.5	6.7	672	2	Q6G521_BARHE	Q6g521 bartonella
210	81.5	6.7	772	2	Q3VNL1_9CHLB	Q3vnl1 pelodictyon
211	81.5	6.7	1019	2	Q83CM1_COXBU	Q83cm1 coxiella bu
212	81.5	6.7	1040	2	Q87TN1_VIBPA	Q87tn1 vibrio para
213	81.5	6.7	1333	2	Q54KL3_DICDI	Q54kl3 dictyosteli
214	81.5	6.7	1687	2	Q6QI17_RAT	Q6qi17 rattus norv
215	81	6.7	145	2	Q695C2_PICAB	Q695c2 picea abies
216	81	6.7	150	2	Q9SPX8_PICAB	Q9spx8 picea abies
217	81	6.7	158	2	Q4RYE8_TETNG	Q4rye8 tetraodon n
218	81	6.7	254	1	CHIT_PETHY	P29021 petunia hyb
219	81	6.7	278	2	Q8KEE7_CHLTE	Q8kee7 chlorobium
220	81	6.7	286	2	Q5PE94_SALPA	Q5pe94 salmonella
221	81	6.7	318	2	Q86SG9_HUMAN	Q86sg9 homo sapien
222	81	6.7	318	2	Q86SH1_HUMAN	Q86sh1 homo sapien
223	81	6.7	318	2	Q86SH3_HUMAN	Q86sh3 homo sapien
224	81	6.7	318	2	Q86UG7_HUMAN	Q86ug7 homo sapien
225	81	6.7	379	2	Q5MG77_PIG	Q5mg77 sus scrofa
226	81	6.7	379	2	Q85AW1_PIG	Q85aw1 sus scrofa
227	81	6.7	379	2	Q8M707_PHAAE	Q8m707 phacochoeru
228	81	6.7	379	2	Q9T568_PIG	Q9t568 sus scrofa
229	81	6.7	409	2	Q4E7K4_9RICK	Q4e7k4 wolbachia e
230	81	6.7	459	2	Q7Y8E6_MOGWO	Q7y8e6 mogera wogu
231	81	6.7	460	2	Q61D03_CAEBR	Q61d03 caenorhabdi
232	81	6.7	461	2	P91197_CAEEL	P91197 caenorhabdi
233	81	6.7	474	2	Q5FHA3_EHRRG	Q5fha3 ehrlichia r
234	81	6.7	545	2	Q97TJ2_CLOAB	Q97tj2 clostridium
235	81	6.7	568	2	Q6BYD1_DEBHA	Q6byd1 debaryomyce
236	81	6.7	591	2	Q9JI49_RAT	Q9ji49 rattus norv
237	81	6.7	622	2	Q9C4V0_SULIS	Q9c4v0 sulfolobus
238	81	6.7	703	2	Q8G1T9_BRUSU	Q8g1t9 brucella su
239	81	6.7	748	2	O44416_9DIPT	O44416 chironomus
240	81	6.7	771	2	Q8A9X0_BACTN	Q8a9x0 bacteroides
241	81	6.7	989	2	Q54NP1_DICDI	Q54np1 dictyosteli
242	81	6.7	1038	2	Q6LVZ3_PHOPR	Q6lvz3 photobacter
243	81	6.7	1156	2	Q4WGM4_ASPFU	Q4wgm4 aspergillus
244	81	6.7	4226	2	Q8IHY1_PLAF7	Q8ihy1 plasmodium
245	80.5	6.6	205	2	Q6D905_ERWCT	Q6d905 erwinia car
246	80.5	6.6	309	2	Q4HLJ8_CAMLA	Q4hlj8 campylobact
247	80.5	6.6	315	2	Q5BKJ9_XENTR	Q5bkj9 xenopus tro
248	80.5	6.6	343	2	Q3YPD2_CALDR	Q3ypd2 callisaurus
249	80.5	6.6	374	2	Q6FG00_ACIAD	Q6fg00 acinetobact
250	80.5	6.6	379	2	Q9XMB7_MARBA	Q9xmb7 marmota bai

251	80.5	6.6	395	1	TRFR_CHICK	O93603	gallus gall	324	79.5	6.5	362	2	Q9CNG0_PASMU	Q9cng0	pasteurella
252	80.5	6.6	420	2	Q2WW43_CLOBE	Q2ww43	clostridium	325	79.5	6.5	364	2	Q9LI65_ARATH	Q9li65	arabidopsis
253	80.5	6.6	641	2	Q4PBM3_USTMA	Q4pbm3	ustilago ma	326	79.5	6.5	369	2	O18053_CAEEL	O18053	caenorhabdi
254	80.5	6.6	741	2	Q4SWG9_TETNG	Q4swg9	tetraodon n	327	79.5	6.5	369	2	Q53R77_ORYSA	Q53r77	oryza sativ
255	80.5	6.6	789	2	Q5CQN2_CRYPV	Q5cqn2	cryptospori	328	79.5	6.5	390	2	Q7N821_PHOLL	Q7n821	photorhabdu
256	80.5	6.6	838	2	Q8UTC7_9HIV1	Q8utc7	human immun	329	79.5	6.5	430	2	Q5CJG9_CRYHO	Q5cjg9	cryptospori
257	80.5	6.6	857	2	Q5U897_9HIV1	Q5u897	human immun	330	79.5	6.5	453	2	Q3MHV9_BOVIN	Q3mhv9	bos taurus
258	80.5	6.6	878	2	Q8EW47_MYCPE	Q8ew47	mycoplasma	331	79.5	6.5	482	2	Q44GY4_CHRSL	Q44gy4	chromohalob
259	80.5	6.6	1048	2	Q5LB81_BACFN	Q5lb81	bacteroides	332	79.5	6.5	504	2	Q2YAH8_NITMU	Q2yah8	nitrosospir
260	80.5	6.6	1048	2	Q64RM7_BACFR	Q64rm7	bacteroides	333	79.5	6.5	525	2	Q2XE94_PSEPU	Q2xe94	pseudomonas
261	80.5	6.6	1608	2	Q54VR7_DICDI	Q54vr7	dictyosteli	334	79.5	6.5	558	2	Q9M1E2_ARATH	Q9m1e2	arabidopsis
262	80	6.6	140	2	Q85PI7_PIG	Q85pi7	sus scrofa	335	79.5	6.5	608	2	Q57M22_SALCH	Q57m22	salmonella
263	80	6.6	308	2	Q4L439_STAHJ	Q4l439	staphylococ	336	79.5	6.5	608	2	Q5PN51_SALPA	Q5pn51	salmonella
264	80	6.6	314	2	Q924X8_MOUSE	Q924x8	mus musculu	337	79.5	6.5	608	2	Q8ZND9_SALTY	Q8znd9	salmonella
265	80	6.6	324	2	Q7S346_NEUCR	Q7s346	neurospora	338	79.5	6.5	608	2	Q8Z523_SALTI	Q8z523	salmonella
266	80	6.6	352	1	OPSD_GOBNI	Q9ygz2	gobius nige	339	79.5	6.5	654	2	Q7TLW5_NPVCF	Q7tlw5	choristoneu
267	80	6.6	352	2	Q9PRJ8_XENLA	Q9prj8	xenopus lae	340	79.5	6.5	682	2	Q83C62_COXBU	Q83c62	coxiella bu
268	80	6.6	355	2	Q5KST3_9ECHI	Q5kst3	luidia quin	341	79.5	6.5	857	2	Q5U8D3_9HIV1	Q5u8d3	human immun
269	80	6.6	356	2	Q9GCS0_9SCIU	Q9gcs0	petinomys s	342	79.5	6.5	1049	2	Q2Z5P9_9GAMM	Q2z5p9	shewanella
270	80	6.6	356	2	Q9GCS1_9SCIU	Q9gcs1	hylopetes p	343	79.5	6.5	1049	2	Q35ST9_9GAMM	Q35st9	shewanella
271	80	6.6	372	2	Q4FP51_PELUB	Q4fp51	pelagibacte	344	79.5	6.5	1049	2	Q36DA9_9GAMM	Q36da9	shewanella
272	80	6.6	379	1	CYB_PIG	P24964	sus scrofa	345	79.5	6.5	1143	2	Q9SUB9_ARATH	Q9sub9	arabidopsis
273	80	6.6	379	2	Q5BQG5_PIG	Q5bqg5	sus scrofa	346	79	6.5	253	2	Q3CEV4_THEET	Q3cev4	thermoanaer
274	80	6.6	379	2	Q5BQG9_9CETA	Q5bqg9	sus philipp	347	79	6.5	289	2	Q9QGQ6_HHV8	Q9qgq6	human herpe
275	80	6.6	379	2	Q5J1T7_PIG	Q5j1t7	sus scrofa	348	79	6.5	292	2	Q44EC2_CHRSL	Q44ec2	chromohalob
276	80	6.6	379	2	Q5MG52_PIG	Q5mg52	sus scrofa	349	79	6.5	297	2	Q5HRB7_STAEQ	Q5hrb7	staphylococ
277	80	6.6	379	2	Q5MG53_PIG	Q5mg53	sus scrofa	350	79	6.5	321	2	Q3KUV2_SHEEP	Q3kuv2	ovis aries
278	80	6.6	379	2	Q5MG60_PIG	Q5mg60	sus scrofa	351	79	6.5	379	1	CYB_CAMBA	Q34028	camelus bac
279	80	6.6	379	2	Q5MG61_PIG	Q5mg61	sus scrofa	352	79	6.5	379	1	CYB_CEPCA	Q9b5r8	cephalophus
280	80	6.6	379	2	Q5MG63_PIG	Q5mg63	sus scrofa	353	79	6.5	379	1	CYB_CEPNI	Q9b5r1	cephalophus
281	80	6.6	379	2	Q5MG65_PIG	Q5mg65	sus scrofa	354	79	6.5	379	1	CYB_CEPRU	Q9b5q6	cephalophus
282	80	6.6	379	2	Q5MG66_PIG	Q5mg66	sus scrofa	355	79	6.5	379	1	CYB_SUSBA	Q8m703	sus barbatu
283	80	6.6	379	2	Q5MG69_PIG	Q5mg69	sus scrofa	356	79	6.5	379	2	Q5KSP5_9ECHI	Q5ksp5	astropecten
284	80	6.6	379	2	Q5MG70_PIG	Q5mg70	sus scrofa	357	79	6.5	379	2	Q36543_SUSBA	Q36543	sus barbatu
285	80	6.6	379	2	Q5MG71_PIG	Q5mg71	sus scrofa	358	79	6.5	379	2	Q3YLB6_MIRCO	Q3ylb6	mirza coque
286	80	6.6	379	2	Q5MG73_PIG	Q5mg73	sus scrofa	359	79	6.5	379	2	Q540T9_CAMBA	Q540t9	camelus bac
287	80	6.6	379	2	Q5MG74_PIG	Q5mg74	sus scrofa	360	79	6.5	379	2	Q5MG76_PIG	Q5mg76	sus scrofa
288	80	6.6	379	2	Q69GE8_PIG	Q69ge8	sus scrofa	361	79	6.5	379	2	Q6GV89_PIG	Q6gv89	sus scrofa
289	80	6.6	379	2	Q6GV86_PIG	Q6gv86	sus scrofa	362	79	6.5	379	2	Q6GV90_PIG	Q6gv90	sus scrofa
290	80	6.6	379	2	Q71KJ5_PIG	Q71kj5	sus scrofa	363	79	6.5	379	2	Q6GV91_PIG	Q6gv91	sus scrofa
291	80	6.6	379	2	Q85QJ9_PIG	Q85qj9	sus scrofa	364	79	6.5	379	2	Q6GV93_PIG	Q6gv93	sus scrofa
292	80	6.6	379	2	Q9MEF7_MARAM	Q9mef7	martes amer	365	79	6.5	379	2	Q6GV94_PIG	Q6gv94	sus scrofa
293	80	6.6	379	2	Q9T4J0_PIG	Q9t4j0	sus scrofa	366	79	6.5	379	2	Q8HFA8_CAMBA	Q8hfa8	camelus bac
294	80	6.6	379	2	Q9T565_PIG	Q9t565	sus scrofa	367	79	6.5	379	2	Q8M702_SUSBA	Q8m702	sus barbatu
295	80	6.6	379	2	Q9T566_PIG	Q9t566	sus scrofa	368	79	6.5	379	2	Q9B5R9_CEPCA	Q9b5r9	cephalophus
296	80	6.6	379	2	Q9T567_PIG	Q9t567	sus scrofa	369	79	6.5	411	2	Q4J7Y6_SULAC	Q4j7y6	sulfolobus
297	80	6.6	379	2	Q2NNJ5_PIG	Q2nnj5	sus scrofa	370	79	6.5	426	2	Q454W3_9BURK	Q454w3	burkholderi
298	80	6.6	379	2	Q564N6_9SCIU	Q564n6	hylopetes p	371	79	6.5	426	2	Q4LVP1_9BURK	Q4lvp1	burkholderi
299	80	6.6	406	2	Q6ZC71_ORYSA	Q6zc71	oryza sativ	372	79	6.5	460	2	Q60K01_CAEBR	Q60k01	caenorhabdi
300	80	6.6	420	2	Q2ZIT7_CALSA	Q2zit7	caldicellul	373	79	6.5	463	2	Q2U171_ASPOR	Q2u171	aspergillus
301	80	6.6	447	2	Q49XK9_STAS1	Q49xk9	staphylococ	374	79	6.5	468	2	Q7VFP4_HELHP	Q7vfp4	helicobacte
302	80	6.6	502	2	Q9B973_9HYME	Q9b973	ceratosolen	375	79	6.5	474	2	Q5HB54_EHRRW	Q5hb54	ehrlichia r
303	80	6.6	643	2	Q6BSN4_DEBHA	Q6bsn4	debaryomyce	376	79	6.5	507	2	Q3SHZ0_THIDA	Q3shz0	thiobacillu
304	80	6.6	703	2	Q8VP06_BRUAB	Q8vp06	brucella ab	377	79	6.5	560	2	Q440J9_SOLUS	Q440j9	solibacter
305	80	6.6	703	2	Q57EC5_BRUAB	Q57ec5	brucella ab	378	79	6.5	595	2	Q6YK44_ORYSA	Q6yk44	oryza sativ
306	80	6.6	703	2	Q2YMX2_BRUA2	Q2ymx2	brucella ab	379	79	6.5	595	2	Q84KR4_ORYSA	Q84kr4	oryza sativ
307	80	6.6	721	2	Q8YG36_BRUME	Q8yg36	brucella me	380	79	6.5	787	2	Q80VI3_MOUSE	Q80vi3	mus musculu
308	80	6.6	889	2	Q6ZC72_ORYSA	Q6zc72	oryza sativ	381	79	6.5	913	2	Q19945_CAEEL	Q19945	caenorhabdi
309	80	6.6	933	2	Q7R539_GIALA	Q7r539	giardia lam	382	79	6.5	1052	2	Q89FH4_BRAJA	Q89fh4	bradyrhizob
310	80	6.6	1047	2	Q8EBL9_SHEON	Q8ebl9	shewanella	383	79	6.5	1063	2	Q3KCV6_PSEPF	Q3kcv6	pseudomonas
311	80	6.6	1059	2	Q4KBN7_PSEF5	Q4kbn7	pseudomonas	384	79	6.5	1250	2	Q60Z17_CAEBR	Q60z17	caenorhabdi
312	79.5	6.5	142	2	Q3YA01_9HYME	Q3ya01	allodape fr	385	79	6.5	1353	1	ADCY9_MOUSE	P51830	mus musculu
313	79.5	6.5	149	2	Q695B0_TSUCA	Q695b0	tsuga canad	386	78.5	6.5	208	2	Q7M881_WOLSU	Q7m881	wolinella s
314	79.5	6.5	149	2	Q695B1_PSEMZ	Q695b1	pseudotsuga	387	78.5	6.5	240	2	Q6P7J5_XENLA	Q6p7j5	xenopus lae
315	79.5	6.5	149	2	Q695B2_PINCE	Q695b2	pinus cembr	388	78.5	6.5	242	2	Q49YX4_STAS1	Q49yx4	staphylococ
316	79.5	6.5	149	2	Q695B4_PICGL	Q695b4	picea glauc	389	78.5	6.5	276	2	Q9WNS8_HHV8	Q9wns8	human herpe
317	79.5	6.5	149	2	Q695B6_PICMA	Q695b6	picea maria	390	78.5	6.5	289	2	Q9WHC1_HHV8	Q9whc1	human herpe
318	79.5	6.5	154	2	Q9SPW4_PICGL	Q9spw4	picea glauc	391	78.5	6.5	322	2	Q18269_CAEEL	Q18269	caenorhabdi
319	79.5	6.5	215	2	Q4QEX0_LEIMA	Q4qex0	leishmania	392	78.5	6.5	328	1	EMB_RAT	O88775	rattus norv
320	79.5	6.5	289	2	Q6IUS6_HHV8	Q6ius6	human herpe	393	78.5	6.5	339	2	Q3YPF4_CALDR	Q3ypf4	callisaurus
321	79.5	6.5	326	2	Q2PRE0_BRARE	Q2pre0	brachydanio	394	78.5	6.5	343	2	Q3YPF5_CALDR	Q3ypf5	callisaurus
322	79.5	6.5	341	2	Q8H8E5_ORYSA	Q8h8e5	oryza sativ	395	78.5	6.5	347	2	Q3YPF1_CALDR	Q3ypf1	callisaurus
323	79.5	6.5	356	2	Q7G4E6_ORYSA	Q7g4e6	oryza sativ	396	78.5	6.5	347	2	Q3YPF9_CALDR	Q3ypf9	callisaurus

397	78.5	6.5	347	2	Q3YPG6_CALDR	Q3ypg6	callisaurus
398	78.5	6.5	363	2	Q8UEG6_AGRT5	Q8ueg6	agrobacteri
399	78.5	6.5	387	2	Q3Q429_9GAMM	Q3q429	shewanella
400	78.5	6.5	423	2	Q9FH91_ARATH	Q9fh91	arabidopsis
401	78.5	6.5	452	2	Q8WF40_9BIVA	Q8wf40	venerupis (
402	78.5	6.5	459	2	Q2YV57_STAAB	Q2yv57	staphylococ
403	78.5	6.5	500	2	Q65RX6_MANSM	Q65rx6	mannheimia
404	78.5	6.5	506	2	Q3EGC7_ACTSC	Q3egc7	actinobacil
405	78.5	6.5	522	2	Q2S9T7_9GAMM	Q2s9t7	hahella che
406	78.5	6.5	593	2	Q64JP8_9AMPH	Q64jp8	scolecomorp
407	78.5	6.5	609	2	Q644J4_9SALA	Q644j4	batrachosep
408	78.5	6.5	648	2	Q76L35_TOBAC	Q76l35	nicotiana t
409	78.5	6.5	754	2	Q54M49_DICDI	Q54m49	dictyosteli
410	78.5	6.5	760	1	ADA25_MOUSE	Q9r159	mus musculu
411	78.5	6.5	791	2	Q3T2P0_9HIV1	Q3t2p0	human immun
412	78.5	6.5	825	2	Q651J1_ORYSA	Q651j1	oryza sativ
413	78.5	6.5	858	2	Q3T2N8_9HIV1	Q3t2n8	human immun
414	78.5	6.5	858	2	Q3T2P1_9HIV1	Q3t2p1	human immun
415	78.5	6.5	858	2	Q3T2P2_9HIV1	Q3t2p2	human immun
416	78.5	6.5	1039	2	Q7MQH1_VIBVY	Q7mqh1	vibrio vuln
417	78.5	6.5	1039	2	Q8DDC6_VIBVU	Q8ddc6	vibrio vuln
418	78.5	6.5	1213	2	Q381I5_9TRYP	Q381i5	trypanosoma
419	78.5	6.5	1421	2	Q5CH19_CRYHO	Q5ch19	cryptospori
420	78	6.4	211	2	Q4XQI5_PLACH	Q4xqi5	plasmodium
421	78	6.4	227	2	Q74HY8_LACJO	Q74hy8	lactobacill
422	78	6.4	285	2	Q92LL3_RHIME	Q92ll3	rhizobium m
423	78	6.4	286	2	Q3PBI6_PARDE	Q3pbi6	paracoccus
424	78	6.4	297	2	Q5HI49_STAAC	Q5hi49	staphylococ
425	78	6.4	297	2	Q8NXT3_STAAW	Q8nxt3	staphylococ
426	78	6.4	309	2	Q6GBL1_STAAS	Q6gbl1	staphylococ
427	78	6.4	309	2	Q7A731_STAAN	Q7a731	staphylococ
428	78	6.4	309	2	Q99VZ6_STAAM	Q99vz6	staphylococ
429	78	6.4	329	2	Q76BK6_PAROL	Q76bk6	paralichthy
430	78	6.4	344	2	Q5QNN8_BRARE	Q5qnn8	brachydanio
431	78	6.4	356	2	Q2SWR4_BURTH	Q2swr4	burkholderi
432	78	6.4	356	2	Q8WF83_9SCIU	Q8wf83	petaurista
433	78	6.4	379	1	CYB_CEPHE	Q9tdl4	cephalorhyn
434	78	6.4	379	1	CYB_PHAAE	Q8m708	phacochoeru
435	78	6.4	379	2	Q5MG67_PIG	Q5mg67	sus scrofa
436	78	6.4	379	2	Q5MG75_PIG	Q5mg75	sus scrofa
437	78	6.4	379	2	Q66M72_PIG	Q66m72	sus scrofa
438	78	6.4	379	2	Q66M73_PIG	Q66m73	sus scrofa
439	78	6.4	379	2	Q8M709_PHAAE	Q8m709	phacochoeru
440	78	6.4	379	2	Q92L18_RHIME	Q92l18	rhizobium m
441	78	6.4	379	2	Q5NUR7_9SCIU	Q5nur7	petaurista
442	78	6.4	379	2	Q9XMC0_9SCIU	Q9xmc0	marmota cau
443	78	6.4	380	2	Q7Y752_9SMEG	Q7y752	zoogoneticu
444	78	6.4	380	2	Q7YHK2_9SMEG	Q7yhk2	zoogoneticu
445	78	6.4	409	2	Q73GC5_WOLPM	Q73gc5	wolbachia p
446	78	6.4	415	2	Q47U43_COLP3	Q47u43	colwellia p
447	78	6.4	457	2	Q8A565_BACTN	Q8a565	bacteroides
448	78	6.4	468	2	Q6ANP9_DESPS	Q6anp9	desulfotale
449	78	6.4	493	2	Q5X388_LEGPA	Q5x388	legionella
450	78	6.4	519	1	PALH_KLULA	Q6cxk7	kluyveromyc
451	78	6.4	555	2	Q869R1_DICDI	Q869r1	dictyosteli
452	78	6.4	617	2	Q5W2Z9_SULIS	Q5w2z9	sulfolobus
453	78	6.4	641	2	Q7ZZW2_PAROL	Q7zzw2	paralichthy
454	78	6.4	832	2	Q8IBT8_PLAF7	Q8ibt8	plasmodium
455	78	6.4	989	2	Q6FP46_CANGA	Q6fp46	candida gla
456	78	6.4	1059	2	Q2XK95_PSEPU	Q2xk95	pseudomonas
457	78	6.4	1059	2	Q88HD4_PSEPK	Q88hd4	pseudomonas
458	78	6.4	1062	2	P95422_PSEAE	P95422	pseudomonas
459	78	6.4	1062	2	Q9I0Y8_PSEAE	Q9i0y8	pseudomonas
460	78	6.4	1280	2	Q86JR7_DICDI	Q86jr7	dictyosteli
461	78	6.4	1780	2	Q61T87_CAEBR	Q61t87	caenorhabdi
462	78	6.4	1783	2	Q18698_CAEEL	Q18698	caenorhabdi
463	78	6.4	1877	2	Q8MQA1_CAEEL	Q8mqa1	caenorhabdi
464	78	6.4	4005	2	Q4SEV9_TETNG	Q4sev9	tetraodon n
465	77.5	6.4	142	2	Q3YA00_9HYME	Q3ya00	allodapula
466	77.5	6.4	146	2	Q695C1_PICAB	Q695c1	picea abies
467	77.5	6.4	151	2	Q9SPX9_PICAB	Q9spx9	picea abies
468	77.5	6.4	218	2	Q932K2_STAAM	Q932k2	staphylococ
469	77.5	6.4	274	2	Q995A5_HHV8	Q995a5	human herpe
470	77.5	6.4	320	2	Q6D431_ERWCT	Q6d431	erwinia car
471	77.5	6.4	328	2	Q3YPG7_CALDR	Q3ypg7	callisaurus
472	77.5	6.4	330	2	Q676M5_9HYST	Q676m5	bathyergus
473	77.5	6.4	336	2	Q3YPD3_CALDR	Q3ypd3	callisaurus
474	77.5	6.4	343	2	Q3YPD7_CALDR	Q3ypd7	callisaurus
475	77.5	6.4	343	2	Q3YPD9_CALDR	Q3ypd9	callisaurus
476	77.5	6.4	343	2	Q3YPF6_CALDR	Q3ypf6	callisaurus
477	77.5	6.4	343	2	Q9B4H0_CALDR	Q9b4h0	callisaurus
478	77.5	6.4	347	2	Q3YPD1_CALDR	Q3ypd1	callisaurus
479	77.5	6.4	347	2	Q3YPD5_CALDR	Q3ypd5	callisaurus
480	77.5	6.4	347	2	Q3YPD6_CALDR	Q3ypd6	callisaurus
481	77.5	6.4	347	2	Q3YPG2_CALDR	Q3ypg2	callisaurus
482	77.5	6.4	347	2	Q3YPG3_CALDR	Q3ypg3	callisaurus
483	77.5	6.4	347	2	Q6YIU5_CALDR	Q6yiu5	callisaurus
484	77.5	6.4	379	1	CYB_LAMVI	Q36227	lama vicugn
485	77.5	6.4	379	2	Q8W9E4_9SCIU	Q8w9e4	sciurus aes
486	77.5	6.4	379	2	Q9T3R3_9SCIU	Q9t3r3	marmota cau
487	77.5	6.4	379	2	Q9TF94_9SCIU	Q9tf94	spermophilu
488	77.5	6.4	379	2	Q9TF95_9SCIU	Q9tf95	spermophilu
489	77.5	6.4	427	2	Q2U189_ASPOR	Q2u189	aspergillus
490	77.5	6.4	434	2	Q6NFZ8_CORDI	Q6nfz8	corynebacte
491	77.5	6.4	437	2	Q7WRI8_STAAU	Q7wri8	staphylococ
492	77.5	6.4	443	2	Q3XTT3_9PROT	Q3xtt3	magnetococc
493	77.5	6.4	452	2	Q7YF45_9BIVA	Q7yf45	venerupis (
494	77.5	6.4	452	2	Q7YF47_9BIVA	Q7yf47	venerupis (
495	77.5	6.4	452	2	Q7YF50_9BIVA	Q7yf50	venerupis (
496	77.5	6.4	452	2	Q7YF51_9BIVA	Q7yf51	venerupis (
497	77.5	6.4	452	2	Q7YF52_9BIVA	Q7yf52	venerupis (
498	77.5	6.4	453	1	SERC1_MOUSE	Q9qzi8	mus musculu
499	77.5	6.4	453	2	Q3UZ93_MOUSE	Q3uz93	m 8 days em
500	77.5	6.4	456	2	Q6BQ78_DEBHA	Q6bq78	debaryomyce
501	77.5	6.4	459	1	NU4M_RABIT	O79436	oryctolagus
502	77.5	6.4	459	2	Q5HJF8_STAAC	Q5hjf8	staphylococ
503	77.5	6.4	459	2	Q6GCQ4_STAAS	Q6gcq4	staphylococ
504	77.5	6.4	459	2	Q6GK94_STAAR	Q6gk94	staphylococ
505	77.5	6.4	459	2	Q7A1X0_STAAW	Q7a1x0	staphylococ
506	77.5	6.4	459	2	Q99X01_STAAN	Q99x01	staphylococ
507	77.5	6.4	467	2	Q2TWC3_ASPOR	Q2twc3	aspergillus
508	77.5	6.4	475	2	Q3S003_RALME	Q3s003	ralstonia m
509	77.5	6.4	494	2	Q87S84_VIBPA	Q87s84	vibrio para
510	77.5	6.4	500	2	O51549_BORBU	O51549	borrelia bu
511	77.5	6.4	522	2	Q3QBK4_9GAMM	Q3qbk4	shewanella
512	77.5	6.4	557	2	P94622_CLOCL	P94622	clostridium
513	77.5	6.4	565	2	Q8A4R9_BACTN	Q8a4r9	bacteroides
514	77.5	6.4	578	2	Q4C464_CROWT	Q4c464	crocosphaer
515	77.5	6.4	624	2	Q4PA14_USTMA	Q4pa14	ustilago ma
516	77.5	6.4	820	2	Q54GB8_DICDI	Q54gb8	dictyosteli
517	77.5	6.4	825	2	Q9FK21_ARATH	Q9fk21	arabidopsis
518	77.5	6.4	1045	2	Q54ZK1_DICDI	Q54zk1	dictyosteli
519	77.5	6.4	1107	2	Q76NT1_DICDI	Q76nt1	dictyosteli
520	77	6.3	207	2	Q5I651_HHV8	Q5i651	human herpe
521	77	6.3	249	2	Q4NF25_9MICC	Q4nf25	arthrobacte
522	77	6.3	251	2	Q69BY7_9TELE	Q69by7	coryphaenoi
523	77	6.3	251	2	Q69BZ4_9PERO	Q69bz4	chaetodon s
524	77	6.3	252	2	Q46BP1_METBA	Q46bp1	methanosarc
525	77	6.3	309	2	Q2YSV8_STAAB	Q2ysv8	staphylococ
526	77	6.3	309	2	Q8CTN3_STAES	Q8ctn3	staphylococ
527	77	6.3	314	2	Q6ZAX4_ORYSA	Q6zax4	oryza sativ
528	77	6.3	328	2	Q9TB46_PLADU	Q9tb46	platynereis
529	77	6.3	330	2	Q3YPD4_CALDR	Q3ypd4	callisaurus
530	77	6.3	343	2	Q3YPE2_CALDR	Q3ype2	callisaurus
531	77	6.3	346	2	Q61B87_CAEBR	Q61b87	caenorhabdi
532	77	6.3	347	2	Q3YPD0_CALDR	Q3ypd0	callisaurus
533	77	6.3	347	2	Q3YPE3_CALDR	Q3ype3	callisaurus
534	77	6.3	379	2	Q5J1T5_9CETA	Q5j1t5	sus celeben
535	77	6.3	379	2	Q5MG68_PIG	Q5mg68	sus scrofa
536	77	6.3	379	2	Q8WBM1_MARAM	Q8wbm1	martes amer
537	77	6.3	379	2	Q9B5Q9_9CETA	Q9b5q9	cephalophus
538	77	6.3	379	2	Q9G4V1_MARAM	Q9g4v1	martes amer
539	77	6.3	379	2	Q9G7S6_PIG	Q9g7s6	sus scrofa
540	77	6.3	379	2	Q9MNV4_MARAM	Q9mnv4	martes amer
541	77	6.3	380	2	Q4U6M3_9SAUR	Q4u6m3	zonosaurus
542	77	6.3	424	2	Q6D859_ERWCT	Q6d859	erwinia car

543	77	6.3	429	2	Q4LAB4_STAHJ	Q4lab4	staphylococ
544	77	6.3	452	2	Q6BQ77_DEBHA	Q6bq77	debaryomyce
545	77	6.3	459	2	Q3S070_RALME	Q3s070	ralstonia m
546	77	6.3	471	2	Q85YM1_9ROSI	Q85ym1	monadenium
547	77	6.3	493	2	Q5WUP6_LEGPL	Q5wup6	legionella
548	77	6.3	516	2	Q9B5Z5_9TURB	Q9b5z5	pseudostylo
549	77	6.3	520	2	Q5VCB9_SPIKU	Q5vcb9	spiroplasma
550	77	6.3	534	2	Q8RWH6_ARATH	Q8rwh6	arabidopsis
551	77	6.3	536	2	Q2I8W8_9HIV1	Q2i8w8	human immun
552	77	6.3	537	2	Q7S496_NEUCR	Q7s496	neurospora
553	77	6.3	577	2	Q85QQ7_9HEXA	Q85qq7	gomphioceph
554	77	6.3	581	1	PRLR_SHEEP	O46561	ovis aries
555	77	6.3	590	2	Q9STC7_DUNBI	Q9stc7	dunaliella
556	77	6.3	677	2	Q7QS58_GIALA	Q7qs58	giardia lam
557	77	6.3	1032	1	Y895_HAEIN	Q57124	haemophilus
558	77	6.3	1032	2	Q4QM13_HAEI8	Q4qm13	haemophilus
559	77	6.3	1061	2	Q986H1_RHILO	Q986h1	rhizobium l
560	77	6.3	1078	2	Q3P638_9GAMM	Q3p638	shewanella
561	77	6.3	1188	2	Q7RWN3_NEUCR	Q7rwn3	neurospora
562	77	6.3	1193	2	Q55B99_DICDI	Q55b99	dictyosteli
563	77	6.3	1203	2	Q55B98_DICDI	Q55b98	dictyosteli
564	77	6.3	1215	2	P93750_ARATH	P93750	arabidopsis
565	77	6.3	2651	2	Q8IAV6_PLAF7	Q8iav6	plasmodium
566	76.5	6.3	207	2	Q36BV5_9GAMM	Q36bv5	shewanella
567	76.5	6.3	222	2	Q7B5K3_LACPL	Q7b5k3	lactobacill
568	76.5	6.3	232	1	G6B_RAT	Q6mg59	rattus norv
569	76.5	6.3	248	2	Q7QYX9_GIALA	Q7qyx9	giardia lam
570	76.5	6.3	268	2	Q6XFA1_9SAUR	Q6xfa1	psammophis
571	76.5	6.3	274	2	Q995B5_HHV8	Q995b5	human herpe
572	76.5	6.3	278	2	Q3GXC4_9ACTO	Q3gxc4	nocardioide
573	76.5	6.3	289	2	Q80ID9_HHV8	Q80id9	human herpe
574	76.5	6.3	289	2	Q80IF2_HHV8	Q80if2	human herpe
575	76.5	6.3	333	2	Q8KVY0_9RHOB	Q8kvy0	ruegeria sp
576	76.5	6.3	343	2	Q859X2_9SAUR	Q859x2	uma exsul.
577	76.5	6.3	343	2	Q85KP0_9SAUR	Q85kp0	uma exsul.
578	76.5	6.3	347	2	Q3YPG5_CALDR	Q3ypg5	callisaurus
579	76.5	6.3	360	2	Q34CE7_RHOPA	Q34ce7	rhodopseudo
580	76.5	6.3	377	2	Q8K0P5_MOUSE	Q8k0p5	mus musculu
581	76.5	6.3	379	1	CYB_CANAU	Q6jwx5	canis aureu
582	76.5	6.3	379	1	CYB_CANFA	Q34101	canis famil
583	76.5	6.3	379	1	CYB_CANLU	Q6y8j2	canis lupus
584	76.5	6.3	379	1	CYB_MARMR	Q9xp34	marmota mar
585	76.5	6.3	379	1	CYB_MARVA	Q9th56	marmota van
586	76.5	6.3	379	2	Q3ZED2_CANLU	Q3zed2	canis lupus
587	76.5	6.3	379	2	Q49RE5_CANFA	Q49re5	canis famil
588	76.5	6.3	379	2	Q49RV1_CANFA	Q49rv1	canis famil
589	76.5	6.3	379	2	Q49RZ0_CANFA	Q49rz0	canis famil
590	76.5	6.3	379	2	Q6JWX7_CANLU	Q6jwx7	canis lupus
591	76.5	6.3	379	2	Q9G3M7_9RODE	Q9g3m7	rhizomys si
592	76.5	6.3	389	2	Q4CXF9_TRYCR	Q4cxf9	trypanosoma
593	76.5	6.3	413	2	Q2WQU1_CLOBE	Q2wqu1	clostridium
594	76.5	6.3	426	2	Q9W3R5_DROME	Q9w3r5	drosophila
595	76.5	6.3	441	2	Q3K7G1_PSEPF	Q3k7g1	pseudomonas
596	76.5	6.3	451	2	O69657_MYCTU	O69657	mycobacteri
597	76.5	6.3	451	2	Q7TVX6_MYCBO	Q7tvx6	mycobacteri
598	76.5	6.3	468	2	Q5A0Y4_CANAL	Q5a0y4	candida alb
599	76.5	6.3	473	2	Q48M64_PSE14	Q48m64	pseudomonas
600	76.5	6.3	478	2	Q5SZW5_HUMAN	Q5szw5	homo sapien
601	76.5	6.3	518	2	Q5K8N9_CRYNE	Q5k8n9	cryptococcu
602	76.5	6.3	538	2	Q9M1T4_ARATH	Q9m1t4	arabidopsis
603	76.5	6.3	541	2	Q4V8T5_BRARE	Q4v8t5	brachydanio
604	76.5	6.3	556	2	Q6BVD3_DEBHA	Q6bvd3	debaryomyce
605	76.5	6.3	557	1	PNS1_CANGA	Q6f1c9	candida gla
606	76.5	6.3	557	2	Q7KVU5_DROME	Q7kvu5	drosophila
607	76.5	6.3	574	2	Q9TW13_LEIME	Q9tw13	leishmania
608	76.5	6.3	598	2	Q9U1G0_LEIME	Q9u1g0	leishmania
609	76.5	6.3	606	2	Q644T5_9SALA	Q644t5	batrachosep
610	76.5	6.3	608	2	Q2WB73_MAGSA	Q2wb73	magnetospir
611	76.5	6.3	614	1	DNAK_ODOSI	P49463	odontella s
612	76.5	6.3	694	2	Q2QLJ8_ORYSA	Q2qlj8	oryza sativ
613	76.5	6.3	722	2	Q9F0W5_PSEFL	Q9f0w5	pseudomonas
614	76.5	6.3	762	2	Q5LDA6_BACFN	Q5lda6	bacteroides
615	76.5	6.3	762	2	Q64UC9_BACFR	Q64uc9	bacteroides
616	76.5	6.3	1055	2	Q36U69_MARHY	Q36u69	marinobacte
617	76.5	6.3	1378	2	Q3UHB0_MOUSE	Q3uhb0	mus musculu
618	76.5	6.3	1378	2	Q68HV2_MOUSE	Q68hv2	mus musculu
619	76.5	6.3	1444	2	Q6A051_MOUSE	Q6a051	mus musculu
620	76.5	6.3	2421	2	Q5CUF6_CRYPV	Q5cuf6	cryptospori
621	76	6.3	144	2	O47929_9HYME	O47929	exoneura tr
622	76	6.3	184	2	Q4F9L5_GRYPE	Q4f9l5	gryllus pen
623	76	6.3	204	2	Q4K938_PSEF5	Q4k938	pseudomonas
624	76	6.3	249	2	Q7R5F7_GIALA	Q7r5f7	giardia lam
625	76	6.3	265	2	Q2ZF96_CALSA	Q2zf96	caldicellul
626	76	6.3	289	1	OPSD_COMDY	O42327	comephorus
627	76	6.3	298	2	Q34CA4_RHOPA	Q34ca4	rhodopseudo
628	76	6.3	308	2	Q2NL45_MOUSE	Q2nl45	mus musculu
629	76	6.3	310	2	Q8VG54_MOUSE	Q8vg54	mus musculu
630	76	6.3	312	2	Q8TKV9_METAC	Q8tkv9	methanosarc
631	76	6.3	330	2	Q85T18_9SAUR	Q85t18	anolis roqu
632	76	6.3	343	2	Q3YPF8_CALDR	Q3ypf8	callisaurus
633	76	6.3	343	2	Q85KP4_9SAUR	Q85kp4	uma exsul.
634	76	6.3	346	2	O16913_CAEEL	O16913	caenorhabdi
635	76	6.3	353	2	Q2Y0W9_HIPHI	Q2y0w9	hippoglossu
636	76	6.3	379	1	CYB_MARME	Q9t3h9	martes mela
637	76	6.3	379	1	CYB_PTEHP	Q8sjz4	pteropus hy
638	76	6.3	379	2	O78726_PIG	O78726	sus scrofa
639	76	6.3	379	2	Q38R65_SHEEP	Q38r65	ovis aries
640	76	6.3	379	2	Q38R67_SHEEP	Q38r67	ovis aries
641	76	6.3	379	2	Q38R69_SHEEP	Q38r69	ovis aries
642	76	6.3	379	2	Q38R70_SHEEP	Q38r70	ovis aries
643	76	6.3	379	2	Q38R71_SHEEP	Q38r71	ovis aries
644	76	6.3	379	2	Q7I1Z0_MARZI	Q7i1z0	martes zibe
645	76	6.3	379	2	Q8M700_9CETA	Q8m700	sus verruco
646	76	6.3	379	2	Q8M701_9CETA	Q8m701	sus verruco
647	76	6.3	379	2	Q8W7D6_MARMT	Q8w7d6	martes mart
648	76	6.3	379	2	Q8WBM0_MARZI	Q8wbm0	martes zibe
649	76	6.3	379	2	Q9B5R7_9CETA	Q9b5r7	cephalophus
650	76	6.3	379	2	Q9GBH0_MARMT	Q9gbh0	martes mart
651	76	6.3	379	2	Q9GBH3_MARAM	Q9gbh3	martes amer
652	76	6.3	379	2	Q588N5_SCILI	Q588n5	sciurus lis
653	76	6.3	379	2	Q588N9_SCILI	Q588n9	sciurus lis
654	76	6.3	379	2	Q9T7P0_9RODE	Q9t7p0	tachyorycte
655	76	6.3	380	2	Q4U6R0_9SAUR	Q4u6r0	zonosaurus
656	76	6.3	380	2	Q7YE34_9LABR	Q7ye34	microspatho
657	76	6.3	380	2	Q7YHK3_9SMEG	Q7yhk3	zoogoneticu
658	76	6.3	392	2	Q36DA5_9GAMM	Q36da5	shewanella
659	76	6.3	393	2	Q5CI38_CRYHO	Q5ci38	cryptospori
660	76	6.3	403	2	Q4DNU1_TRYCR	Q4dnu1	trypanosoma
661	76	6.3	405	2	Q6L2S9_PICTO	Q6l2s9	picrophilus
662	76	6.3	408	2	Q3B003_SYNS9	Q3b003	synechococc
663	76	6.3	410	2	Q9XP09_9HYME	Q9xp09	parapantele
664	76	6.3	417	2	Q3IGF3_PSEHT	Q3igf3	pseudoalter
665	76	6.3	430	2	Q6Y0P9_STAAU	Q6y0p9	staphylococ
666	76	6.3	431	2	Q4EPL8_LISMO	Q4epl8	listeria mo
667	76	6.3	431	2	Q6LWG4_LACPL	Q6lwg4	lactobacill
668	76	6.3	431	2	Q8Y7H9_LISMO	Q8y7h9	listeria mo
669	76	6.3	445	2	Q76L72_9EUCA	Q76l72	euphausia s
670	76	6.3	447	2	Q8VUH5_STAAU	Q8vuh5	staphylococ
671	76	6.3	447	2	Q6G7E5_STAAS	Q6g7e5	staphylococ
672	76	6.3	447	2	Q8NVE0_STAAW	Q8nve0	staphylococ
673	76	6.3	447	2	Q99S97_STAAN	Q99s97	staphylococ
674	76	6.3	447	2	Q5HE36_STAAC	Q5he36	staphylococ
675	76	6.3	453	2	Q6UKF6_9BILA	Q6ukf6	phoronis ps
676	76	6.3	475	2	Q2WIM6_CLOBE	Q2wim6	clostridium
677	76	6.3	483	2	Q5LZW7_STRT1	Q5lzw7	streptococc
678	76	6.3	483	2	Q5M4H8_STRT2	Q5m4h8	streptococc
679	76	6.3	505	2	Q972X7_SULTO	Q972x7	sulfolobus
680	76	6.3	515	1	LRTM2_MOUSE	Q8bga3	mus musculu
681	76	6.3	515	2	Q8C8L1_MOUSE	Q8c8l1	mus musculu
682	76	6.3	527	2	Q41D91_9BACI	Q41d91	exiguobacte
683	76	6.3	529	2	Q65M41_BACLD	Q65m41	bacillus li
684	76	6.3	532	1	YHCA_BACSU	P54585	bacillus su
685	76	6.3	536	2	Q5Q1C2_9CORO	Q5q1c2	infectious
686	76	6.3	539	2	Q5Q1C1_9CORO	Q5q1c1	infectious
687	76	6.3	540	2	Q4RN73_TETNG	Q4rn73	tetraodon n
688	76	6.3	543	2	Q9DXY6_9CORO	Q9dxy6	infectious

689	76	6.3	559	2	Q7QR36_GIALA	Q7qr36 giardia lam	762	75.5	6.2	1024	2	Q5NXR2_AZOSE	Q5nxr2 azoarcus sp		
690	76	6.3	561	2	O17947_CAEEL	O17947 caenorhabdi	763	75.5	6.2	1099	2	Q18633_CAEEL	Q18633 caenorhabdi		
691	76	6.3	574	2	Q3ILR2_PSEHT	Q3ilr2 pseudoalter	764	75.5	6.2	1173	2	Q6NR54_DROME	Q6nr54 drosophila		
692	76	6.3	604	2	O93700_9CREN	O93700 sulfolobus	765	75.5	6.2	1683	2	Q86KY1_DICDI	Q86ky1 dictyosteli		
693	76	6.3	633	2	Q2Y0X0_HIPHI	Q2y0x0 hippoglossu	766	75.5	6.2	4226	2	Q9N9H5_PLAFA	Q9n9h5 plasmodium		
694	76	6.3	688	2	Q7Q074_ANOGA	Q7q074 anopheles g	767	75	6.2	111	2	Q9XEF7_ARATH	Q9xef7 arabidopsis		
695	76	6.3	695	2	Q33LU3_METHU	Q33lu3 methanospir	768	75	6.2	176	2	Q8TIK1_METAC	Q8tik1 methanosarc		
696	76	6.3	742	2	Q23766_9DIPT	Q23766 chironomus	769	75	6.2	252	2	Q69BY8_9TELE	Q69by8 trachyrincu		
697	76	6.3	751	1	CPB3_CAEEL	O01835 caenorhabdi	770	75	6.2	253	2	Q8AWJ8_9PERC	Q8awj8 chloroscomb		
698	76	6.3	806	2	Q61QC8_CAEBR	Q61qc8 caenorhabdi	771	75	6.2	284	2	Q2NST2_SODGL	Q2nst2 sodalis glo		
699	76	6.3	1011	2	Q24273_DROME	Q24273 drosophila	772	75	6.2	299	2	Q8AWR5_BRARE	Q8awr5 brachydanio		
700	76	6.3	1043	2	Q6LNM7_PHOPR	Q6lnm7 photobacter	773	75	6.2	312	2	Q6MFX2_RAT	Q6mfx2 rattus norv		
701	76	6.3	1087	2	Q9VNP2_DROME	Q9vnp2 drosophila	774	75	6.2	330	2	Q85T15_9SAUR	Q85t15 anolis roqu		
702	76	6.3	1645	2	Q582H4_9TRYP	Q582h4 trypanosoma	775	75	6.2	330	2	Q85T16_9SAUR	Q85t16 anolis roqu		
703	76	6.3	2783	2	Q4RI15_TETNG	Q4ri15 tetraodon n	776	75	6.2	339	2	Q61CY0_CAEBR	Q61cy0 caenorhabdi		
704	75.5	6.2	108	2	Q2VTP0_PHLGI	Q2vtp0 phlebiopsis	777	75	6.2	343	2	Q3YPG0_CALDR	Q3ypg0 callisaurus		
705	75.5	6.2	111	2	Q90X36_BRARE	Q90x36 brachydanio	778	75	6.2	347	2	Q6YIW1_PHRCO	Q6yiw1 phrynosoma		
706	75.5	6.2	138	2	P71459_LACPL	P71459 lactobacill	779	75	6.2	353	2	Q3DMY9_STRAG	Q3dmy9 streptococc		
707	75.5	6.2	142	2	Q8HMW9_9HYME	Q8hmw9 allodape mu	780	75	6.2	360	2	Q8HIC0_9SCIU	Q8hic0 callosciuru		
708	75.5	6.2	146	2	Q695B9_PICGL	Q695b9 picea glauc	781	75	6.2	373	2	Q8Z089_ANASP	Q8z089 anabaena sp		
709	75.5	6.2	146	2	Q695C0_PICGL	Q695c0 picea glauc	782	75	6.2	379	1	CYB_CEPNG	Q9b5r0 cephalophus		
710	75.5	6.2	151	2	Q9SPW5_PICGL	Q9spw5 picea glauc	783	75	6.2	379	1	CYB_GULGU	P56697 gulo gulo (		
711	75.5	6.2	185	2	Q4F9L1_TENMO	Q4f9l1 tenebrio mo	784	75	6.2	379	1	CYB_MESHI	Q35000 mesomys his		
712	75.5	6.2	222	2	Q88ZC6_LACPL	Q88zc6 lactobacill	785	75	6.2	379	2	P92579_BUBDE	P92579 bubalus dep		
713	75.5	6.2	239	2	Q75QB4_9ENTO	Q75qb4 human coxsa	786	75	6.2	379	2	P92867_BUBDE	P92867 bubalus dep		
714	75.5	6.2	239	2	Q6DCQ3_XENLA	Q6dcq3 xenopus lae	787	75	6.2	379	2	Q3HNI3_GULGU	Q3hni3 gulo gulo (		
715	75.5	6.2	250	2	Q4MML4_BACCE	Q4mml4 bacillus ce	788	75	6.2	379	2	Q3HNI4_GULGU	Q3hni4 gulo gulo (		
716	75.5	6.2	275	2	Q6GIG5_STAAR	Q6gig5 staphylococ	789	75	6.2	379	2	Q7IYN8_9CETA	Q7iyn8 cephalophus		
717	75.5	6.2	343	2	Q3YPE5_CALDR	Q3ype5 callisaurus	790	75	6.2	379	2	Q8HBR1_CAMBA	Q8hbr1 camelus bac		
718	75.5	6.2	343	2	Q3YPE6_CALDR	Q3ype6 callisaurus	791	75	6.2	379	2	Q8HFA7_CAMBA	Q8hfa7 camelus bac		
719	75.5	6.2	343	2	Q3YPE7_CALDR	Q3ype7 callisaurus	792	75	6.2	379	2	Q9B1D2_CEPNA	Q9b1d2 cephalophus		
720	75.5	6.2	343	2	Q3YPF0_CALDR	Q3ypf0 callisaurus	793	75	6.2	379	2	Q9B5Q3_9CETA	Q9b5q3 cephalophus		
721	75.5	6.2	343	2	Q85CB0_9SAUR	Q85cb0 uma exsul.	794	75	6.2	379	2	Q9B5R6_CEPLE	Q9b5r6 cephalophus		
722	75.5	6.2	343	2	Q85KP1_9SAUR	Q85kp1 uma exsul.	795	75	6.2	379	2	Q9B5S1_9CETA	Q9b5s1 cephalophus		
723	75.5	6.2	347	2	Q3YPE9_CALDR	Q3ype9 callisaurus	796	75	6.2	379	2	Q9XLD8_KOBEL	Q9xld8 kobus ellip		
724	75.5	6.2	347	2	Q6YIU9_HOLMA	Q6yiu9 holbrookia	797	75	6.2	379	2	Q9XLD9_KOBEL	Q9xld9 kobus ellip		
725	75.5	6.2	348	2	Q8MQU1_PARLI	Q8mqu1 paracentrot	798	75	6.2	379	2	Q7GI04_MESHI	Q7gi04 mesomys his		
726	75.5	6.2	355	2	Q465J2_METBA	Q465j2 methanosarc	799	75	6.2	379	2	Q9XK52_9SCIU	Q9xk52 marmota sib		
727	75.5	6.2	364	2	Q92PR2_RHIME	Q92pr2 rhizobium m	800	75	6.2	380	2	Q9T578_9RODE	Q9t578 acomys sp.		
728	75.5	6.2	378	2	Q70EH3_9RODE	Q70eh3 saccostomus	801	75	6.2	380	2	Q4U6L7_9SAUR	Q4u6l7 zonosaurus		
729	75.5	6.2	379	2	Q3HNH8_GULGU	Q3hnh8 gulo gulo (	802	75	6.2	380	2	Q7YE73_9LABR	Q7ye73 chromis xan		
730	75.5	6.2	379	2	Q3HNI9_GULGU	Q3hni9 gulo gulo (	803	75	6.2	385	2	Q9PFR8_XYLFA	Q9pfr8 xylella fas		
731	75.5	6.2	379	2	Q3HNJ1_GULGU	Q3hnj1 gulo gulo (	804	75	6.2	389	2	Q4L3Z7_STAHJ	Q4l3z7 staphylococ		
732	75.5	6.2	379	2	Q9GBG7_GULGU	Q9gbg7 gulo gulo (	805	75	6.2	395	2	Q3JKS6_BURP1	Q3jks6 burkholderi		
733	75.5	6.2	379	2	O20611_9HYST	O20611 coetomys da	806	75	6.2	396	2	Q8D2Q7_WIGBR	Q8d2q7 wiggleswort		
734	75.5	6.2	379	2	O21789_9HYST	O21789 ctenomys fr	807	75	6.2	417	2	Q697E1_ECOLI	Q697e1 escherichia		
735	75.5	6.2	379	2	Q6T8R4_SPEPA	Q6t8r4 spermophilu	808	75	6.2	452	2	Q6GMG6_BRARE	Q6gmg6 brachydanio		
736	75.5	6.2	379	2	Q9XP28_MARCA	Q9xp28 marmota cal	809	75	6.2	475	2	Q46EY2_METBA	Q46ey2 methanosarc		
737	75.5	6.2	380	2	Q94SX5_COLSA	Q94sx5 cololabis s	810	75	6.2	479	2	Q3FXD5_9BURK	Q3fxd5 rhodoferax		
738	75.5	6.2	384	2	Q37623_PROWI	Q37623 prototheca	811	75	6.2	487	2	Q37NN7_RHOPA	Q37nn7 rhodopseudo		
739	75.5	6.2	409	1	MNTH_YERPE	Q8zck2 yersinia pe	812	75	6.2	490	2	Q4SGF2_TETNG	Q4sgf2 tetraodon n		
740	75.5	6.2	409	2	Q668N2_YERPS	Q668n2 yersinia ps	813	75	6.2	519	2	Q6RI96_RHIFR	Q6ri96 rhizobium f		
741	75.5	6.2	429	2	Q41UT5_FERAC	Q41ut5 ferroplasma	814	75	6.2	521	2	Q4X1B7_ASPFU	Q4x1b7 aspergillus		
742	75.5	6.2	431	2	Q9S333_PROMA	Q9s333 prochloroco	815	75	6.2	522	2	Q2UCA0_ASPOR	Q2uca0 aspergillus		
743	75.5	6.2	476	2	Q9SIA5_ARATH	Q9sia5 arabidopsis	816	75	6.2	527	2	Q8KU76_ENTFA	Q8ku76 enterococcu		
744	75.5	6.2	494	2	Q7MNM2_VIBVY	Q7mnm2 vibrio vuln	817	75	6.2	566	2	Q73YM0_MYCPA	Q73ym0 mycobacteri		
745	75.5	6.2	494	2	Q8DET3_VIBVU	Q8det3 vibrio vuln	818	75	6.2	570	2	Q9B510_TETBI	Q9b510 tetrodontop		
746	75.5	6.2	564	2	Q5AQF8_EMENI	Q5aqf8 aspergillus	819	75	6.2	581	1	PRLR_BOVIN	Q28172 bos taurus		
747	75.5	6.2	578	2	Q85UI2_CIOSA	Q85ui2 ciona savig	820	75	6.2	726	2	Q6C7B9_YARLI	Q6c7b9 yarrowia li		
748	75.5	6.2	593	2	Q6BM61_DEBHA	Q6bm61 debaryomyce	821	75	6.2	853	2	O93245_ONCMY	O93245 oncorhynchu		
749	75.5	6.2	609	2	Q2X9I6_PSEPU	Q2x9i6 pseudomonas	822	75	6.2	880	2	Q3VWQ4_PROAE	Q3vwq4 prosthecoch		
750	75.5	6.2	609	2	Q88FZ5_PSEPK	Q88fz5 pseudomonas	823	75	6.2	887	2	Q4I9I5_GIBZE	Q4i9i5 gibberella		
751	75.5	6.2	687	2	Q3WD50_9ACTO	Q3wd50 frankia sp.	824	75	6.2	982	2	Q09938_CAEEL	Q09938 caenorhabdi		
752	75.5	6.2	702	2	Q5S2D2_MACMU	Q5s2d2 macaca mula	825	75	6.2	1041	2	Q3XLS8_9PROT	Q3xls8 magnetococc		
753	75.5	6.2	702	2	Q5S2D3_MACFA	Q5s2d3 macaca fasc	826	75	6.2	1072	2	Q2UU52_ASPOR	Q2uu52 aspergillus		
754	75.5	6.2	788	1	QOXM_SULAC	P39481 sulfolobus	827	75	6.2	2201	1	TENA_HUMAN	P24821 homo sapien		
755	75.5	6.2	801	2	Q4N2A4_THEPA	Q4n2a4 theileria p	828	75	6.2	2201	2	Q5T7S3_HUMAN	Q5t7s3 homo sapien		
756	75.5	6.2	824	2	Q40713_ORYSA	Q40713 oryza sativ	829	75	6.2	2233	2	Q4LE33_HUMAN	Q4le33 homo sapien		
757	75.5	6.2	849	2	Q8T3V2_DROME	Q8t3v2 drosophila	830	74.5	6.1	146	2	Q8LXC1_MARAM	Q8lxc1 martes amer		
758	75.5	6.2	858	2	Q5U888_9HIV1	Q5u888 human immun	831	74.5	6.1	202	2	Q6ZV01_HUMAN	Q6zv01 homo sapien		
759	75.5	6.2	864	2	Q6BGY9_DEBHA	Q6bgy9 debaryomyce	832	74.5	6.1	208	2	Q392V0_BURS3	Q392v0 burkholderi		
760	75.5	6.2	886	2	Q8KAY9_CHLTE	Q8kay9 chlorobium	833	74.5	6.1	239	1	TSN9_MOUSE	Q8bju2 mus musculu		
761	75.5	6.2	1020	2	Q4KHX4_PSEF5	Q4khx4 pseudomonas	834	74.5	6.1	239	2	Q3TQQ0_MOUSE	Q3tqq0 m 2 cells e		

835	74.5	6.1	246	2	Q9MF63_BETVU	Q9mf63	beta vulgar
836	74.5	6.1	265	2	Q896Z5_CLOTE	Q896z5	clostridium
837	74.5	6.1	268	2	Q6NIZ8_CORDI	Q6niz8	corynebacte
838	74.5	6.1	289	2	O93938_YEAST	O93938	saccharomyc
839	74.5	6.1	289	2	Q9WHC9_HHV8	Q9whc9	human herpe
840	74.5	6.1	296	2	Q4EFP8_LISMO	Q4efp8	listeria mo
841	74.5	6.1	296	2	Q722C5_LISMF	Q722c5	listeria mo
842	74.5	6.1	310	2	Q7V7B4_PROMM	Q7v7b4	prochloroco
843	74.5	6.1	318	2	Q970J0_SULTO	Q970j0	sulfolobus
844	74.5	6.1	328	2	Q6JP46_9MARC	Q6jp46	radula comp
845	74.5	6.1	330	2	Q85T11_9SAUR	Q85t11	anolis roqu
846	74.5	6.1	332	2	Q8ZXG2_PYRAE	Q8zxg2	pyrobaculum
847	74.5	6.1	343	2	Q85CS6_9SAUR	Q85cs6	uma paraphy
848	74.5	6.1	343	2	Q85KN5_9SAUR	Q85kn5	uma paraphy
849	74.5	6.1	343	2	Q85KN6_9SAUR	Q85kn6	uma paraphy
850	74.5	6.1	343	2	Q85KN8_9SAUR	Q85kn8	uma paraphy
851	74.5	6.1	343	2	Q85KN9_9SAUR	Q85kn9	uma paraphy
852	74.5	6.1	343	2	Q85KP2_9SAUR	Q85kp2	uma exsul.
853	74.5	6.1	346	2	Q9GCS2_TAMHU	Q9gcs2	tamiasciuru
854	74.5	6.1	347	2	Q3YPF7_CALDR	Q3ypf7	callisaurus
855	74.5	6.1	360	2	Q317F7_DESDG	Q317f7	desulfovibr
856	74.5	6.1	376	2	Q9TH54_MARMO	Q9th54	marmota mon
857	74.5	6.1	377	2	Q93F46_EDWTA	Q93f46	edwardsiell
858	74.5	6.1	378	2	Q8NLL3_CORGL	Q8nll3	corynebacte
859	74.5	6.1	378	2	Q94Y65_TAMHU	Q94y65	tamiasciuru
860	74.5	6.1	379	1	CYB_AMMHA	Q9tf30	ammospermop
861	74.5	6.1	379	1	CYB_CHROW	Q9b9f5	chrotogale
862	74.5	6.1	379	1	CYB_CTECO	O21764	ctenomys co
863	74.5	6.1	379	1	CYB_HIPEQ	Q34717	hippotragus
864	74.5	6.1	379	2	Q5F4E8_9CHIR	Q5f4e8	harpiocepha
865	74.5	6.1	379	2	Q5F4G7_9CHIR	Q5f4g7	myotis sica
866	74.5	6.1	379	2	Q9TH46_9SCIU	Q9th46	marmota bro
867	74.5	6.1	379	2	Q9XMB8_9SCIU	Q9xmb8	marmota bro
868	74.5	6.1	383	2	Q3KFP9_PSEPF	Q3kfp9	pseudomonas
869	74.5	6.1	407	2	Q6MDT1_PARUW	Q6mdt1	parachlamyd
870	74.5	6.1	410	2	Q6E822_9HEMI	Q6e822	umbonia ata
871	74.5	6.1	416	2	Q6M1T5_CORGL	Q6m1t5	corynebacte
872	74.5	6.1	428	2	Q7P9H7_RICSI	Q7p9h7	rickettsia
873	74.5	6.1	429	1	ARSB_STAXY	Q01255	staphylococ
874	74.5	6.1	432	1	RMUC_RICCN	Q92gr5	rickettsia
875	74.5	6.1	453	2	Q7V4H7_PROMM	Q7v4h7	prochloroco
876	74.5	6.1	456	2	Q39U75_GEOMG	Q39u75	geobacter m
877	74.5	6.1	458	1	TCR_STAHY	P36890	staphylococ
878	74.5	6.1	462	2	Q6GQP2_BRARE	Q6gqp2	brachydanio
879	74.5	6.1	468	2	Q9KUT2_VIBCH	Q9kut2	vibrio chol
880	74.5	6.1	473	2	Q9W1Y9_DROME	Q9w1y9	drosophila
881	74.5	6.1	478	2	Q66H95_RAT	Q66h95	rattus norv
882	74.5	6.1	518	2	Q83MI2_TROW8	Q83mi2	tropheryma
883	74.5	6.1	518	2	Q83MP0_TROWT	Q83mp0	tropheryma
884	74.5	6.1	522	2	Q35UI4_9GAMM	Q35ui4	shewanella
885	74.5	6.1	522	2	Q369G7_9GAMM	Q369g7	shewanella
886	74.5	6.1	522	2	Q8JRZ2_9BACU	Q8jrz2	phthorimaea
887	74.5	6.1	530	2	Q4YWN6_PLABE	Q4ywn6	plasmodium
888	74.5	6.1	559	2	Q8JR34_9CORO	Q8jr34	infectious
889	74.5	6.1	565	2	Q446U8_SOLUS	Q446u8	solibacter
890	74.5	6.1	565	2	Q5L7X4_BACFN	Q5l7x4	bacteroides
891	74.5	6.1	565	2	Q64N48_BACFR	Q64n48	bacteroides
892	74.5	6.1	591	2	Q4SBH4_TETNG	Q4sbh4	tetraodon n
893	74.5	6.1	618	2	Q9LQ76_ARATH	Q9lq76	arabidopsis
894	74.5	6.1	618	2	Q9ZTZ7_ARATH	Q9ztz7	arabidopsis
895	74.5	6.1	641	2	Q88E58_PSEPK	Q88e58	pseudomonas
896	74.5	6.1	677	2	Q77LV0_9NUCL	Q77lv0	helicoverpa
897	74.5	6.1	677	2	Q99GS9_9NUCL	Q99gs9	helicoverpa
898	74.5	6.1	729	1	NU5C_ADICA	Q85fh9	adiantum ca
899	74.5	6.1	740	2	Q6NUU5_BRARE	Q6nuu5	brachydanio
900	74.5	6.1	763	2	Q811Q4_MOUSE	Q811q4	mus musculu
901	74.5	6.1	829	2	Q4QDT5_LEIMA	Q4qdt5	leishmania
902	74.5	6.1	1034	2	Q37JQ7_RHOPA	Q37jq7	rhodopseudo
903	74.5	6.1	1054	2	Q75HC2_ORYSA	Q75hc2	oryza sativ
904	74.5	6.1	1059	2	Q8JHB1_SQUAC	Q8jhb1	squalus aca
905	74.5	6.1	1059	2	Q8JHB3_SQUAC	Q8jhb3	squalus aca
906	74.5	6.1	1062	2	Q89NG9_BRAJA	Q89ng9	bradyrhizob
907	74.5	6.1	1087	2	Q2TYZ6_ASPOR	Q2tyz6	aspergillus
908	74.5	6.1	1091	2	Q8JHB5_SQUAC	Q8jhb5	squalus aca
909	74.5	6.1	1439	2	Q5CPF4_CRYPV	Q5cpf4	cryptospori
910	74.5	6.1	1469	2	Q5CJY6_CRYHO	Q5cjy6	cryptospori
911	74.5	6.1	1709	1	SN_HUMAN	Q9bzz2	homo sapien
912	74.5	6.1	3880	2	Q2TYJ0_ASPOR	Q2tyj0	aspergillus
913	74	6.1	114	2	Q8X1T9_PHONA	Q8x1t9	pholiota na
914	74	6.1	140	2	Q85PI9_CANFA	Q85pi9	canis famil
915	74	6.1	142	2	Q3Y9Z4_9HYME	Q3y9z4	halterapis
916	74	6.1	176	2	Q4F9L3_9HEMI	Q4f913	leptocoris
917	74	6.1	263	1	LGT_STRT1	Q5m0j6	streptococc
918	74	6.1	268	2	Q822A6_CHLCV	Q822a6	chlamydophi
919	74	6.1	282	2	Q9PUZ5_9PERC	Q9puz5	balistes sp
920	74	6.1	293	2	Q3CR79_ALTAT	Q3cr79	pseudoalter
921	74	6.1	307	2	Q7TR51_MOUSE	Q7tr51	mus musculu
922	74	6.1	311	2	Q4IXC3_AZOVI	Q4ixc3	azotobacter
923	74	6.1	330	2	Q85T09_9SAUR	Q85t09	anolis roqu
924	74	6.1	330	2	Q85T21_9SAUR	Q85t21	anolis roqu
925	74	6.1	347	2	Q624U8_CAEBR	Q624u8	caenorhabdi
926	74	6.1	369	2	Q70VE5_SORMI	Q70ve5	sorex minut
927	74	6.1	379	1	CYB_CAMDR	P24952	camelus dro
928	74	6.1	379	1	CYB_KOBEL	O99342	kobus ellip
929	74	6.1	379	1	CYB_MYOFO	Q7y815	myotis form
930	74	6.1	379	2	O99339_NEOMO	O99339	neotragus m
931	74	6.1	379	2	Q33948_BUBBU	Q33948	bubalus bub
932	74	6.1	379	2	Q5BQG7_9CETA	Q5bqg7	sus philipp
933	74	6.1	379	2	Q5F4G8_MYOFO	Q5f4g8	myotis form
934	74	6.1	379	2	Q5J1T3_9CETA	Q5j1t3	potamochoer
935	74	6.1	379	2	Q5J1T4_9CETA	Q5j1t4	potamochoer
936	74	6.1	379	2	Q5MG78_PIG	Q5mg78	sus scrofa
937	74	6.1	379	2	Q6GV88_PIG	Q6gv88	sus scrofa
938	74	6.1	379	2	Q8HB83_CAMDR	Q8hb83	camelus dro
939	74	6.1	379	2	Q9B5R4_CEPMO	Q9b5r4	cephalophus
940	74	6.1	379	2	Q35087_9HYST	Q35087	mesomys sp.
941	74	6.1	379	2	Q35093_9HYST	Q35093	mesomys sp.
942	74	6.1	379	2	Q8W9L6_GLAVO	Q8w916	glaucomys v
943	74	6.1	379	2	Q94ND7_9HYST	Q94nd7	ctenomys tu
944	74	6.1	379	2	Q94PB4_TAMAM	Q94pb4	tamias amoe
945	74	6.1	379	2	Q94WY4_9HYST	Q94wy4	ctenomys tu
946	74	6.1	379	2	Q9TF64_SPELA	Q9tf64	spermophilu
947	74	6.1	379	2	Q9TH47_MARCA	Q9th47	marmota cal
948	74	6.1	380	2	Q4U6L9_9SAUR	Q4u6l9	zonosaurus
949	74	6.1	380	2	Q4U6M0_9SAUR	Q4u6m0	zonosaurus
950	74	6.1	380	2	Q4U6M1_9SAUR	Q4u6m1	zonosaurus
951	74	6.1	380	2	Q4U6M4_9SAUR	Q4u6m4	zonosaurus
952	74	6.1	380	2	Q4U6Q7_9SAUR	Q4u6q7	zonosaurus
953	74	6.1	385	2	Q3R1B6_XYLFA	Q3r1b6	xylella fas
954	74	6.1	385	2	Q3RAB4_XYLFA	Q3rab4	xylella fas
955	74	6.1	385	2	Q3RI08_XYLFA	Q3ri08	xylella fas
956	74	6.1	385	2	Q87B96_XYLFT	Q87b96	xylella fas
957	74	6.1	399	2	Q5L1X9_GEOKA	Q5l1x9	geobacillus
958	74	6.1	404	2	Q40PX6_DESAC	Q40px6	desulfuromo
959	74	6.1	405	2	O69757_PSEFL	O69757	pseudomonas
960	74	6.1	406	2	Q483X7_COLP3	Q483x7	colwellia p
961	74	6.1	410	2	Q6E8J0_9HEMI	Q6e8j0	heteronotus
962	74	6.1	420	2	Q2KGM2_MAGGR	Q2kgm2	magnaporthe
963	74	6.1	430	2	Q6Y0N7_STAAU	Q6y0n7	staphylococ
964	74	6.1	431	2	Q92C53_LISIN	Q92c53	listeria in
965	74	6.1	442	2	Q41T49_FERAC	Q41t49	ferroplasma
966	74	6.1	448	1	PEVR2_HUMAN	Q9nwf4	homo sapien
967	74	6.1	469	2	Q7Q579_ANOGA	Q7q579	anopheles g
968	74	6.1	474	2	Q3YRZ4_EHRCJ	Q3yrz4	ehrlichia c
969	74	6.1	485	2	Q7VSU8_BORPE	Q7vsu8	bordetella
970	74	6.1	485	2	Q7WF39_BORBR	Q7wf39	bordetella
971	74	6.1	501	2	Q6GIR4_STAAR	Q6gir4	staphylococ
972	74	6.1	505	2	Q82SC4_NITEU	Q82sc4	nitrosomona
973	74	6.1	509	2	Q4B4X2_9BURK	Q4b4x2	polaromonas
974	74	6.1	519	2	Q4JBN0_SULAC	Q4jbn0	sulfolobus
975	74	6.1	528	2	Q9B981_9HYME	Q9b981	blastophaga
976	74	6.1	545	2	Q5Q1C0_9CORO	Q5q1c0	infectious
977	74	6.1	546	2	Q2WBX5_PLADU	Q2wbx5	platynereis
978	74	6.1	555	2	Q9M171_ARATH	Q9m171	arabidopsis
979	74	6.1	579	2	Q4PGT4_USTMA	Q4pgt4	ustilago ma
980	74	6.1	581	2	Q4HZA7_GIBZE	Q4hza7	gibberella

981	74	6.1	591	2	Q5BN32_CANAL	Q5bn32	candida alb
982	74	6.1	602	2	Q6C4W0_YARLI	Q6c4w0	yarrowia li
983	74	6.1	687	2	Q8W3M2_CITUN	Q8w3m2	citrus unsh
984	74	6.1	713	2	Q6CPC7_KLULA	Q6cpc7	kluyveromyc
985	74	6.1	716	2	Q3P5I8_9GAMM	Q3p5i8	shewanella
986	74	6.1	756	2	Q7M762_MOUSE	Q7m762	mus musculu
987	74	6.1	768	2	Q33H50_METHU	Q33h50	methanospir
988	74	6.1	826	2	Q7TSL4_RAT	Q7tsl4	rattus norv
989	74	6.1	857	2	Q91XN5_RAT	Q91xn5	rattus norv
990	74	6.1	1873	2	Q83044_9CLOS	Q83044	lettuce inf
991	74	6.1	2022	2	Q51FJ8_ENTHI	Q51fj8	entamoeba h
992	74	6.1	2113	2	Q46BK6_METBA	Q46bk6	methanosarc
993	73.5	6.0	80	2	Q4ZUS1_PSEU2	Q4zus1	pseudomonas
994	73.5	6.0	126	2	Q4I7X6_GIBZE	Q4i7x6	gibberella
995	73.5	6.0	140	2	Q9XMB1_9CUCU	Q9xmb1	palorus gen
996	73.5	6.0	142	2	Q8HIP6_9HYME	Q8hip6	compsomelis
997	73.5	6.0	142	2	Q8HKK7_9HYME	Q8hkk7	allodape sk
998	73.5	6.0	191	2	Q8ELD6_OCEIH	Q8eld6	oceanobacil
999	73.5	6.0	202	2	Q5I675_HHV8	Q5i675	human herpe
1000	73.5	6.0	243	2	Q8WEL5_9HYME	Q8wel5	pogonomyrme
1001	73.5	6.0	248	2	Q2XFI7_PSEPU	Q2xfi7	pseudomonas
1002	73.5	6.0	250	2	Q81WR6_BACAN	Q81wr6	bacillus an
1003	73.5	6.0	251	2	Q49N48_BEMTA	Q49n48	bemisia tab
1004	73.5	6.0	257	2	Q23189_CAEEL	Q23189	caenorhabdi
1005	73.5	6.0	261	1	CLD18_HUMAN	P56856	homo sapien
1006	73.5	6.0	280	2	Q300C7_STRSU	Q300c7	streptococc
1007	73.5	6.0	318	2	Q33A79_ORYSA	Q33a79	oryza sativ
1008	73.5	6.0	343	2	Q3YPE4_CALDR	Q3ype4	callisaurus
1009	73.5	6.0	344	2	Q676S8_9HYST	Q676s8	coetomys wh
1010	73.5	6.0	347	2	Q6YIV8_PHRHE	Q6yiv8	phrynosoma
1011	73.5	6.0	347	2	Q6YIV9_9SAUR	Q6yiv9	phrynosoma
1012	73.5	6.0	350	2	Q6BNJ6_DEBHA	Q6bnj6	debaryomyce
1013	73.5	6.0	353	2	Q9PT68_XENLA	Q9pt68	xenopus lae
1014	73.5	6.0	360	2	Q6BMS1_DEBHA	Q6bms1	debaryomyce
1015	73.5	6.0	373	2	Q8CU33_STAES	Q8cu33	staphylococ
1016	73.5	6.0	379	1	CYB_ASTPE	Q33818	asterina pe
1017	73.5	6.0	379	1	CYB_GLASA	O48372	glaucomys s
1018	73.5	6.0	379	1	CYB_TRASR	Q9t9b7	tragelaphus
1019	73.5	6.0	379	2	Q3HNI0_GULGU	Q3hni0	gulo gulo (
1020	73.5	6.0	379	2	O20613_9HYST	O20613	cryptomys c
1021	73.5	6.0	379	2	Q5NUR5_9SCIU	Q5nur5	petaurista
1022	73.5	6.0	379	2	Q6T8R1_SPEPA	Q6t8r1	spermophilu
1023	73.5	6.0	379	2	Q94WX4_9HYST	Q94wx4	ctenomys au
1024	73.5	6.0	379	2	Q9TF05_MARMO	Q9tf05	marmota mon
1025	73.5	6.0	379	2	Q9TF65_9SCIU	Q9tf65	spermophilu
1026	73.5	6.0	379	2	Q9TF67_9SCIU	Q9tf67	spermophilu
1027	73.5	6.0	379	2	Q9TH53_MARMO	Q9th53	marmota mon
1028	73.5	6.0	379	2	Q9TH55_MARMO	Q9th55	marmota mon
1029	73.5	6.0	387	2	Q9SIC2_ARATH	Q9sic2	arabidopsis
1030	73.5	6.0	428	2	Q83E21_COXBU	Q83e21	coxiella bu
1031	73.5	6.0	429	1	ARSB_STAAU	P30329	staphylococ
1032	73.5	6.0	429	2	Q9AC73_STAAN	Q9ac73	staphylococ
1033	73.5	6.0	431	2	Q4RTL1_TETNG	Q4rtl1	tetraodon n
1034	73.5	6.0	459	2	Q955S3_MICRF	Q955s3	microcebus
1035	73.5	6.0	463	2	Q4A008_STAS1	Q4a008	staphylococ
1036	73.5	6.0	463	2	Q6HNC2_BACHK	Q6hnc2	bacillus th
1037	73.5	6.0	477	2	Q7WCB2_BORPA	Q7wcb2	bordetella
1038	73.5	6.0	499	2	Q5RFW0_BRARE	Q5rfw0	brachydanio
1039	73.5	6.0	507	2	Q978U2_THEVO	Q978u2	thermoplasm
1040	73.5	6.0	508	2	Q2ULC3_ASPOR	Q2ulc3	aspergillus
1041	73.5	6.0	511	2	Q4Q5M9_LEIMA	Q4q5m9	leishmania
1042	73.5	6.0	515	2	Q512T5_ENTHI	Q512t5	entamoeba h
1043	73.5	6.0	522	2	Q2ZC00_9GAMM	Q2zc00	shewanella
1044	73.5	6.0	544	2	Q97M46_CLOAB	Q97m46	clostridium
1045	73.5	6.0	569	2	Q65ZH5_CAEEL	Q65zh5	caenorhabdi
1046	73.5	6.0	586	2	Q4KE19_PSEF5	Q4ke19	pseudomonas
1047	73.5	6.0	593	2	Q8W104_ARATH	Q8w104	arabidopsis
1048	73.5	6.0	640	2	Q2XDI9_PSEPU	Q2xdi9	pseudomonas
1049	73.5	6.0	640	2	Q48NU1_PSE14	Q48nu1	pseudomonas
1050	73.5	6.0	640	2	Q4ZMG1_PSEU2	Q4zmg1	pseudomonas
1051	73.5	6.0	640	2	Q88QU0_PSEPK	Q88qu0	pseudomonas
1052	73.5	6.0	644	1	C1QR1_MOUSE	O89103	mus musculu
1053	73.5	6.0	644	2	Q3U2X0_MOUSE	Q3u2x0	mus musculu
1054	73.5	6.0	654	2	Q8EUQ4_MYCPE	Q8euq4	mycoplasma
1055	73.5	6.0	720	2	Q6YXQ6_PHYPA	Q6yxq6	physcomitre
1056	73.5	6.0	756	2	O44417_CHIPA	O44417	chironomus
1057	73.5	6.0	756	2	O44418_CHIPA	O44418	chironomus
1058	73.5	6.0	808	2	Q54SC3_DICDI	Q54sc3	dictyosteli
1059	73.5	6.0	815	2	Q86AZ6_DICDI	Q86az6	dictyosteli
1060	73.5	6.0	858	2	Q3T2N9_9HIV1	Q3t2n9	human immun
1061	73.5	6.0	879	1	FPRP_RAT	Q62786	rattus norv
1062	73.5	6.0	970	2	Q86AL6_DICDI	Q86al6	dictyosteli
1063	73.5	6.0	1014	2	Q2XJI7_PSEPU	Q2xji7	pseudomonas
1064	73.5	6.0	1014	2	Q88PE4_PSEPK	Q88pe4	pseudomonas
1065	73.5	6.0	1034	2	Q379W4_RHOPA	Q379w4	rhodopseudo
1066	73.5	6.0	1061	2	Q92SH0_RHIME	Q92sh0	rhizobium m
1067	73.5	6.0	1071	2	Q3JA51_NITOC	Q3ja51	nitrosococc
1068	73.5	6.0	1253	2	Q6CUJ1_KLULA	Q6cuj1	kluyveromyc
1069	73.5	6.0	1342	2	Q2QS53_ORYSA	Q2qs53	oryza sativ
1070	73.5	6.0	1443	2	Q5A450_CANAL	Q5a450	candida alb
1071	73.5	6.0	1479	2	Q5CQB4_CRYPV	Q5cqb4	cryptospori
1072	73.5	6.0	1501	2	Q75JS9_DICDI	Q75js9	dictyosteli
1073	73.5	6.0	1540	2	Q559R8_DICDI	Q559r8	dictyosteli
1074	73.5	6.0	1543	1	MRP2_MOUSE	Q8vi47	mus musculu
1075	73.5	6.0	1543	2	Q8VI46_MOUSE	Q8vi46	mus musculu
1076	73.5	6.0	1605	2	Q8AYF1_XENLA	Q8ayf1	xenopus lae
1077	73.5	6.0	1761	2	Q6CTB0_KLULA	Q6ctb0	kluyveromyc
1078	73	6.0	140	2	Q85PI8_SHEEP	Q85pi8	ovis aries
1079	73	6.0	196	2	Q7VRH4_BLOFL	Q7vrh4	blochmannia
1080	73	6.0	207	2	Q5I635_HHV8	Q5i635	human herpe
1081	73	6.0	207	2	Q5I645_HHV8	Q5i645	human herpe
1082	73	6.0	207	2	Q5I650_HHV8	Q5i650	human herpe
1083	73	6.0	215	2	Q3ENR8_BACTI	Q3enr8	bacillus th
1084	73	6.0	215	2	Q4MMU0_BACCE	Q4mmu0	bacillus ce
1085	73	6.0	215	2	Q635I8_BACCZ	Q635i8	bacillus ce
1086	73	6.0	215	2	Q6HE74_BACHK	Q6he74	bacillus th
1087	73	6.0	215	2	Q818Z4_BACCR	Q818z4	bacillus ce
1088	73	6.0	215	2	Q81MD5_BACAN	Q81md5	bacillus an
1089	73	6.0	215	2	Q731K5_BACC1	Q731k5	bacillus ce
1090	73	6.0	256	1	YCA5_YEAST	P25587	saccharomyc
1091	73	6.0	268	2	Q43GL4_9CHLB	Q43gl4	chlorobium
1092	73	6.0	280	2	Q9K8S9_BACHD	Q9k8s9	bacillus ha
1093	73	6.0	289	1	OPSD_ABYKO	O42294	abyssocottu
1094	73	6.0	296	2	Q2T0B4_BURTH	Q2t0b4	burkholderi
1095	73	6.0	298	2	Q9A571_CAUCR	Q9a571	caulobacter
1096	73	6.0	300	2	O20849_DIPDO	O20849	dipsosaurus
1097	73	6.0	308	2	Q9PW10_CHICK	Q9pw10	gallus gall
1098	73	6.0	312	2	Q465P5_METBA	Q465p5	methanosarc
1099	73	6.0	312	2	Q8VFE2_MOUSE	Q8vfe2	mus musculu
1100	73	6.0	313	2	Q3AA06_CARHZ	Q3aa06	carboxydoth
1101	73	6.0	319	2	Q32R40_EPTBU	Q32r40	eptatretus
1102	73	6.0	321	2	Q3KUS9_SHEEP	Q3kus9	ovis aries
1103	73	6.0	321	2	Q3KUT5_SHEEP	Q3kut5	ovis aries
1104	73	6.0	321	2	Q3KUW7_SHEEP	Q3kuw7	ovis aries
1105	73	6.0	321	2	Q3KUW9_SHEEP	Q3kuw9	ovis aries
1106	73	6.0	321	2	Q3KUX5_SHEEP	Q3kux5	ovis aries
1107	73	6.0	321	2	Q3KUY2_SHEEP	Q3kuy2	ovis aries
1108	73	6.0	321	2	Q3KV46_SHEEP	Q3kv46	ovis aries
1109	73	6.0	321	2	Q3KV47_SHEEP	Q3kv47	ovis aries
1110	73	6.0	339	2	Q3G787_9DELT	Q3g787	pelobacter
1111	73	6.0	340	2	Q8HD58_9HYST	Q8hd58	kannabateom
1112	73	6.0	347	2	Q4RVS8_TETNG	Q4rvs8	tetraodon n
1113	73	6.0	352	2	O93887_CRYNE	O93887	cryptococcu
1114	73	6.0	352	2	Q6DY59_PSEAM	Q6dy59	pseudopleur
1115	73	6.0	354	2	Q2L675_9ECHI	Q2l675	acanthaster
1116	73	6.0	354	2	Q6LJK9_PHOPR	Q6ljk9	photobacter
1117	73	6.0	360	2	Q8HD59_9HYST	Q8hd59	kannabateom
1118	73	6.0	360	2	Q8HIC1_9SCIU	Q8hic1	callosciuru
1119	73	6.0	371	2	Q94Y45_TAMSO	Q94y45	tamias sono
1120	73	6.0	372	2	Q94Y75_TAMAM	Q94y75	tamias amoe
1121	73	6.0	373	2	Q94Y48_TAMSE	Q94y48	tamias sene
1122	73	6.0	376	2	Q94Y73_TAMAM	Q94y73	tamias amoe
1123	73	6.0	379	1	CYB_CEPMA	Q9b5r2	cephalophus
1124	73	6.0	379	1	CYB_CEPMO	Q9b5r3	cephalophus
1125	73	6.0	379	1	CYB_ERIEU	Q36368	erinaceus e
1126	73	6.0	379	1	CYB_OREOR	Q9t9a6	oreotragus

1127	73	6.0	379	1	CYB_SHEEP	P24959	ovis aries
1128	73	6.0	379	1	CYB_SPEAI	Q9tf14	spermophilu
1129	73	6.0	379	1	CYB_SPEAN	Q9tf89	spermophilu
1130	73	6.0	379	1	CYB_SPEBE	Q9t469	spermophilu
1131	73	6.0	379	1	CYB_TAMSE	Q94y47	tamias sene
1132	73	6.0	379	2	Q38R77_SHEEP	Q38r77	ovis aries
1133	73	6.0	379	2	Q38R78_SHEEP	Q38r78	ovis aries
1134	73	6.0	379	2	Q38R81_SHEEP	Q38r81	ovis aries
1135	73	6.0	379	2	Q38R83_SHEEP	Q38r83	ovis aries
1136	73	6.0	379	2	Q38R86_SHEEP	Q38r86	ovis aries
1137	73	6.0	379	2	Q3S263_BOVIN	Q3s263	bos taurus
1138	73	6.0	379	2	Q5MA65_SHEEP	Q5ma65	ovis aries
1139	73	6.0	379	2	Q6XBW5_9CARN	Q6xbw5	genetta joh
1140	73	6.0	379	2	Q70RT7_9CETA	Q70rt7	platanista
1141	73	6.0	379	2	Q71FJ2_CIVCI	Q71fj2	civettictis
1142	73	6.0	379	2	Q8HQF0_PLEAU	Q8hqf0	plecotus au
1143	73	6.0	379	2	Q9B5Q4_9CETA	Q9b5q4	cephalophus
1144	73	6.0	379	2	Q9B5Q5_9CETA	Q9b5q5	cephalophus
1145	73	6.0	379	2	Q9B5Q7_9CETA	Q9b5q7	cephalophus
1146	73	6.0	379	2	Q9B5S0_9CETA	Q9b5s0	cephalophus
1147	73	6.0	379	2	Q9MI63_9CETA	Q9mi63	platanista
1148	73	6.0	379	2	Q9TDQ9_MUNMU	Q9tdq9	muntiacus m
1149	73	6.0	379	2	Q9TGH3_TRASR	Q9tgh3	tragelaphus
1150	73	6.0	379	2	Q9XLE3_CEPMA	Q9xle3	cephalophus
1151	73	6.0	379	2	Q9XP69_9CETA	Q9xp69	cephalophus
1152	73	6.0	379	2	Q4W261_9CETA	Q4w261	ovis ammon
1153	73	6.0	379	2	Q4W263_9CETA	Q4w263	ovis ammon
1154	73	6.0	379	2	Q4W266_9CETA	Q4w266	ovis nivico
1155	73	6.0	379	2	O20549_9HYST	O20549	ctenomys ha
1156	73	6.0	379	2	Q5NUR6_9SCIU	Q5nur6	petaurista
1157	73	6.0	379	2	Q6XAG4_CAVPO	Q6xag4	cavia porce
1158	73	6.0	379	2	Q94PT4_TAMSI	Q94pt4	tamias sibi
1159	73	6.0	379	2	Q94Y74_TAMAM	Q94y74	tamias amoe
1160	73	6.0	379	2	Q9G3N7_9RODE	Q9g3n7	eospalax fo
1161	73	6.0	379	2	Q9TEF9_CAVPO	Q9tef9	cavia porce
1162	73	6.0	379	2	Q9TF08_SPELA	Q9tf08	spermophilu
1163	73	6.0	379	2	Q9TF13_SPEAI	Q9tf13	spermophilu
1164	73	6.0	379	2	Q9TF72_9SCIU	Q9tf72	spermophilu
1165	73	6.0	379	2	Q9TF87_SPEAN	Q9tf87	spermophilu
1166	73	6.0	380	1	CYB_SAITA	Q9t5n4	saiga tatar
1167	73	6.0	380	2	Q644A1_9SALA	Q644a1	bolitogloss
1168	73	6.0	380	2	Q674Z4_9TELE	Q674z4	papyrocranu
1169	73	6.0	380	2	Q7YE29_9LABR	Q7ye29	neopomacent
1170	73	6.0	380	2	Q7YHI9_9SMEG	Q7yhi9	goodea grac
1171	73	6.0	404	2	Q4T2B0_TETNG	Q4t2b0	tetraodon n
1172	73	6.0	412	1	AATC_MOUSE	P05201	mus musculu
1173	73	6.0	413	2	Q3UJH8_MOUSE	Q3ujh8	mus musculu
1174	73	6.0	421	2	Q3BDW9_ACTPL	Q3bdw9	actinobacil
1175	73	6.0	424	2	Q7P4Z0_FUSNV	Q7p4z0	fusobacteri
1176	73	6.0	440	2	Q56YB8_ARATH	Q56yb8	arabidopsis
1177	73	6.0	440	2	Q8RCP9_THETN	Q8rcp9	thermoanaer
1178	73	6.0	457	2	Q7RJ14_PLAYO	Q7rj14	plasmodium
1179	73	6.0	458	1	TCR_BACCE	P0a4k7	bacillus ce
1180	73	6.0	458	1	TCR_BACST	P07561	bacillus st
1181	73	6.0	458	1	TCR_BACSU	P0a4k8	bacillus su
1182	73	6.0	458	1	TCR_STRAG	P13924	streptococc
1183	73	6.0	458	1	TCR_STRPN	P0a4k6	streptococc
1184	73	6.0	458	2	Q3Y254_ENTFC	Q3y254	enterococcu
1185	73	6.0	458	2	Q53HX6_PASHA	Q53hx6	pasteurella
1186	73	6.0	458	2	Q79P53_BACCE	Q79p53	bacillus ce
1187	73	6.0	458	2	Q7B6N8_ENTFA	Q7b6n8	enterococcu
1188	73	6.0	458	2	Q79CL3_9ZZZZ	Q79cl3	plasmid pbc
1189	73	6.0	482	2	Q60QI9_CAEBR	Q60qi9	caenorhabdi
1190	73	6.0	484	2	Q7MBA4_PHOLL	Q7mba4	photorhabdu
1191	73	6.0	484	2	Q92PU8_RHIME	Q92pu8	rhizobium m
1192	73	6.0	489	2	Q316W8_DESDG	Q316w8	desulfovibr
1193	73	6.0	498	2	Q5PG84_SALPA	Q5pg84	salmonella
1194	73	6.0	498	2	Q8ZQ35_SALTY	Q8zq35	salmonella
1195	73	6.0	501	2	Q2YSK4_STAAB	Q2ysk4	staphylococ
1196	73	6.0	501	2	Q6GBA3_STAAS	Q6gba3	staphylococ
1197	73	6.0	501	2	Q7A1I0_STAAW	Q7a1i0	staphylococ
1198	73	6.0	501	2	Q7A6T5_STAAN	Q7a6t5	staphylococ
1199	73	6.0	501	2	Q99VP6_STAAM	Q99vp6	staphylococ
1200	73	6.0	501	2	Q5HHU5_STAAC	Q5hhu5	staphylococ
1201	73	6.0	514	1	G6PD_BOSIN	Q7ys37	bos indicus
1202	73	6.0	544	2	Q8JQ37_9CORO	Q8jq37	infectious
1203	73	6.0	582	2	O65670_ARATH	O65670	arabidopsis
1204	73	6.0	676	2	Q3K770_PSEPF	Q3k770	pseudomonas
1205	73	6.0	679	2	Q9LJY0_ARATH	Q9ljy0	arabidopsis
1206	73	6.0	703	2	Q59LI1_CANAL	Q59li1	candida alb
1207	73	6.0	707	1	CN101_HUMAN	Q9nx78	homo sapien
1208	73	6.0	713	2	Q33WR5_9GAMM	Q33wr5	shewanella
1209	73	6.0	718	1	SC5A3_CANFA	P31637	canis famil
1210	73	6.0	727	2	Q2S6T0_9GAMM	Q2s6t0	hahella che
1211	73	6.0	729	2	Q2U1S6_ASPOR	Q2u1s6	aspergillus
1212	73	6.0	852	2	Q8UT82_9HIV1	Q8ut82	human immun
1213	73	6.0	870	2	Q6E7I0_9HIV1	Q6e7i0	human immun
1214	73	6.0	879	2	Q8C6Q7_MOUSE	Q8c6q7	mus musculu
1215	73	6.0	1154	2	Q7XPW1_ORYSA	Q7xpw1	oryza sativ
1216	73	6.0	1207	2	Q4X1R2_ASPFU	Q4x1r2	aspergillus
1217	73	6.0	1224	1	BRWD2_HUMAN	Q9bzh6	homo sapien
1218	73	6.0	1243	2	Q9P2J6_HUMAN	Q9p2j6	homo sapien
1219	73	6.0	1291	1	CD45_MOUSE	P06800	mus musculu
1220	73	6.0	1295	2	Q3XSX3_9PROT	Q3xsx3	magnetococc
1221	73	6.0	1343	2	Q64730_MOUSE	Q64730	mus musculu
1222	73	6.0	1378	2	Q2QYQ5_ORYSA	Q2qyq5	oryza sativ
1223	73	6.0	2405	2	Q4UGK4_THEAN	Q4ugk4	theileria a
1224	73	6.0	2405	2	Q4UGK5_THEAN	Q4ugk5	theileria a
1225	73	6.0	2607	2	Q4JQF9_MAIZE	Q4jqf9	zea mays (m
1226	72.5	6.0	117	2	Q6UKG2_9BILA	Q6ukg2	phoronis ps
1227	72.5	6.0	144	2	Q951D9_9HYME	Q951d9	panteliella
1228	72.5	6.0	146	2	Q8LU08_MARAM	Q8lu08	martes amer
1229	72.5	6.0	146	2	Q8LU09_MARAM	Q8lu09	martes amer
1230	72.5	6.0	189	2	Q5NIA5_FRATT	Q5nia5	francisella
1231	72.5	6.0	191	2	Q4F9M2_9NEOP	Q4f9m2	hydropsyche
1232	72.5	6.0	194	2	Q5TSI0_ANOGA	Q5tsi0	anopheles g
1233	72.5	6.0	202	2	Q5I670_HHV8	Q5i670	human herpe
1234	72.5	6.0	208	2	Q4LRX4_9BURK	Q4lrx4	burkholderi
1235	72.5	6.0	215	1	Y457_ANASP	P0a3k0	anabaena sp
1236	72.5	6.0	215	1	Y457_ANAVA	P0a3k1	anabaena va
1237	72.5	6.0	254	2	Q8KU90_ENTFA	Q8ku90	enterococcu
1238	72.5	6.0	255	2	Q3M956_ANAVT	Q3m956	anabaena va
1239	72.5	6.0	263	2	Q2M4W4_9HYME	Q2m4w4	ceratosolen
1240	72.5	6.0	264	2	Q458C3_9BURK	Q458c3	burkholderi
1241	72.5	6.0	275	2	Q5HHG2_STAAC	Q5hhg2	staphylococ
1242	72.5	6.0	275	2	Q6GB03_STAAS	Q6gb03	staphylococ
1243	72.5	6.0	275	2	Q7A1D7_STAAW	Q7a1d7	staphylococ
1244	72.5	6.0	275	2	Q7A6L0_STAAN	Q7a6l0	staphylococ
1245	72.5	6.0	275	2	Q99VF4_STAAM	Q99vf4	staphylococ
1246	72.5	6.0	283	2	Q6G5H9_BARHE	Q6g5h9	bartonella
1247	72.5	6.0	288	2	Q6G0Y0_BARQU	Q6g0y0	bartonella
1248	72.5	6.0	290	1	YCF38_CYAPA	P48278	cyanophora
1249	72.5	6.0	297	2	Q9AIY4_CARRU	Q9aiy4	carsonella
1250	72.5	6.0	306	2	Q8FKK8_ECOL6	Q8fkk8	escherichia
1251	72.5	6.0	317	2	Q4APA5_9CHLB	Q4apa5	chlorobium
1252	72.5	6.0	320	2	Q8NH95_HUMAN	Q8nh95	homo sapien
1253	72.5	6.0	321	2	Q4SCG5_TETNG	Q4scg5	tetraodon n
1254	72.5	6.0	343	2	Q85C21_9SAUR	Q85c21	uma paraphy
1255	72.5	6.0	363	2	Q35NR4_9BRAD	Q35nr4	bradyrhizob
1256	72.5	6.0	379	2	O20615_9HYST	O20615	cryptomys h
1257	72.5	6.0	379	2	Q6T8R2_SPEPA	Q6t8r2	spermophilu
1258	72.5	6.0	379	2	Q9TF06_9SCIU	Q9tf06	spermophilu
1259	72.5	6.0	379	2	Q9TF22_SPETO	Q9tf22	spermophilu
1260	72.5	6.0	397	2	Q41536_WHEAT	Q41536	triticum ae
1261	72.5	6.0	413	2	Q573D3_9VIRU	Q573d3	acidianus f
1262	72.5	6.0	414	2	Q62YM2_BACLD	Q62ym2	bacillus li
1263	72.5	6.0	414	2	Q65N72_BACLD	Q65n72	bacillus li
1264	72.5	6.0	416	2	O24725_NOCSK	O24725	nocardioide
1265	72.5	6.0	437	2	Q3P209_9GAMM	Q3p209	shewanella
1266	72.5	6.0	453	2	Q84WQ0_ARATH	Q84wq0	arabidopsis
1267	72.5	6.0	456	2	Q3KHS0_PSEPF	Q3khs0	pseudomonas
1268	72.5	6.0	470	2	Q68EK2_BRARE	Q68ek2	brachydanio
1269	72.5	6.0	501	2	Q49VS4_STAS1	Q49vs4	staphylococ
1270	72.5	6.0	505	2	Q44KJ6_CHRSL	Q44kj6	chromohalob
1271	72.5	6.0	509	1	HKT9_ORYSA	Q8l4k5	oryza sativ
1272	72.5	6.0	511	2	Q5MG94_IPOBA	Q5mg94	ipomoea bat

1273	72.5	6.0	512	2	Q3ND44_9PROT	Q3nd44	nitrosomona
1274	72.5	6.0	523	2	Q4I045_GIBZE	Q4i045	gibberella
1275	72.5	6.0	566	2	Q2PTK8_LISMO	Q2ptk8	listeria mo
1276	72.5	6.0	571	2	Q33KR2_METHU	Q33kr2	methanospir
1277	72.5	6.0	575	2	Q62657_RAT	Q62657	rattus norv
1278	72.5	6.0	578	2	Q979U5_THEVO	Q979u5	thermoplasm
1279	72.5	6.0	580	2	Q54R76_DICDI	Q54r76	dictyosteli
1280	72.5	6.0	580	2	Q5N7A3_ORYSA	Q5n7a3	oryza sativ
1281	72.5	6.0	592	2	Q50YH7_ENTHI	Q50yh7	entamoeba h
1282	72.5	6.0	597	2	Q59LX0_CANAL	Q59lx0	candida alb
1283	72.5	6.0	606	2	Q9XXR3_CAEEL	Q9xxr3	caenorhabdi
1284	72.5	6.0	608	2	Q4E390_TRYCR	Q4e390	trypanosoma
1285	72.5	6.0	616	1	S6A20_RAT	Q64093	rattus norv
1286	72.5	6.0	619	2	Q62701_RAT	Q62701	rattus norv
1287	72.5	6.0	623	2	Q4HZD5_GIBZE	Q4hzd5	gibberella
1288	72.5	6.0	623	2	Q7S238_NEUCR	Q7s238	neurospora
1289	72.5	6.0	623	2	Q7MCW8_VIBVY	Q7mcw8	vibrio vuln
1290	72.5	6.0	640	2	Q88A50_PSESM	Q88a50	pseudomonas
1291	72.5	6.0	660	2	Q7V3L0_PROMP	Q7v3l0	prochloroco
1292	72.5	6.0	794	2	Q7R595_GIALA	Q7r595	giardia lam
1293	72.5	6.0	852	2	Q4JG89_9HIV1	Q4jg89	human immun
1294	72.5	6.0	860	2	Q2N0T4_9HIV1	Q2n0t4	human immun
1295	72.5	6.0	862	2	Q5G7C5_9HIV1	Q5g7c5	human immun
1296	72.5	6.0	904	2	O59666_SCHPO	O59666	schizosacch
1297	72.5	6.0	1022	2	Q2SJY0_9GAMM	Q2sjy0	hahella che
1298	72.5	6.0	1032	2	Q9CLS7_PASMU	Q9cls7	pasteurella
1299	72.5	6.0	1073	2	Q9W1T8_DROME	Q9w1t8	drosophila
1300	72.5	6.0	1243	2	Q93564_CAEEL	Q93564	caenorhabdi
1301	72.5	6.0	1357	2	Q5CGW7_CRYHO	Q5cgw7	cryptospori
1302	72.5	6.0	1359	2	Q5CQL4_CRYPV	Q5cql4	cryptospori
1303	72.5	6.0	1467	2	Q7RHL5_PLAYO	Q7rhl5	plasmodium
1304	72	5.9	128	2	O03245_9HYME	O03245	opius dissi
1305	72	5.9	128	2	P92861_9HYME	P92861	pauesia jun
1306	72	5.9	142	2	Q8HIR1_9HYME	Q8hir1	braunsapis
1307	72	5.9	144	2	Q8L8T4_ARATH	Q8l8t4	arabidopsis
1308	72	5.9	146	2	Q54S97_DICDI	Q54s97	dictyosteli
1309	72	5.9	220	2	Q6RBY2_MARMO	Q6rby2	marmota mon
1310	72	5.9	222	2	Q317B0_DESDG	Q317b0	desulfovibr
1311	72	5.9	226	2	Q59PT7_CANAL	Q59pt7	candida alb
1312	72	5.9	235	2	Q3RPH9_RALME	Q3rph9	ralstonia m
1313	72	5.9	253	2	Q8AWK7_9PERC	Q8awk7	trachinus d
1314	72	5.9	253	2	Q8AWN9_9PERC	Q8awn9	forsterygio
1315	72	5.9	262	2	Q7Y650_9CETA	Q7y650	platanista
1316	72	5.9	267	2	Q2MF79_BEMTA	Q2mf79	bemisia tab
1317	72	5.9	277	2	Q4ZWT2_PSEU2	Q4zwt2	pseudomonas
1318	72	5.9	288	2	Q3Y2D3_ENTFC	Q3y2d3	enterococcu
1319	72	5.9	289	1	OPSD_BATMU	O42300	batrachocot
1320	72	5.9	301	2	Q8JMA5_9NUCL	Q8jma5	mamestra co
1321	72	5.9	309	2	Q9V4C6_DROME	Q9v4c6	drosophila
1322	72	5.9	314	2	Q5LPL4_SILPO	Q5lpl4	silicibacte
1323	72	5.9	321	2	Q3KUW2_SHEEP	Q3kuw2	ovis aries
1324	72	5.9	325	2	Q51FF7_ENTHI	Q51ff7	entamoeba h
1325	72	5.9	328	2	Q8UV77_BRARE	Q8uv77	brachydanio
1326	72	5.9	330	2	Q85T13_9SAUR	Q85t13	anolis roqu
1327	72	5.9	330	2	Q85T23_9SAUR	Q85t23	anolis roqu
1328	72	5.9	330	2	Q85T28_9SAUR	Q85t28	anolis roqu
1329	72	5.9	344	1	ISIA_ANASP	Q8yq35	anabaena sp
1330	72	5.9	357	2	Q5LPP4_SILPO	Q5lpp4	silicibacte
1331	72	5.9	375	2	Q6LYB9_METMP	Q6lyb9	methanococc
1332	72	5.9	378	2	Q3ZEC7_PARHE	Q3zec7	paradoxurus
1333	72	5.9	378	2	Q5SLE2_THET8	Q5sle2	thermus the
1334	72	5.9	378	2	Q72H63_THET2	Q72h63	thermus the
1335	72	5.9	378	2	Q94Y42_TAMST	Q94y42	tamias stri
1336	72	5.9	379	1	CYB_AEPME	Q9t9a5	aepyceros m
1337	72	5.9	379	1	CYB_GAZGA	O48336	gazella gaz
1338	72	5.9	379	1	CYB_LUTLU	Q34900	lutra lutra
1339	72	5.9	379	1	CYB_MARFA	Q9teb4	martes flav
1340	72	5.9	379	1	CYB_MARFL	Q9xmc1	marmota fla
1341	72	5.9	379	1	CYB_MARZI	Q9teb5	martes zibe
1342	72	5.9	379	1	CYB_ORYLE	Q9t9a8	oryx leucor
1343	72	5.9	379	1	CYB_VIVIN	Q6xbw7	viverricula
1344	72	5.9	379	2	Q33949_BUBBU	Q33949	bubalus bub
1345	72	5.9	379	2	Q3MNI9_GENGE	Q3mni9	genetta gen
1346	72	5.9	379	2	Q3MNJ1_GENGE	Q3mnj1	genetta gen
1347	72	5.9	379	2	Q4KXM8_9CHIR	Q4kxm8	myotis aura
1348	72	5.9	379	2	Q5EG31_BOVIN	Q5eg31	bos taurus
1349	72	5.9	379	2	Q70RR1_PONBL	Q70rr1	pontoporia
1350	72	5.9	379	2	Q71FI1_GENGE	Q71fi1	genetta gen
1351	72	5.9	379	2	Q7YBY4_9CHIR	Q7yby4	myotis tric
1352	72	5.9	379	2	Q85PM8_PARHE	Q85pm8	paradoxurus
1353	72	5.9	379	2	Q8W8Q1_MARFO	Q8w8q1	martes foin
1354	72	5.9	379	2	Q9MNV1_MARMT	Q9mnv1	martes mart
1355	72	5.9	379	2	Q9MNV3_MARAM	Q9mnv3	martes amer
1356	72	5.9	379	2	Q9T4L9_MARZI	Q9t4l9	martes zibe
1357	72	5.9	379	2	Q9TEB6_MARZI	Q9teb6	martes zibe
1358	72	5.9	379	2	Q4W259_9CETA	Q4w259	ovis ammon
1359	72	5.9	379	2	Q4W265_9CETA	Q4w265	ovis ammon
1360	72	5.9	379	2	Q4W268_9CETA	Q4w268	ovis nivico
1361	72	5.9	379	2	Q4W269_9CETA	Q4w269	ovis nivico
1362	72	5.9	379	2	Q36096_9HYST	Q36096	trinomys pa
1363	72	5.9	379	2	Q5YKK0_CAVPO	Q5ykk0	cavia porce
1364	72	5.9	379	2	Q6XAG1_9HYST	Q6xag1	cavia tschu
1365	72	5.9	379	2	Q94Y41_TAMST	Q94y41	tamias stri
1366	72	5.9	379	2	Q9TF86_9SCIU	Q9tf86	spermophilu
1367	72	5.9	380	2	O03399_9RODE	O03399	acomys sp.
1368	72	5.9	380	2	Q4U6Q9_9SAUR	Q4u6q9	zonosaurus
1369	72	5.9	380	2	Q4U6R1_9SAUR	Q4u6r1	zonosaurus
1370	72	5.9	380	2	Q7YE28_9LABR	Q7ye28	neopomacent
1371	72	5.9	380	2	Q7YHG1_9SMEG	Q7yhg1	xenotoca va
1372	72	5.9	380	2	Q7YHJ0_9SMEG	Q7yhj0	goodea grac
1373	72	5.9	385	2	Q6MSW4_MYCMS	Q6msw4	mycoplasma
1374	72	5.9	415	2	Q6UVS0_PSEAK	Q6uvs0	pseudendocl
1375	72	5.9	417	2	Q7YH69_9CEST	Q7yh69	taenia asia
1376	72	5.9	418	2	Q33US0_9GAMM	Q33us0	shewanella
1377	72	5.9	420	2	Q5NHP3_FRATT	Q5nhp3	francisella
1378	72	5.9	422	2	Q736J7_BACC1	Q736j7	bacillus ce
1379	72	5.9	441	1	PGAC_ECO57	Q8xar5	escherichia
1380	72	5.9	441	1	PGAC_ECOLI	P75905	escherichia
1381	72	5.9	441	2	Q8FJ31_ECOL6	Q8fj31	escherichia
1382	72	5.9	443	2	Q7V6J9_PROMM	Q7v6j9	prochloroco
1383	72	5.9	447	2	Q92YL5_RHIME	Q92yl5	rhizobium m
1384	72	5.9	449	2	Q6L279_PICTO	Q6l279	picrophilus
1385	72	5.9	455	2	O45936_CAEEL	O45936	caenorhabdi
1386	72	5.9	458	2	Q8RLD5_ENTFC	Q8rld5	enterococcu
1387	72	5.9	459	2	Q94Q77_MIRCO	Q94q77	mirza coque
1388	72	5.9	459	2	Q94YD5_SORUN	Q94yd5	sorex ungui
1389	72	5.9	475	1	AMO1_SCHPO	O74315	schizosacch
1390	72	5.9	483	2	Q9G8V8_9CRYP	Q9g8v8	rhodomonas
1391	72	5.9	488	2	Q4NC02_9MICC	Q4nc02	arthrobacte
1392	72	5.9	491	2	Q2QYN4_ORYSA	Q2qyn4	oryza sativ
1393	72	5.9	499	2	Q2QYN3_ORYSA	Q2qyn3	oryza sativ
1394	72	5.9	534	2	Q6Y411_9ECHI	Q6y411	ophiura lut
1395	72	5.9	555	2	Q5LHM4_BACFN	Q5lhm4	bacteroides
1396	72	5.9	555	2	Q64YJ9_BACFR	Q64yj9	bacteroides
1397	72	5.9	557	2	Q54IT7_DICDI	Q54it7	dictyosteli
1398	72	5.9	579	2	O57322_AMBTI	O57322	ambystoma t
1399	72	5.9	581	1	PRLR_CEREL	Q28235	cervus elap
1400	72	5.9	591	2	Q5A1D7_CANAL	Q5a1d7	candida alb
1401	72	5.9	601	2	Q644F5_9SALA	Q644f5	hemidactyli
1402	72	5.9	602	2	Q5QS43_PSEPE	Q5qs43	pseudocheir
1403	72	5.9	607	2	Q8LPM4_CITSI	Q8lpm4	citrus sine
1404	72	5.9	614	1	SC5A7_DROME	Q9ve46	drosophila
1405	72	5.9	617	2	O65272_ARATH	O65272	arabidopsis
1406	72	5.9	663	2	Q4SP61_TETNG	Q4sp61	tetraodon n
1407	72	5.9	729	2	Q59K69_CANAL	Q59k69	candida alb
1408	72	5.9	752	2	Q3SFU4_THIDA	Q3sfu4	thiobacillu
1409	72	5.9	786	2	Q9XF71_TOBAC	Q9xf71	nicotiana t
1410	72	5.9	854	2	O93244_ONCMY	O93244	oncorhynchu
1411	72	5.9	904	2	Q6NBZ4_RHOPA	Q6nbz4	rhodopseudo
1412	72	5.9	913	2	Q6BIQ9_DEBHA	Q6biq9	debaryomyce
1413	72	5.9	916	2	Q9VT80_DROME	Q9vt80	drosophila
1414	72	5.9	940	2	Q5YEV6_OREMO	Q5yev6	oreochromis
1415	72	5.9	982	1	YS96_CAEEL	Q09965	caenorhabdi
1416	72	5.9	1003	2	Q4UIV2_THEAN	Q4uiv2	theileria a
1417	72	5.9	1022	2	Q83DH8_COXBU	Q83dh8	coxiella bu
1418	72	5.9	1079	2	Q4P0D0_USTMA	Q4p0d0	ustilago ma

1419	72	5.9	1079	2	Q703G5_USTMA	Q703g5 ustilago ma
1420	72	5.9	1178	2	Q9NF95_LEIMA	Q9nf95 leishmania
1421	72	5.9	1253	2	Q19523_CAEEL	Q19523 caenorhabdi
1422	72	5.9	1290	2	Q4RGQ4_TETNG	Q4rgq4 tetraodon n
1423	72	5.9	1449	2	Q8T675_DICDI	Q8t675 dictyosteli
1424	72	5.9	1583	1	MIS4_SCHPO	Q09725 schizosacch
1425	71.5	5.9	118	1	B2MG_ORNAN	Q864t7 ornithorhyn
1426	71.5	5.9	128	2	O79128_9HYME	O79128 braunsapis
1427	71.5	5.9	131	2	Q61QC1_CAEBR	Q61qc1 caenorhabdi
1428	71.5	5.9	142	2	Q8HIQ9_9HYME	Q8hiq9 brevineura
1429	71.5	5.9	146	2	Q8LXC0_MARAM	Q8lxc0 martes amer
1430	71.5	5.9	146	2	Q8LXB9_MARAM	Q8lxb9 martes amer
1431	71.5	5.9	152	2	Q6MZ91_MYCUL	Q6mz91 mycobacteri
1432	71.5	5.9	166	2	Q37ML5_RHOPA	Q37ml5 rhodopseudo
1433	71.5	5.9	168	2	Q2SD61_9GAMM	Q2sd61 hahella che
1434	71.5	5.9	183	2	Q9VHG9_DROME	Q9vhg9 drosophila
1435	71.5	5.9	202	2	Q6ZV02_HUMAN	Q6zv02 homo sapien
1436	71.5	5.9	206	2	Q3DJU0_STRAG	Q3dju0 streptococc
1437	71.5	5.9	230	2	Q3XTX4_9PROT	Q3xtx4 magnetococc
1438	71.5	5.9	233	2	Q4VH01_9RODE	Q4vh01 heteromys d
1439	71.5	5.9	235	2	Q6DR08_ARATH	Q6dr08 arabidopsis
1440	71.5	5.9	235	2	Q6E283_ARATH	Q6e283 arabidopsis
1441	71.5	5.9	268	2	Q6XFA2_MALMO	Q6xfa2 malpolon mo
1442	71.5	5.9	299	2	Q6BQG8_DEBHA	Q6bqg8 debaryomyce
1443	71.5	5.9	307	2	Q7RP65_PLAYO	Q7rp65 plasmodium
1444	71.5	5.9	314	2	Q8VFZ5_MOUSE	Q8vfz5 mus musculu
1445	71.5	5.9	324	2	Q4RXK4_TETNG	Q4rxk4 tetraodon n
1446	71.5	5.9	332	2	Q93ZH9_ARATH	Q93zh9 arabidopsis
1447	71.5	5.9	336	2	Q46WP4_RALEJ	Q46wp4 ralstonia e
1448	71.5	5.9	343	2	Q54EK7_DICDI	Q54ek7 dictyosteli
1449	71.5	5.9	343	2	Q85AL2_UMASC	Q85al2 uma scopari
1450	71.5	5.9	343	2	Q85AT3_UMASC	Q85at3 uma scopari
1451	71.5	5.9	343	2	Q85KN7_9SAUR	Q85kn7 uma paraphy
1452	71.5	5.9	343	2	Q85KP3_9SAUR	Q85kp3 uma exsul.
1453	71.5	5.9	343	2	Q9B4H4_UMASC	Q9b4h4 uma scopari
1454	71.5	5.9	343	2	Q9B4H6_UMASC	Q9b4h6 uma scopari
1455	71.5	5.9	347	2	Q676M3_9HYST	Q676m3 bathyergus
1456	71.5	5.9	347	2	Q3YPF2_CALDR	Q3ypf2 callisaurus
1457	71.5	5.9	348	2	Q676L8_9HYST	Q676l8 bathyergus
1458	71.5	5.9	349	2	Q899J8_CLOTE	Q899j8 clostridium
1459	71.5	5.9	349	2	Q676M6_9HYST	Q676m6 bathyergus
1460	71.5	5.9	353	2	Q7Z1Q4_CAEEL	Q7z1q4 caenorhabdi
1461	71.5	5.9	353	2	Q9F0B7_LACDE	Q9f0b7 lactobacill
1462	71.5	5.9	354	1	OPSD_ZEUFA	O42604 zeus faber
1463	71.5	5.9	356	2	Q9GCR8_9SCIU	Q9gcr8 belomys pea
1464	71.5	5.9	361	2	Q676M1_9HYST	Q676m1 bathyergus
1465	71.5	5.9	363	1	MRAY_TREPA	O83365 treponema p
1466	71.5	5.9	366	1	Y1196_METJA	Q58596 methanococc
1467	71.5	5.9	378	2	Q94X35_9LABR	Q94x35 cymatogaste
1468	71.5	5.9	379	1	CYB_LAMPA	Q34916 lama guanic
1469	71.5	5.9	379	2	Q5GH07_LAMVI	Q5gh07 vicugna vic
1470	71.5	5.9	379	2	Q5GH08_LAMPA	Q5gh08 lama glama
1471	71.5	5.9	379	2	Q676M4_9HYST	Q676m4 bathyergus
1472	71.5	5.9	379	2	Q6T8R5_SPEPA	Q6t8r5 spermophilu
1473	71.5	5.9	379	2	Q6T8R6_SPEPA	Q6t8r6 spermophilu
1474	71.5	5.9	379	2	Q94WW6_9HYST	Q94ww6 ctenomys la
1475	71.5	5.9	379	2	Q94WW7_9HYST	Q94ww7 ctenomys la
1476	71.5	5.9	379	2	Q9TF62_SPETO	Q9tf62 spermophilu
1477	71.5	5.9	379	2	Q9TF68_9SCIU	Q9tf68 spermophilu
1478	71.5	5.9	379	2	Q7YE02_9LABR	Q7ye02 stegastes p
1479	71.5	5.9	381	1	CYB_SMIMA	O20433 sminthopsis
1480	71.5	5.9	381	2	Q9XP74_SMIVI	Q9xp74 sminthopsis
1481	71.5	5.9	385	2	Q3XS19_9PROT	Q3xs19 magnetococc
1482	71.5	5.9	386	2	Q3V7P4_YERPS	Q3v7p4 yersinia ps
1483	71.5	5.9	386	2	Q8ZFC4_YERPE	Q8zfc4 yersinia pe
1484	71.5	5.9	398	1	TRFR_HUMAN	P34981 homo sapien
1485	71.5	5.9	398	2	Q2M339_HUMAN	Q2m339 homo sapien
1486	71.5	5.9	407	2	Q2NSN1_SODGL	Q2nsn1 sodalis glo
1487	71.5	5.9	412	2	Q624D3_CAEBR	Q624d3 caenorhabdi
1488	71.5	5.9	424	2	Q7VMU9_HAEDU	Q7vmu9 haemophilus
1489	71.5	5.9	429	2	Q6GIZ4_STAAR	Q6giz4 staphylococ
1490	71.5	5.9	439	2	Q5FYG3_HOMCO	Q5fyg3 homalodisca
1491	71.5	5.9	444	2	O34502_BACSU	O34502 bacillus su
1492	71.5	5.9	445	2	Q8CNG8_STAES	Q8cng8 staphylococ
1493	71.5	5.9	445	2	Q5HM61_STAEQ	Q5hm61 staphylococ
1494	71.5	5.9	447	2	Q2YYH6_STAAB	Q2yyh6 staphylococ
1495	71.5	5.9	449	2	Q7W0C7_BORPE	Q7w0c7 bordetella
1496	71.5	5.9	454	2	Q2NG40_9EURY	Q2ng40 methanospha
1497	71.5	5.9	455	2	Q33F71_METHU	Q33f71 methanospir
1498	71.5	5.9	495	2	O63853_SARGL	O63853 sarcophyton
1499	71.5	5.9	509	1	HKT3_ORYSA	Q81481 oryza sativ
1500	71.5	5.9	524	2	Q3NWI0_9GAMM	Q3nwi0 shewanella

ALIGNMENTS

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RESULT 1
Q6UWS1_HUMAN
ID   Q6UWS1_HUMAN   PRELIMINARY;   PRT;   229 AA.
AC   Q6UWS1;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   TCCE518.
GN   ORFNames=UNQ518;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA   Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA   Wood W.I., Godowski P.J., Gray A.M.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   ---------------------------------------------------------------------
DR   EMBL; AY358671; AAQ89034.1; -; mRNA.
DR   Ensembl; ENSG00000168955; Homo sapiens.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR008661; L6_membrane.
DR   Pfam; PF05805; L6_membrane; 1.
SQ   SEQUENCE   229 AA;  25109 MW;  1718ED342C58C903 CRC64;

  Query Match           100.0%;  Score 1215;  DB 2;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-99;
  Matches  229;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGL 60
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Db          1 MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGL 60

Qy         61 MAIPATTMSLTARKRACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPS 120
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Qy        121 NSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSE 180

Qy        181 ENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV 229
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Db        181 ENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV 229


RESULT 2
Q5U609_HUMAN
ID   Q5U609_HUMAN   PRELIMINARY;   PRT;   229 AA.
AC   Q5U609;
DT   07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT   07-DEC-2004, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   TM4SF20 protein.
GN   Name=TM4SF20;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Colon;
RG   NIH MGC Project;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   ---------------------------------------------------------------------
DR   EMBL; BC035754; AAH35754.1; -; mRNA.
DR   Ensembl; ENSG00000168955; Homo sapiens.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR008661; L6_membrane.
DR   Pfam; PF05805; L6_membrane; 1.
SQ   SEQUENCE   229 AA;  25137 MW;  B750504AFD7C247D CRC64;

  Query Match             99.7%;  Score 1211;  DB 2;  Length 229;
  Best Local Similarity   99.6%;  Pred. No. 6.5e-99;
  Matches  228;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGL 60
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          1 MTCCEGWTSCNGFSLLVLLLLGVVLNVIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGL 60

Qy         61 MAIPATTMSLTARKRACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MAIPATTMSLTARKRACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPS 120

Qy        121 NSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSE 180


Qy        181 ENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV 229
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV 229


RESULT 3
Q53R12_HUMAN
ID   Q53R12_HUMAN   PRELIMINARY;   PRT;   229 AA.
AC   Q53R12;
DT   24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   24-MAY-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Hypothetical protein FLJ22800.
GN   Name=FLJ22800;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Nguyen C., Harris A., Meyer R.;
RT   "The sequence of Homo sapiens BAC clone RP11-563C6.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Waterston R.H.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Waterston R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RA   Wilson R.K.;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AC097662; AAY24253.1; -; Genomic_DNA.
DR   Ensembl; ENSG00000168955; Homo sapiens.
DR   GO; GO:0016021; C:integral to membrane; IEA.
KW   Hypothetical protein.
SQ   SEQUENCE   229 AA;  25075 MW;  1718E0594997A1A1 CRC64;

  Query Match             99.5%;  Score 1209;  DB 2;  Length 229;
  Best Local Similarity   99.6%;  Pred. No. 9.7e-99;
  Matches  228;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGL 60

Qy         61 MAIPATTMSLTARKRACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPS 120
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         61 MAIPATTMSLTARKRACCNNRTGMFLSSLFSVITVIGALYCMLISIQALLKGPLMCNSPS 120

Qy        121 NSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSE 180

Qy        181 ENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV 229
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Db        181 ENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV 229


RESULT 4
Q9H5X9_HUMAN
ID   Q9H5X9_HUMAN   PRELIMINARY;   PRT;   229 AA.
AC   Q9H5X9;
DT   01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2001, sequence version 1.
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DT   07-FEB-2006, entry version 11.
DE   Hypothetical protein FLJ22800.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Ileal mucosa;
RA   Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
RA   Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
RA   Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,
RA   Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
RA   Isogai T., Sugano S.;
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AK026453; BAB15488.1; -; mRNA.
DR   Ensembl; ENSG00000168955; Homo sapiens.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR008661; L6_membrane.
DR   Pfam; PF05805; L6_membrane; 1.
SQ   SEQUENCE   229 AA;  25103 MW;  B7505D2798B34CDF CRC64;

  Query Match             99.2%;  Score 1205;  DB 2;  Length 229;
  Best Local Similarity   99.1%;  Pred. No. 2.2e-98;
  Matches  227;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGL 60
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 MTCCEGWTSCNGFSLLVLLLLGVVLNVIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGL 60

Qy         61 MAIPATTMSLTARKRACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPS 120
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db         61 MAIPATTMSLTARKRACCNNRTGMFLSSLFSVITVIGALYCMLISIQALLKGPLMCNSPS 120

Qy        121 NSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSE 180

Qy        181 ENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV 229
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV 229


RESULT 5
Q3T0Z4_BOVIN
ID   Q3T0Z4_BOVIN   PRELIMINARY;   PRT;   230 AA.
AC   Q3T0Z4;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-MAR-2006, entry version 4.
DE   Hypothetical protein.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Crossbred x Angus; TISSUE=Ileum;
RA   Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,
RA   Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C.,
RA   Wagner L., Bala M., Barbazuk S., Barber S., Babakaiff R., Beland J.,
RA   Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,
RA   Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D.,
RA   Siddiqui A., Holt R., Jones S.J., Marra M.A.;
RL   Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; BC102196; AAI02197.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR008661; L6_membrane.
DR   Pfam; PF05805; L6_membrane; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   230 AA;  25214 MW;  FF48895B0B2F6932 CRC64;

  Query Match             76.7%;  Score 931.5;  DB 2;  Length 230;
  Best Local Similarity   74.3%;  Pred. No. 3.6e-74;
  Matches  171;  Conservative   27;  Mismatches   31;  Indels    1;  Gaps    1;

Qy          1 MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGL 60
              |||||||||||||||||||||||| |||||||:: |:|||| :||||||||||||||||:
Db          1 MTCCEGWTSCNGFSLLVLLLLGVTLNAIPLILNFVDEDQFFENPISCFEWWFPGIIGAGV 60

Qy         61 MAIPATTMSLTARKRACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPS 120
              |||||||||| |||||||||:|||||||  : |||||| ||:|:||||| :|||:||| |
Db         61 MAIPATTMSLAARKRACCNNKTGMFLSSLLNAITVIGAAYCLLVSIQALAEGPLICNSQS 120

Qy        121 NSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSE 180
              |: ::|||||||::  : |||:||||| ||| | |  | |:  :| |: ||  : ||:|
Db        121 NTTSSCEFSLKNLTANYKESFDLQWFFEDSCVPHTDSNNPSITNTTANNWRVYNLHFNSI 180

Qy        181 ENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLC-GVSKRRSQIV 229
              ||:||:|||||||||||||:|||||||:||| |||| |||  |||||
Db        181 ENQHRIIHFSVFLGLLLVGILEILFGLSQIIIGFFGCLCGGVSNGRSQIV 230


RESULT 6
Q9CQY8_MOUSE
ID   Q9CQY8_MOUSE   PRELIMINARY;   PRT;   226 AA.
AC   Q9CQY8;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 20.
DE   11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length
DE   enriched library, clone:5033426G15 product:similar to CDNA: FLJ22800
DE   FIS, CLONE KAIA2630 (10 day old male pancreas cDNA, RIKEN full-length
DE   enriched library, clone:1810018L02 product:similar to CDNA: FLJ22800
DE   FIS, CLONE KAIA2630).
GN   Name=Tm4sf20;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
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RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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CC ---
DR EMBL; AK017195; BAB30629.1; -; mRNA.
DR EMBL; AK007532; BAB25093.1; -; mRNA.
DR Ensembl; ENSMUSG00000026149; Mus musculus.
DR MGI; MGI:1913511; Tm4sf20.
DR GO; GO:0005615; C:extracellular space; RCA.
DR GO; GO:0016021; C:integral to membrane; RCA.
DR InterPro; IPR008661; L6_membrane.
DR Pfam; PF05805; L6_membrane; 1.
SQ SEQUENCE 226 AA; 24760 MW; 3FE6BA1C6A335EAD CRC64;

Query Match 76.1%; Score 924.5; DB 2; Length 226;
Best Local Similarity 74.2%; Pred. No. 1.5e-73;
Matches 170; Conservative 27; Mismatches 29; Indels 3; Gaps 2;

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Qy          1 MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGL 60
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Qy         61 MAIPATTMSLTARKRACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPS 120
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Qy        181 ENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV 229
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RESULT 7
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ID   Q9D3Q0_MOUSE   PRELIMINARY;   PRT;   226 AA.
AC   Q9D3Q0;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 21.
DE   11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length
DE   enriched library, clone:5033430P14 product:similar to CDNA: FLJ22800
DE   FIS, CLONE KAIA2630.
GN   Name=Tm4sf20; Synonyms=1810018L02Rik;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
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RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
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RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
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RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
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RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
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RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
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RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
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RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AK017209; BAB30635.1; -; mRNA.
DR   Ensembl; ENSMUSG00000026149; Mus musculus.
DR   MGI; MGI:1913511; 1810018L02Rik.
DR   MGI; MGI:1913511; Tm4sf20.
DR   GO; GO:0005615; C:extracellular space; RCA.
DR   GO; GO:0016021; C:integral to membrane; RCA.
DR   InterPro; IPR008661; L6_membrane.
DR   Pfam; PF05805; L6_membrane; 1.
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  Query Match             75.6%;  Score 918.5;  DB 2;  Length 226;
  Best Local Similarity   73.8%;  Pred. No. 5e-73;
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Qy         61 MAIPATTMSLTARKRACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPS 120
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RESULT 8
Q9D3R0_MOUSE
ID   Q9D3R0_MOUSE   PRELIMINARY;   PRT;   226 AA.
AC   Q9D3R0;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 21.
DE   11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length
DE   enriched library, clone:5033405M13 product:similar to CDNA: FLJ22800
DE   FIS, CLONE KAIA2630.
GN   Name=Tm4sf20; Synonyms=1810018L02Rik;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
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RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
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RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
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RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AK017154; BAB30618.1; -; mRNA.
DR   Ensembl; ENSMUSG00000026149; Mus musculus.
DR   MGI; MGI:1913511; 1810018L02Rik.
DR   MGI; MGI:1913511; Tm4sf20.
DR   GO; GO:0005615; C:extracellular space; RCA.
DR   GO; GO:0016021; C:integral to membrane; RCA.
DR   InterPro; IPR008661; L6_membrane.
DR   Pfam; PF05805; L6_membrane; 1.
SQ   SEQUENCE   226 AA;  24714 MW;  8BE6BE5C2D1EDDC0 CRC64;

  Query Match             75.1%;  Score 912.5;  DB 2;  Length 226;
  Best Local Similarity   73.8%;  Pred. No. 1.7e-72;
  Matches  169;  Conservative   27;  Mismatches   30;  Indels    3;  Gaps    2;

Qy          1 MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGL 60
              |||||||||||||||:|:|||||:| ||| :|||| |  |||||||:|||||||||||
Db          1 MTCCEGWTSCNGFSLLILILLGVVINCIPLGISLVEADSTSQNPISCYEWWFPGIIGAGL 60

Qy         61 MAIPATTMSLTARKRACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPS 120
              |||||||||| |||||| ||:||||||| |||||:||:||||:|:||||:|||:||: :
Db         61 MAIPATTMSLAARKRACGNNKTGMFLSSLFSVITVVGAVYCMLVSLQALLEGPLICNTQA 120

Qy        121 NSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSE 180
              ||   |||||||:|   |||||| |||| :|  || |  || |: | | |:     : :||
Db        121 NSTVTCEFSLKNLSKFDPESFNLLWFFNGTCVSPTDFKNPTINN-MVSNWKIP--NSNSE 177

Qy        181 ENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV 229
              |::||: ||||| |||||||:|||||||:||||||||||:||||||
Db        178 EDRHRIFHFSVFMSLLLVGILELLFGLSQILIGFLGCLCGVSQRRSQIV 226


RESULT 9
Q4KL96_XENLA
ID   Q4KL96_XENLA   PRELIMINARY;   PRT;   242 AA.
AC   Q4KL96;
DT   02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT   02-AUG-2005, sequence version 1.
DT   07-FEB-2006, entry version 2.
DE   Hypothetical protein (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
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RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; BC099340; AAH99340.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   242 AA;  25805 MW;  286B614727816l6E CRC64;

  Query Match             43.5%;  Score 528;  DB 2;  Length 242;
  Best Local Similarity   42.5%;  Pred. No. 2e-38;
  Matches   97;  Conservative   46;  Mismatches   77;  Indels    8;  Gaps    3;

Qy          1 MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGL 60
              ||| |||:|||||  ||:| || :  |  |||   ||: :   :||||:||| ||::| ||
Db         15 MTCTEGWSSCNGFFLLILSLLAIAFNLTPLIADYVEDGRLFVSPISCYEWWLPGLVGGGL 74

Qy         61 MAIPATTMSLTARKRACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPS 120
              : :|| :|:| |||:  ||:| ||  |:  ||:::|||:|| :||: |: ||||:| : |
Db         75 LVLPAVSMTLAARKKGSCNSRGGMLASALLSVVSIIGAVYCTIISLFAVAKGPLICETGS 134

Qy        121 NSNANCEFSLKNIS--DIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASG-WRASSFHF 177
              |  ::|:::| |:|        |:| |  | :| |     :     | | |     :
Db        135 NELSSCDYTLANLSSNSFKELQFDLAWLRNTTCIP-----RVDPAMTAAQGIIHQRNLSI 189

Qy        178 DSEENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRR 225
              :  |   ::|| :||: | ::|::|||  :||   |  | :|| ||||
Db        190 ELNEETQKIIHITVFVALAIIGLVEVLVAVSQAAAGIFGFICGTSKRR 237


RESULT 10
Q4KLD0_XENLA
ID   Q4KLD0_XENLA   PRELIMINARY;   PRT;   205 AA.
AC   Q4KLD0;
DT   02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT   02-AUG-2005, sequence version 1.
DT   07-FEB-2006, entry version 2.
DE   Hypothetical protein (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; BC099286; AAH99286.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR008661; L6_membrane.
DR   PANTHER; PTHR14198; L6_membrane; 1.
DR   Pfam; PF05805; L6_membrane; 1.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   205 AA;  21982 MW;  7149A36D0D1F5B0C CRC64;

  Query Match             17.9%;  Score 217.5;  DB 2;  Length 205;
  Best Local Similarity   27.7%;  Pred. No. 5.2e-11;
  Matches   64;  Conservative   46;  Mismatches   84;  Indels   37;  Gaps    9;

Qy          2 TCCEGWTSCN---GFSLLVLLLLGVVLNAIPLIVSL-VEEDQFSQNPISCFEWWFPGIIG 57
              | | |   |:   | ||    :: :: | : |    ||  | : : ::    :  ||||
Db          5 TMCTG--KCSKFIGISLFPFSIICIIANILLLFPGFGVEAIQDAGSRMTPEVLYLGGIIG 62

Qy         58 AG-LMAIPATTMSLTARKRACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMC 116
                | |: |||  :  | ::: ||||| |||||  |: | ::||:| : :|   :: ||:
Db         63 GGFLVLIPAIHILATGQRKNCCNNRCGMFLSIIFAAIGLVGAVYALTVSAFGMVYGPV-- 120

Qy        117 NSPSNSNANCEFSLKNISDIHPESF--NLQWFFNDSCAPPTGFNKPTSNDTMASGWRASS 174
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Db        121 ---------CEFRNSTGALVWGQIFKDNIKNFSNESYL----FNKDL--------WQLC- 158

Qy        175 FHFDSEENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRR 225
                  : :   : : |:|  :|    :|::  : |:| |  |||||  :::
Db        159 ----EKPDNVAVFNISLFSIVLTASAIEIILCVVQVVNGLAGCLCGTCQKK 205


RESULT 11
Q66KQ0_XENLA
ID   Q66KQ0_XENLA   PRELIMINARY;   PRT;   203 AA.
AC   Q66KQ0;
DT   11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2004, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   MGC85546 protein.
GN   Name=MGC85546;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC078602; AAH78602.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR008661; L6_membrane.
DR   PANTHER; PTHR14198; L6_membrane; 1.
DR   Pfam; PF05805; L6_membrane; 1.
SQ   SEQUENCE   203 AA;  21693 MW;  F47FDDFDDBD7C5F4 CRC64;

  Query Match             16.1%;  Score 195.5;  DB 2;  Length 203;
  Best Local Similarity   32.1%;  Pred. No. 4.6e-09;

  Matches   72;  Conservative   23;  Mismatches   76;  Indels   53;  Gaps    9;

Qy         10 CNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAG-LMAIPATTM 68
              | |: |||| |  :| | | |      |    ||| :| | |:| || ||| || :||
Db          9 CIGYFLLVLALFCIVAN-ILLYFPNGETQYASQNHLSRFVWFFQGIGGAGLLMLLPAGVF 67

Qy         69 SLTARKRAC-------CNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPSN 121
                  :  |        |      | |   ::| | || ||::||    |::|||  ||
Db         68 IGLEHEDCCGCCGHEKCGKSCAMLSSILAALIGVAGAGYCVVISALGLVEGPLCLNSGEW 127

Qy        122 SNANCEFSLKNISDIHPESFNLQWFFN----DSCAPPTGFNKPTSNDTMASGWRASSFHF 177
              | |   ||          | |:  |     :|: |   |    | |:
Db        128 SYA---FS----------GTNGQYLTNHQSWSTCSEPK--NVVVWNVTL---------- 161

Qy        178 DSEENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGV 221
                      ||: |||     ::|:  | ||: | :| :|||
Db        162 ----------FSILLGL---SGIQVILCLIQIINGLIGGICGV 191


RESULT 12
Q4T901_TETNG
ID   Q4T901_TETNG   PRELIMINARY;   PRT;   199 AA.
AC   Q4T901;
DT   19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   19-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 4.
DE   Chromosome 1 SCAF7673, whole genome shotgun sequence. (Fragment).
GN   ORFNames=GSTENG00004984001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15496914; DOI=10.1038/nature03025;
RA   Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; CAAE01007673; CAF90631.1; -; Genomic_DNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR008661; L6_membrane.
DR   PANTHER; PTHR14198; L6_membrane; 1.
DR   Pfam; PF05805; L6_membrane; 1.
FT   NON_TER     199     199
SQ   SEQUENCE   199 AA;  20583 MW;  3F7A5AF20422979B CRC64;

  Query Match             15.9%;  Score 193;  DB 2;  Length 199;
  Best Local Similarity   25.4%;  Pred. No. 7.5e-09;
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  Matches   58;  Conservative   38;  Mismatches   84;  Indels   48;  Gaps    7;

Qy          3 CCEGWTSCNGFSLLVLLLLGVVLNAIPLIV--SLVEEDQFSQNPISCFEWWFPGIIGAGL 60
              |  |:  | | ||| | :: |: | :      : ||::  ::       |:| ||:|:|:
Db          2 CSGGFAKCLGISLLPLSIVCVLCNILLFFPGGTSVEKENITEQ-----VWYFGGIVGSGV 56

Qy         61 MAIPATTMSLTARKRAC--------CNNRTGMFLSSFFSVITVIGALYCMLISIQALLKG 112
              : |    : |  :   |        |  |  |  |: |: : |:|| |  :|| |: :|
Db         57 LMIFPALVFLGLKNNDCCGCCGNESCGRRFAMLSSALFAGVGVLGAGYSFIISAVAINRG 116

Qy        113 PLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRA 172
              |    | : : |      |  :   | : |   :||  | |              |
Db        117 PKCVVSYNGTQAEWSTPFSNGDYL---SNSTAW---NSCLGPEG----------VVSW-- 158

Qy        173 SSFHFDSEENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCG 220
                            | |:|  ||::|::::     |:| | || :||
Db        159 ---------------HLSLFSVLLVMGLIQIALCAVQVVNGLLGAVCG 191


RESULT 13
Q5U519_XENLA
ID   Q5U519_XENLA   PRELIMINARY;   PRT;   203 AA.
AC   Q5U519;
DT   07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT   07-DEC-2004, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   LOC495395 protein.
GN   Name=LOC495395;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RA   Klein S., Gerhard D.S.;
RL   Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; BC084866; AAH84866.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR008661; L6_membrane.
DR   PANTHER; PTHR14198; L6_membrane; 1.
DR   Pfam; PF05805; L6_membrane; 1.
SQ   SEQUENCE   203 AA;  21691 MW;  C74FA6B16A9E7273 CRC64;

  Query Match           15.7%;  Score 190.5;  DB 2;  Length 203;
  Best Local Similarity   29.1%;  Pred. No. 1.3e-08;
  Matches   66;  Conservative   30;  Mismatches   86;  Indels   45;  Gaps    8;

Qy          3 CCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAG-LM 61
              |     | |:|||:| :  :  | | |     |    |:| :| | |:| || ||| ||
Db          2 CYGSCARCIGYSLLILAIFCIAAN-ILLYFPNGETKYASENHLSRFVWFFQGIGGAGLLM 60

Qy         62 AIPATTMSLTARKRAC-------CNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPL 114
                :||       ::  |       |     | |   ::| | || ||::||   |::|||
Db         61 LLPAGVFIGLEQEDCCGCCGHERCGKSCAMLSSILAALIGVAGAGYCVVISALGLVEGPL 120

Qy        115 MCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASS 174
                |:   | |  : : | ::          |    :|  |   |    | |:
Db        121 CLNNGDWSYAFSDTNGKYLTKYQ------TW---STCIEPR--NVVVRNVTL-------- 161

Qy        175 FHFDSEENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGV 221
                          ||: |||     ::|:  | ||: | :| :|||
Db        162 -------------FSILLGL---SGIQVILCLIQIINGLIGGICGV 191


RESULT 14
Q4S8Y9_TETNG
ID   Q4S8Y9_TETNG   PRELIMINARY;   PRT;   142 AA.
AC   Q4S8Y9;
DT   19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   19-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 4.
DE   Chromosome 7 SCAF14703, whole genome shotgun sequence.
GN   ORFNames=GSTENG00022131001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15496914; DOI=10.1038/nature03025;
RA   Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
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```

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CC   ----------------------------------------------------------------------
DR   EMBL; CAAE01014703; CAG02893.1; -; Genomic_DNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR008661; L6_membrane.
DR   PANTHER; PTHR14198; L6_membrane; 1.
DR   Pfam; PF05805; L6_membrane; 1.
SQ   SEQUENCE   142 AA;  14740 MW;  29F40A0CCA0762AC CRC64;

  Query Match             15.1%;  Score 183.5;  DB 2;  Length 142;
  Best Local Similarity   29.8%;  Pred. No. 3.7e-08;
  Matches   53;  Conservative   28;  Mismatches   56;  Indels   41;  Gaps    8;

Qy         54 GIIGAGLMA-IPATTMSLTARKRACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKG 112
              |:|| | |  :||  : ||   ::|| || |||||  |: : ||| || : ::  ||  |
Db          3 GLIGGGAMVLLPALYIHLTG-TQSCCANRCGMFLSIGFAGVGVIGGLYSLTVASLALQNG 61

Qy        113 PLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTM--ASGW 170
              ||           |:              :| |         | | | |  : :  :| |
Db         62 PL-----------CQM------------LSLVWI--------TPF-KDTKGEYLSDSSSW 89

Qy        171 RASSFHFDSEENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQI 228
              :  :   :  |      | :|  || :  ||::    |:| | :|||||   ::: :
Db         90 KLCTAPANVVE-----FHIGMFATLLALSCLEIILCAIQMVNGLVGCLCGTCAKKTVV 142


RESULT 15
Q7SYW6_XENLA
ID   Q7SYW6_XENLA   PRELIMINARY;   PRT;   197 AA.
AC   Q7SYW6;
DT   01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2003, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Tm4sf4-prov protein.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RA   Klein S., Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
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CC   ----------------------------------------------------------------------
DR   EMBL; BC054239; AAH54239.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR008661; L6_membrane.
DR   PANTHER; PTHR14198; L6_membrane; 1.
DR   Pfam; PF05805; L6_membrane; 1.
SQ   SEQUENCE   197 AA;  20576 MW;  9B7CD56419EB7E99 CRC64;

  Query Match             15.0%;  Score 182;  DB 2;  Length 197;
  Best Local Similarity   25.8%;  Pred. No. 7e-08;
  Matches   59;  Conservative   30;  Mismatches   88;  Indels   52;  Gaps    8;

Qy          3 CCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA 62
              |  |   | | :|: | :| :: | :          |:   : ||   |:| ||:|:|::
Db          2 CSGGCAKCLGITLIPLAILCILANILLFFPGGTIADK--NDHISDEVWYFGGIVGSGVLM 59

Qy         63 IPATTMSLTARKRAC--------CNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPL 114
              |    : |  :  |         |  |  || |  |: |  :|| || ::|  |: |||
Db         60 IFPALVFLGLKNNDCCGCCGNESCGKRFAMFTSIIFAAIGFVGAGYCFIVSAVAIDKGP- 118

Qy        115 MCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASS 174
                      |:|   | :   |:  | |   |   ||              | :
Db        119 ----------KCDFGNGNYTYASQET-ELSW--KDCVEPPN----------IGEWNLTL 154

Qy        175 FHFDSEENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSK 223
              |                  | ||: |:  ||  : | : | :|  :||  |
Db        155 F---------------CLLLLMSGVQAVLCAI-QAINGLIGTICGDCK 186


Search completed: November 21, 2006, 20:08:29
Job time : 391.447 secs
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OM protein - protein search, using sw model
Run on:         November 21, 2006, 20:10:39 ; Search time 90.5199 Seconds
                                          (without alignments)
                                          404.080 Million cell updates/sec
Title:          US-10-063-553-48_COPY_111_190
Perfect score:  449
Sequence:       1 KGPLMCNSPSNSNANCEFSL.....RASSFHFDSEENKHRLIHFS 80
Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5
Searched:       2589679 seqs, 457216429 residues
Total number of hits satisfying chosen parameters:      2589679
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries
Database :       A_Geneseq_8:*
                1:  geneseqp1980s:*
                2:  geneseqp1990s:*
                3:  geneseqp2000s:*
                4:  geneseqp2001s:*
                5:  geneseqp2002s:*
                6:  geneseqp2003as:*
                7:  geneseqp2003bs:*
                8:  geneseqp2004s:*
     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.
                                SUMMARIES
  No.   Score  Match Length DB  ID                          Description
RESULT 1
ID   AAY66703 standard; protein; 229 AA.
DE   Membrane-bound protein PRO994.
PN   WO9963088-A2.
PD   09-DEC-1999.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 3;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 2
ID   AAU29122 standard; protein; 229 AA.
DE   Human PRO polypeptide sequence #99.
PN   WO200168848-A2.
PD   20-SEP-2001.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 4;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 3
ID   AAB87549 standard; protein; 229 AA.
DE   Human PRO994.
PN   WO200116318-A2.
PD   08-MAR-2001.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 4;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 4
ID   AAB65226 standard; protein; 229 AA.
DE   Human PRO994 (UNQ518) protein sequence SEQ ID NO:258.
PN   WO200073454-A1.
PD   07-DEC-2000.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 4;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 5
ID   ABG95874 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein PRO994.
PN   US2002119130-A1.
PD   29-AUG-2002.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 5;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 6
ID   ABU58498 standard; protein; 229 AA.
DE   Human PRO polypeptide #99.
PN   US2003027272-A1.
PD   06-FEB-2003.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 7
ID   ABU88046 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003032127-A1.
PD   13-FEB-2003.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 8
ID   ABU84361 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003032112-A1.
PD   13-FEB-2003.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 9
ID   ABR66235 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003027278-A1.
PD   06-FEB-2003.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 10
ID   ABR65625 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003036159-A1.
PD   20-FEB-2003.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 11
ID   ABU99565 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003040070-A1.
PD   27-FEB-2003.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 12
ID   ABU58041 standard; protein; 229 AA.
DE   Human PRO polypeptide #73.
PN   US2003027163-A1.
PD   06-FEB-2003.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 13
ID   ABU59119 standard; protein; 229 AA.
DE   Novel human secreted or transmembrane protein PRO994.
PN   US2002132252-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 14
ID   ABU82631 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein PRO994.
PN   US2003032023-A1.
PD   13-FEB-2003.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 15
ID   ABU82804 standard; protein; 229 AA.
DE   Human PRO polypeptide #99.
PN   US2003032113-A1.
PD   13-FEB-2003.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 16
ID   ABU89925 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003036147-A1.
PD   20-FEB-2003.
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Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 17
ID ABR68174 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 18
ID ABU60550 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, #103.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 19
ID ABU96227 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 20
ID ABU92658 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 21
ID ABO08735 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 22
ID ABO02787 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 23
ID ABR74941 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 24
ID ABR94703 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 25
ID ABU13932 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 26
ID ABU85676 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 27
ID ABU98836 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 28
ID ABU98051 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 29
ID ABU91757 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 30
ID ABU89450 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 31
ID ABU86291 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 32
ID ABU67504 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 33
ID ABU80532 standard; protein; 229 AA.
DE Human PRO protein #99.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 34
ID ABU72517 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 35
ID ABU90899 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 36
ID ABO33958 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.

PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 37
ID ABR99450 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 38
ID ABR98840 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 39
ID ABO16363 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 40
ID ABR92263 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 41
ID ABO18904 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 42
ID ABR78325 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 43
ID ABU71975 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 44
ID ABU85061 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 45
ID ABO00200 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 46
ID ABO11532 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 47
ID ABO02177 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 48
ID ABU88751 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 49
ID ABU83446 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 50
ID ABO06247 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 51
ID ABR59283 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 52
ID ABO09345 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 53
ID ABO19209 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 54
ID ABO11227 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 55
ID ABR66845 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 56
ID ABO16058 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040060-A1.
PD 27-FEB-2003.

Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 57
ID ABO13764 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 58
ID ABU71529 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 59
ID ABU65667 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, SEQ ID 198.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 60
ID ABO07515 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 61
ID ABO03702 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 62
ID ABR67150 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 63
ID ABO15753 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 64
ID ABU56034 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, PRO994.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 65
ID ABU72310 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 66
ID ABU65362 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 67
ID ABU95307 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US20030036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 68
ID ABU71210 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 69
ID ABO07820 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 70
ID ABR70061 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 71
ID ABR69394 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US20030036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 72
ID ABO01535 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 73
ID ABU81337 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US20030017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 74
ID ABR60134 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US20030032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 75
ID ABU90983 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 76
ID ABR67869 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027269-A1.
PD 06-FEB-2003.

Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 77
ID ABR65257 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 78
ID ABR68479 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 79
ID ABR71891 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 80
ID ABU59266 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, #103.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 81
ID ABU85371 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 82
ID ABU89061 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 83
ID ABU83141 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 84
ID ABU94997 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 85
ID ABU90545 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 86
ID ABU84056 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 87
ID ABU93707 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 88
ID ABO25963 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 89
ID ABR64952 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 90
ID ABO27304 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO994.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 91
ID ABR68784 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 92
ID ABO06600 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 93
ID ABR99145 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 94
ID ABU57029 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 95
ID ABU85981 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 96
ID ABU82268 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;

RESULT 97
ID ABU87279 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 98
ID ABU83751 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 99
ID ABO08125 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 100
ID ABU92499 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 101
ID ABU81836 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 102
ID ABU66000 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 103
ID ABU81169 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 104
ID ABR59829 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 105
ID ABU94017 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 106
ID ABU99870 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 107
ID ABR66540 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 108
ID ABR90958 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 109
ID ABO53284 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 110
ID ABU58972 standard; protein; 229 AA.
DE Human sectreted/transmembrane protein, #103.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 111
ID ABU94385 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 112
ID ABU79267 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 113
ID ABU86596 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 114
ID ABU86901 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 115
ID ABU94690 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 116
ID ABO04617 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 117

ID ABR70366 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 118
ID ABU92350 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 119
ID ABU98531 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 120
ID ABR65930 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 121
ID ABR64647 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 122
ID ABU59415 standard; protein; 229 AA.
DE Novel human secreted or transmembrane protein PRO812.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 123
ID ABU79572 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 124
ID ABU92963 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 125
ID ABU95922 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 126
ID ABU91142 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 127
ID ABU90235 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 128
ID ABO09650 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 129
ID ABO10922 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 130
ID ABR70976 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 131
ID ABU98286 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 132
ID ABU87584 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 133
ID ABU91452 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 134
ID ABU89291 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 135
ID ABU84666 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 136
ID ABR69756 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 137
ID ABU80133 standard; protein; 229 AA.
DE Human PRO protein #99.
PN US2003036139-A1.

PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 138
ID ABU82498 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 139
ID ABU92181 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 140
ID ABU93402 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 141
ID ABO09955 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 142
ID ABO09040 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 143
ID ABU96462 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 144
ID ABU10887 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 145
ID ABU10608 standard; protein; 229 AA.
DE Human secreted/transmembrane protein #99.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 146
ID ABU81639 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 147
ID ABU72132 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 148
ID ABU95617 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 149
ID ABU96826 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 150
ID ABR70671 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 151
ID ABO05022 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 152
ID ABO08430 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 153
ID ABU88578 standard; protein; 229 AA.
DE Human secreted and transmembrane polypeptide PRO994.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 154
ID ABO34092 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 155
ID ABO05637 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 156
ID ABR74026 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 157

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ID   ABR95618 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003054455-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 158
ID   ABR80915 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003049741-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 159
ID   ABR81220 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003049743-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 160
ID   ABM00916 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003049769-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 161
ID   ABR88518 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068743-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 162
ID   ABM77339 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003054479-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 163
ID   ABO28823 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003068685-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 164
ID   ABO31568 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003068725-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 165
ID   ABM07985 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068752-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 166
ID   ABO40465 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003068682-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 167
ID   ABO35890 standard; protein; 229 AA.
DE   Human PRO polypeptide #99.
PN   US2003068701-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 168
ID   ABO44029 standard; protein; 229 AA.
DE   Human PRO polypeptide #99.
PN   US2003068755-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 169
ID   ADA77950 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003073180-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 170
ID   ABM24824 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003104539-A1.
PD   05-JUN-2003.
  Query Match             100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 171
ID   ABO03092 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003036131-A1.
PD   20-FEB-2003.
  Query Match             100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 172
ID   ABR90348 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003040075-A1.
PD   27-FEB-2003.
  Query Match             100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 173
ID   ABM17262 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003054459-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 174
ID   ABR95008 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003044930-A1.
PD   06-MAR-2003.
  Query Match             100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 175
ID   ABR95313 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003040071-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 6;  Length 229;
```

Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 176
ID ADB17105 standard; protein; 229 AA.
DE Human transmembrane PRO polypeptide (SeqID 48).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 177
ID ABO21551 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 178
ID ABR97815 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 179
ID ABR87603 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 180
ID ABM77644 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 181
ID ABM27874 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 182
ID ABM06155 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 183
ID ABM03661 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 184
ID ABM35112 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 185
ID ABM26349 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 186
ID ABO48131 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 187
ID ABR92873 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 188
ID ABO24634 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 189
ID ADA37769 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 190
ID ABM11645 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 191
ID ABM02746 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 192
ID ABM16042 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 193
ID ABO27603 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 194
ID ABM29094 standard; protein; 229 AA.

DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 195
ID ABM07070 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 196
ID ABM21164 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 197
ID ABM09510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 198
ID ABO41380 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 199
ID ABO36195 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 200
ID ABO43724 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 201
ID ABM76424 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 202
ID ABM76120 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 203
ID ABM25739 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 204
ID ABM26044 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 205
ID ADA21455 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO994.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 206
ID ABO03397 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 207
ID ABO02482 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 208
ID ABO44262 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO 994.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 209
ID ABR90653 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 210
ID ABR73721 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 211
ID ABO16973 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 212
ID ABR94398 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 213
ID ABR75905 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044929-A1.

PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 214
ID ABR71281 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 215
ID ABR93178 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 216
ID ABR93483 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 217
ID ADA10242 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, PRO994.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 218
ID ABR87908 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 219
ID ABO27908 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 220
ID ABO30043 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 221
ID ABO33252 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 222
ID ABM04940 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 223
ID ABM08900 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 224
ID ABO36500 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 225
ID ABO35585 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 226
ID ABO39550 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 227
ID ABM10425 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 228
ID ABM11950 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 229
ID ABO52096 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 230
ID ABO52401 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 231
ID ADA19910 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;

RESULT 232
ID ABO23719 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 233
ID ADB17293 standard; protein; 229 AA.
DE Human transmembrane PRO polypeptide (SeqID 48).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 234
ID ADA17786 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 235
ID ABR97205 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 236
ID ABR86993 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 237
ID ABM11035 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 238
ID ABM28179 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 239
ID ABO32178 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 240
ID ABM15305 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 241
ID ABM06460 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 242
ID ABM04271 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 243
ID ABM22384 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 244
ID ABM07680 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 245
ID ABO40770 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 246
ID ABM35417 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 247
ID ABM33180 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 248
ID ABO52706 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 249
ID ABO50266 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 250
ID ABU99260 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040055-A1.
PD 27-FEB-2003.

Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 251
ID ABO04312 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 252
ID ABO05942 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 253
ID ABM18482 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 254
ID ADA27894 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 255
ID ABR97510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 256
ID ABR80610 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 257
ID ABM01221 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 258
ID ABR88823 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 259
ID ABM13475 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 260
ID ABM20859 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 261
ID ABO41990 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 262
ID ABO42600 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 263
ID ABM10120 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 264
ID ABO38635 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 265
ID ABM32875 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 266
ID ABM22689 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 267
ID ABM74900 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 268
ID ADA79742 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 269
ID ABR96290 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;

RESULT 270
ID ABM02441 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 271
ID ABR86383 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 272
ID ABR86688 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 273
ID ABM16652 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 274
ID ABM29704 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 275
ID ABO29128 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 276
ID ABM23909 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 277
ID ABM23299 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 278
ID ABM22079 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 279
ID ABO37720 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 280
ID ABM28484 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 281
ID ABM28789 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 282
ID ABM66433 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 283
ID ABM75815 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 284
ID ABM34095 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 285
ID ABM34400 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 286
ID ABO20331 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 287
ID ABO21246 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 288
ID ABO22161 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 289
ID ADA20082 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 290
ID ABO34190 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO 994.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 291
ID ABR96595 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 292
ID ADA94474 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 293
ID ABR85773 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 294
ID ABR99755 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 295
ID ABM00306 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 296
ID ABM00611 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 297
ID ABO29738 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 298
ID ABM23604 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 299
ID ABM29399 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 300
ID ABO38330 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 301
ID ABO45630 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 302
ID ABM20554 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 303
ID ADA81469 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 304
ID ABO16668 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 305
ID ABO18294 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 306
ID ABO22721 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 307
ID ABO23026 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 308
ID ABR92568 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 309
ID ABR81525 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 310
ID ABM77949 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 311
ID ABR89738 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 312
ID ABM26654 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 313
ID ABM13780 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 314
ID ABO28518 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 315
ID ABO30348 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 316
ID ABM07375 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 317
ID ABM03966 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 318
ID ABO37110 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 319
ID ABO41685 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 320
ID ABO35280 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 321
ID ABM25129 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 322
ID ABO47521 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 323
ID ABO47826 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 324
ID ABO48436 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 325
ID ABO51486 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 326
ID ABO51791 standard; protein; 229 AA.
DE Human PRO polypeptide #99.

PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 327
ID ABO50571 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 328
ID ABR79695 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 329
ID ABM16957 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 330
ID ABO17989 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 331
ID ABO20941 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 332
ID ABR96900 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 333
ID ADA38699 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 334
ID ABM12255 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 335
ID ABM16347 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 336
ID ABM24214 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 337
ID ABM14695 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 338
ID ABM04576 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 339
ID ABM06765 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 340
ID ABM09205 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 341
ID ABO39245 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 342
ID ABM75510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 343
ID ABM25434 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 344
ID ABM19944 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 345
ID ABO46850 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049762-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 346
ID ABO47155 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 347
ID ADA83267 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 348
ID ABR71586 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 349
ID ABR72196 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 350
ID ABR98535 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 351
ID ABO06905 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 352
ID ABR84858 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 353
ID ABR73416 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 354
ID ABR76510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 355
ID ABR73111 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 356
ID ABM18177 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 357
ID ABO20636 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 358
ID ABO25379 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 359
ID ABO25684 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 360
ID ABR94093 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 361
ID ADA92820 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 362
ID ABR80000 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 363
ID ABM11340 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 364
ID ABO32947 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;

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RESULT 365
ID   ABO30653 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003064466-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 366
ID   ABO30958 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003064468-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 367
ID   ABM27264 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068760-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 368
ID   ABM30009 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068769-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 369
ID   ABM05545 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003045700-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 370
ID   ABM15610 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068698-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 371
ID   ABM08595 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068759-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 372
ID   ABO42295 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003049748-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 373
ID   ABO38025 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003068765-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 374
ID   ABO45935 standard; protein; 229 AA.
DE   Human PRO polypeptide #99.
PN   US2003049754-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 375
ID   ABM66738 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068688-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 376
ID   ADB20310 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003082767-A1.
PD   01-MAY-2003.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 377
ID   ABM19639 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003104552-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 378
ID   ABO49351 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003049774-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 379
ID   ABO49656 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003049775-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 380
ID   ADA78562 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003073181-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 381
ID   ABR88213 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068720-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 382
ID   ADA00379 standard; protein; 229 AA.
DE   Human secreted/transmembrane polypeptide PRO 994.
PN   US2003027992-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 383
ID   ABM26959 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
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PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 384
ID ABM03356 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 385
ID ABO39855 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 386
ID ABO49961 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 387
ID ABO50876 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 388
ID ABO05332 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 389
ID ABR74636 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 390
ID ABR77115 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 391
ID ABM17872 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 392
ID ABR95923 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 393
ID ABO21856 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 394
ID ABO20026 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 395
ID ABO24329 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 396
ID ABR86078 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 397
ID ABM10730 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 398
ID ABM76729 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 399
ID ABR89433 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 400
ID ABM12560 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 401
ID ABM05850 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 402
ID ABO34975 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068728-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 403
ID ABM03051 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 404
ID ABM19029 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 405
ID ABM19334 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 406
ID ABO46545 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 407
ID ABO49046 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 408
ID ABR69089 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 409
ID ABR89128 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 410
ID ABR72501 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 411
ID ABR74331 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;

RESULT 412
ID ABO18599 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 413
ID ABR80305 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 414
ID ABM01526 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 415
ID ABM02136 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 416
ID ABR87298 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 417
ID ABM12865 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 418
ID ABM30619 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 419
ID ABM24519 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 420
ID ABO29433 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 421
ID ABO31263 standard; protein; 229 AA.

DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 422
ID ABM14390 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 423
ID ABM09815 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 424
ID ABO38940 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 425
ID ABM34705 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 426
ID ABO51181 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 427
ID ABO04007 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 428
ID ABO10477 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 429
ID ABO53178 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 430
ID ABR77720 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 431
ID ABR78930 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 432
ID ABO24024 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 433
ID ABR93788 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 434
ID ABM01831 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 435
ID ABM78254 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 436
ID ABR90043 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 437
ID ADA22381 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO994.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 438
ID ABM27569 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 439
ID ABM13170 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 440
ID ABO31873 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.

PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 441
ID ABM14085 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 442
ID ABM08290 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 443
ID ABO40160 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 444
ID ABM74595 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 445
ID ABM33790 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 446
ID ABM20249 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 447
ID ABO48741 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 448
ID ABO22548 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 449
ID ABR72806 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;

RESULT 450
ID ABO15448 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 451
ID ABR85163 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 452
ID ABO15143 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 453
ID ABO17278 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 454
ID ABM17567 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 455
ID ADA06547 standard; protein; 229 AA.
DE Human secreted/transmembrane PRO polypeptide #73.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 456
ID ADA39240 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 457
ID ABR85468 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 458
ID ABM77034 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 459
ID ABO28213 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;

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  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 460
ID   ABM22994 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068757-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 461
ID   ABM30314 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068723-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 462
ID   ABM21774 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068741-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 463
ID   ABM21469 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068744-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 464
ID   ABM15000 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068766-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 465
ID   ABO41075 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003068694-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 466
ID   ABO36805 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003068715-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 467
ID   ABO37415 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003068726-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 468
ID   ABM75205 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003104544-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 469
ID   ABM33485 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003096357-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 470
ID   ABO46240 standard; protein; 229 AA.
DE   Human PRO polypeptide #99.
PN   US2003049760-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 471
ID   ADA82633 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003049755-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 472
ID   ADB85621 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003049735-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 473
ID   ADB96266 standard; protein; 229 AA.
DE   Human PRO polypeptide #73.
PN   US2003054403-A1.
PD   20-MAR-2003.
  Query Match             100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 474
ID   ABM31839 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068680-A1.
PD   10-APR-2003.
  Query Match             100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 475
ID   ABM31229 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068762-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 476
ID   ADB85941 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003054472-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 477
ID   ABM32144 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068708-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 478
ID   ABM32449 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
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PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 479
ID ADB68300 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 480
ID ADB68107 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 481
ID ABM31534 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 482
ID ABM30924 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 483
ID ADB90924 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 484
ID ADC57738 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 485
ID ADC55102 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 486
ID ADC11969 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 487
ID ADC07004 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 488
ID ADC56391 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 489
ID ADC17183 standard; protein; 229 AA.
DE Mammalian PRO polypeptide (SeqID 48).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 490
ID ADC07446 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 491
ID ADC11436 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 492
ID ADC14881 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 493
ID ADC52376 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 494
ID ADC14558 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 495
ID ADD08090 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 496
ID ADC81915 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 497
ID ADD07557 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.

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  Query Match           100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 498
ID   ADC82448 standard; protein; 229 AA.
DE   Human PRO polypeptide #73.
PN   US2003059833-A1.
PD   27-MAR-2003.
  Query Match           100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 499
ID   ADD05671 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003087376-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 500
ID   ADD08628 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003073090-A1.
PD   17-APR-2003.
  Query Match           100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 501
ID   ADD06877 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2002193300-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 502
ID   ADC83124 standard; protein; 229 AA.
DE   Human PRO polypeptide #73.
PN   US2003059783-A1.
PD   27-MAR-2003.
  Query Match           100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 503
ID   ADD55231 standard; protein; 229 AA.
DE   Human PRO polypeptide #73.
PN   US2003077593-A1.
PD   24-APR-2003.
  Query Match           100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 504
ID   ADD36052 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003105298-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 505
ID   ADD56189 standard; protein; 229 AA.
DE   Human PRO polypeptide #73.
PN   US2003077594-A1.
PD   24-APR-2003.
  Query Match           100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 506
ID   ADD54627 standard; protein; 229 AA.
DE   Human PRO polypeptide #73.
PN   US2002132253-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 507
ID   ADE26781 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003087304-A1.
PD   08-MAY-2003.
  Query Match           100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 508
ID   ADE26248 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003087305-A1.
PD   08-MAY-2003.
  Query Match           100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 509
ID   ADF67185 standard; protein; 229 AA.
DE   Human PRO994 amino acid sequence SEQ ID NO:258.
PN   US2002198148-A1.
PD   26-DEC-2002.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 510
ID   ADG01053 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003078387-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 511
ID   ADG08606 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003180793-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 512
ID   ADG02666 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003207397-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 513
ID   ADG01373 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003207399-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 514
ID   ADF95548 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003207398-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 515
ID   ADF95227 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003180795-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
RESULT 516
ID   ADG12363 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003207392-A1.
PD   06-NOV-2003.
  Query Match           100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-43;
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RESULT 517
ID ADH24080 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 518
ID ADH34106 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 519
ID ADH29939 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 520
ID ADH23910 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 521
ID ADH09023 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 522
ID ADG85314 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 523
ID ADH24590 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 524
ID ADH37446 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 525
ID ADH02035 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 526
ID ADH37616 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 527
ID ADG85654 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 528
ID ADH24250 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 529
ID ADH38544 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 530
ID ADG83665 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 531
ID ADH29473 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 532
ID ADH27589 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 533
ID ADH37786 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 534
ID ADH37963 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 535
ID ADH57383 standard; protein; 229 AA.

DE Novel human secreted and transmembrane protein PRO994.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 536
ID ADH53525 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 537
ID ADH53695 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 538
ID ADH52031 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 539
ID ADH49886 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 540
ID ADI25396 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 541
ID ADH90189 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 542
ID ADI25566 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 543
ID ADH97740 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 544
ID ADI35439 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 545
ID ADI03588 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 546
ID ADI11945 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 547
ID ADH90019 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 548
ID ADH99931 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 549
ID ADH98420 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 550
ID ADI11095 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 551
ID ADI11605 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 552
ID ADH98250 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 553
ID ADH98590 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

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  Query Match            100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 554
ID   ADH98080 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181673-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 555
ID   ADI05068 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003180848-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 556
ID   ADI03418 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181654-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 557
ID   ADI04813 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181657-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 558
ID   ADH78267 standard; protein; 229 AA.
DE   Human PRO polypeptide #24.
PN   US2003181668-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 559
ID   ADI19611 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181676-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 560
ID   ADH90359 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181699-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 561
ID   ADI03078 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181653-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 562
ID   ADH77927 standard; protein; 229 AA.
DE   Human PRO polypeptide #24.
PN   US2003181666-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 563
ID   ADH97910 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181674-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 564
ID   ADI01295 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003190669-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 565
ID   ADI01990 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181652-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 566
ID   ADI03248 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181655-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 567
ID   ADI11435 standard; protein; 229 AA.
DE   Human PRO polypeptide #24.
PN   US2003181681-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 568
ID   ADI02337 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003181650-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 569
ID   ADI11775 standard; protein; 229 AA.
DE   Human PRO polypeptide #24.
PN   US2003181685-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 570
ID   ADI05412 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003190716-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 571
ID   ADH79484 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003191290-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 449;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
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RESULT 572
ID ADI19441 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 573
ID ADI05242 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 574
ID ADH79654 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 575
ID ADI01480 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 576
ID ADI01650 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 577
ID ADI01820 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 578
ID ADH79824 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 579
ID ADI04642 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 580
ID ADI02778 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 581
ID ADH78097 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 582
ID ADI25736 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 583
ID ADI25906 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 584
ID ADK65418 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 585
ID ADH98760 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 586
ID ADH80001 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 587
ID ADL32804 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 588
ID ADM30338 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 589
ID ADL93732 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 590
ID ABM85217 standard; protein; 229 AA.

DE Human protein sequence hCP1734062.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 591
ID ADC52186 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 592
ID ADE74335 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 593
ID ADE74947 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 594
ID ADF35384 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 595
ID ADG11634 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 596
ID ADF96160 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 597
ID ADG04431 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 598
ID ADG00591 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 599
ID ADH06618 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 600
ID ADH06448 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 601
ID ADG68869 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 602
ID ADH27759 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 603
ID ADH25100 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 604
ID ADH33732 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 605
ID ADG82847 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 606
ID ADH02375 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 607
ID ADH07982 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 608
ID ADG69379 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;

RESULT 609
ID ADH39200 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 610
ID ADH26128 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 611
ID ADG83940 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 612
ID ADH19504 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 613
ID ADG85484 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 614
ID ADH06278 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 615
ID ADH30108 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 616
ID ADH24420 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 617
ID ADH33097 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 618
ID ADG69549 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 619
ID ADH07812 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 620
ID ADG85824 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 621
ID ADH39370 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 622
ID ADH33562 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 623
ID ADH33902 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 624
ID ADH01112 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 625
ID ADG69719 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 626
ID ADH20997 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 627
ID ADH02205 standard; protein; 229 AA.
DE Human PRO polypeptide #24.

PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 628
ID ADG69209 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 629
ID ADG85994 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 630
ID ADH24930 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 631
ID ADH39547 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 632
ID ADH20037 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 633
ID ADH02545 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 634
ID ADG69039 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 635
ID ADH07642 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 636
ID ADG86164 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 637
ID ADH24760 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 638
ID ADH25808 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 639
ID ADH38374 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 640
ID ADH57213 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 641
ID ADH52201 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 642
ID ADH49567 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 643
ID ADH90529 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 644
ID ADI11265 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 645
ID ADH98930 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003190698-A1.
PD 09-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 646
ID ADI02160 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 647
ID ADH90699 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 648
ID ADJ54836 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 649
ID ADJ98574 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 650
ID ADJ98744 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 651
ID ADH78903 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 652
ID ADJ99137 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 653
ID ADJ99307 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 654
ID ADJ98925 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 655
ID ADH79073 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 656
ID ADK00933 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 657
ID ADK14454 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 658
ID ADJ64607 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 659
ID ADM31503 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 660
ID ADM36550 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 661
ID ADM40355 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 662
ID ADM80903 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.9e-43;
RESULT 663
ID ADN37963 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;

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  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 664
ID   ADR14507 standard; protein; 229 AA.
DE   Human NF-kappaB pathway-associated protein SeqID508.
PN   WO2004065577-A2.
PD   05-AUG-2004.
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
  Query Match             100.0%;  Score 449;  DB 8;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 665
ID   ADY77743 standard; protein; 229 AA.
DE   Neoplastic disease detection protein PRO994.
PN   US2005059102-A1.
PD   17-MAR-2005.
PA   (EATO/) EATON D L.
PA   (FILV/) FILVAROFF E.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GRIM/) GRIMALDI J C.
PA   (GURN/) GURNEY A L.
PA   (WATA/) WATANABE C K.
PA   (WOOD/) WOOD W I.
  Query Match             100.0%;  Score 449;  DB 9;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 666
ID   AEA38511 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein, #141.
PN   US2005112725-A1.
PD   26-MAY-2005.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 9;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 667
ID   AED50193 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2005163766-A1.
PD   28-JUL-2005.
  Query Match             100.0%;  Score 449;  DB 9;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 668
ID   AEF12574 standard; protein; 229 AA.
DE   Human PRO994 protein SEQ ID NO:48.
PN   US2006008901-A1.
PD   12-JAN-2006.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 449;  DB 10;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 669
ID   AEF74263 standard; protein; 229 AA.
DE   Human PRO994 protein SEQ ID NO:48.
PN   US2005260647-A1.
PD   24-NOV-2005.
PA   (EATO/) EATON D L.
PA   (FILV/) FILVAROFF E.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GRIM/) GRIMALDI J C.
PA   (GURN/) GURNEY A L.
PA   (WATA/) WATANABE C K.
PA   (WOOD/) WOOD W L.
  Query Match             100.0%;  Score 449;  DB 10;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-43;
RESULT 670
ID   ABM85216 standard; protein; 230 AA.
DE   Mouse protein sequence mCP5099.
PN   WO2003073826-A2.
PD   12-SEP-2003.
PA   (SAGR-) SAGRES DISCOVERY.
  Query Match             52.9%;  Score 237.5;  DB 7;  Length 230;
  Best Local Similarity   53.8%;  Pred. No. 7.7e-19;
RESULT 671
ID   ADT66602 standard; protein; 413 AA.
DE   Murine aspartate aminotransferase protein.
PN   WO2004070383-A2.
PD   19-AUG-2004.
PA   (CHEF ) GRUENENTHAL GMBH.
  Query Match             16.3%;  Score 73;  DB 8;  Length 413;
  Best Local Similarity   26.2%;  Pred. No. 16;
RESULT 672
ID   ADP90666 standard; protein; 527 AA.
DE   Mouse extracellular matrix protein #6.
PN   JP2004180541-A.
PD   02-JUL-2004.
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA   (RIKA ) RIKAGAKU KENKYUSHO.
PA   (DANA-) DANAFOMU KK.
  Query Match             15.7%;  Score 70.5;  DB 8;  Length 527;
  Best Local Similarity   30.9%;  Pred. No. 41;
RESULT 673
ID   AAB61263 standard; protein; 631 AA.
DE   Human monocyte inhibitory receptor precursor.
PN   WO200100810-A1.
PD   04-JAN-2001.
PA   (MILL-) MILLENNIUM PHARM INC.
  Query Match             15.6%;  Score 70;  DB 4;  Length 631;
  Best Local Similarity   24.0%;  Pred. No. 59;
RESULT 674
ID   ABB71337 standard; protein; 1079 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 40803.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
  Query Match             15.6%;  Score 70;  DB 4;  Length 1079;
  Best Local Similarity   28.3%;  Pred. No. 1.2e+02;
RESULT 675
ID   AAG84914 standard; protein; 610 AA.
DE   Shrimp white spot Bacilliform virus (WSBV) protein 5.
PN   WO200138351-A2.
PD   31-MAY-2001.
PA   (PENY-) PE CORP NY.
PA   (THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.
PA   (SINO-) SINOGENOMAX CO LTD.
  Query Match             15.5%;  Score 69.5;  DB 4;  Length 610;
  Best Local Similarity   30.8%;  Pred. No. 65;
RESULT 676
ID   ABB98338 standard; protein; 292 AA.
DE   Human anti-tenascin C monoclonal antibody SEQ ID NO 2.
PN   JP2002234900-A.
PD   23-AUG-2002.
PA   (MIED-) MIE DAIGAKUCHO.
  Query Match             15.1%;  Score 68;  DB 6;  Length 292;
  Best Local Similarity   66.7%;  Pred. No. 38;
RESULT 677
ID   ADP04284 standard; protein; 292 AA.
DE   Human tenascin C fibronectin III-like domain BCD domain polypeptide.
PN   JP2004138489-A.
PD   13-MAY-2004.
PA   (MENE-) MENEKI SEIBUTSU KENKYUSHO KK.
PA   (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
  Query Match             15.1%;  Score 68;  DB 8;  Length 292;
  Best Local Similarity   66.7%;  Pred. No. 38;
RESULT 678
ID   ADW18489 standard; protein; 362 AA.
DE   Pinus radiata transcription factor protein NAC family Seq 2279.
PN   WO2005001050-A2.
PD   06-JAN-2005.
PA   (ARBO-) ARBORGEN LLC.
  Query Match             15.1%;  Score 68;  DB 9;  Length 362;
  Best Local Similarity   26.7%;  Pred. No. 50;
RESULT 679
ID   AEE80568 standard; protein; 1658 AA.
DE   Human ovarian cancer marker fragment SEQ ID NO 935.
PN   WO2005116850-A2.
PD   08-DEC-2005.
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PA (COMP-) COMPUGEN LTD.
Query Match 15.1%; Score 68; DB 10; Length 1658;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
RESULT 680
ID AEE80569 standard; protein; 1673 AA.
DE Human ovarian cancer marker fragment SEQ ID NO 936.
PN WO2005116850-A2.
PD 08-DEC-2005.
PA (COMP-) COMPUGEN LTD.
Query Match 15.1%; Score 68; DB 10; Length 1673;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
RESULT 681
ID AEE80579 standard; protein; 1730 AA.
DE Human ovarian cancer marker fragment SEQ ID NO 946.
PN WO2005116850-A2.
PD 08-DEC-2005.
PA (COMP-) COMPUGEN LTD.
Query Match 15.1%; Score 68; DB 10; Length 1730;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
RESULT 682
ID AEE80572 standard; protein; 1928 AA.
DE Human ovarian cancer marker fragment SEQ ID NO 939.
PN WO2005116850-A2.
PD 08-DEC-2005.
PA (COMP-) COMPUGEN LTD.
Query Match 15.1%; Score 68; DB 10; Length 1928;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
RESULT 683
ID ADN05803 standard; protein; 2000 AA.
DE Antipsoriatic protein sequence #1065.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 15.1%; Score 68; DB 8; Length 2000;
Best Local Similarity 66.7%; Pred. No. 4.3e+02;
RESULT 684
ID AEE80578 standard; protein; 2065 AA.
DE Human ovarian cancer marker fragment SEQ ID NO 945.
PN WO2005116850-A2.
PD 08-DEC-2005.
PA (COMP-) COMPUGEN LTD.
Query Match 15.1%; Score 68; DB 10; Length 2065;
Best Local Similarity 66.7%; Pred. No. 4.5e+02;
RESULT 685
ID AEE80577 standard; protein; 2067 AA.
DE Human ovarian cancer marker fragment SEQ ID NO 944.
PN WO2005116850-A2.
PD 08-DEC-2005.
PA (COMP-) COMPUGEN LTD.
Query Match 15.1%; Score 68; DB 10; Length 2067;
Best Local Similarity 66.7%; Pred. No. 4.5e+02;
RESULT 686
ID AEE80574 standard; protein; 2091 AA.
DE Human ovarian cancer marker fragment SEQ ID NO 941.
PN WO2005116850-A2.
PD 08-DEC-2005.
PA (COMP-) COMPUGEN LTD.
Query Match 15.1%; Score 68; DB 10; Length 2091;
Best Local Similarity 66.7%; Pred. No. 4.5e+02;
RESULT 687
ID ABO01379 standard; protein; 2108 AA.
DE Human protein NOV35b.
PN WO2003023008-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.1%; Score 68; DB 6; Length 2108;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 688
ID ADN96130 standard; protein; 2108 AA.
DE Human NOVX polypeptide #92.
PN US2004067490-A1.
PD 08-APR-2004.
PA (ZHON/) ZHONG M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (SPYT/) SPYTEK K A.
PA (KEKU/) KEKUDA R.
PA (TAUP/) TAUPIER R J.
PA (ANDE/) ANDERSON D W.
PA (VERN/) VERNET C A M.
PA (CATT/) CATTERTON E.
PA (MILL/) MILLER C E.
PA (SHEN/) SHENOY S G.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (TCHE/) TCHERNEV V T.
PA (PADI/) PADIGARU M.
PA (GUSE/) GUSEV V Y.
PA (MALY/) MALYANKAR U M.
PA (BURG/) BURGESS C E.
PA (GERL/) GERLACH V.
PA (CASM/) CASMAN S J.
PA (RIEG/) RIEGER D K.
PA (GROS/) GROSSE W M.
PA (SMIT/) SMITHSON G.
PA (PEYM/) PEYMAN J A.
PA (STAR/) STARLING G.
PA (ROTH/) ROTHENBERG M E.
PA (LARO/) LAROCHELLE W J.
PA (SHIM/) SHIMKETS R A.
PA (CRAB/) CRABTREE J.
PA (RAST/) RASTELLI L.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (MACD/) MACDOUGALL J R.
PA (ELLE/) ELLERMAN K.
PA (CHAP/) CHAPOVAL A.
Query Match 15.1%; Score 68; DB 8; Length 2108;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 689
ID AAO30847 standard; protein; 2110 AA.
DE Human cell adhesion and extracellular matrix protein (CADECM)-37.
PN WO2003047526-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 15.1%; Score 68; DB 7; Length 2110;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 690
ID ADM80773 standard; protein; 2110 AA.
DE Human CADECM-2 protein SEQ ID NO:2.
PN WO2004015396-A2.
PD 19-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 15.1%; Score 68; DB 8; Length 2110;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 691
ID AEE80570 standard; protein; 2110 AA.
DE Human ovarian cancer marker fragment SEQ ID NO 937.
PN WO2005116850-A2.
PD 08-DEC-2005.
PA (COMP-) COMPUGEN LTD.
Query Match 15.1%; Score 68; DB 10; Length 2110;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 692
ID AEE80571 standard; protein; 2110 AA.
DE Human ovarian cancer marker fragment SEQ ID NO 938.
PN WO2005116850-A2.
PD 08-DEC-2005.
PA (COMP-) COMPUGEN LTD.
Query Match 15.1%; Score 68; DB 10; Length 2110;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 693
ID ABM83292 standard; protein; 2116 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3541.

PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 15.1%; Score 68; DB 8; Length 2116;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 694
ID ABM83291 standard; protein; 2122 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3540.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 15.1%; Score 68; DB 8; Length 2122;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 695
ID ABG70361 standard; protein; 2167 AA.
DE Novel human thrombopoietin variant protein, NV-20.
PN US2002068342-A1.
PD 06-JUN-2002.
PA (KHOS/) KHOSRAVI R.
PA (BERN/) BERNSTEIN J.
Query Match 15.1%; Score 68; DB 5; Length 2167;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
RESULT 696
ID AAR94562 standard; protein; 2199 AA.
DE Human cytotactin.
PN WO9608513-A1.
PD 21-MAR-1996.
PA (SCRI) SCRIPPS RES INST.
Query Match 15.1%; Score 68; DB 2; Length 2199;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
RESULT 697
ID ABO01378 standard; protein; 2199 AA.
DE Human protein NOV35a.
PN WO2003023008-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.1%; Score 68; DB 6; Length 2199;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
RESULT 698
ID ADN96128 standard; protein; 2199 AA.
DE Human NOVX polypeptide #91.
PN US2004067490-A1.
PD 08-APR-2004.
PA (ZHON/) ZHONG M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (SPYT/) SPYTEK K A.
PA (KEKU/) KEKUDA R.
PA (TAUP/) TAUPIER R J.
PA (ANDE/) ANDERSON D W.
PA (VERN/) VERNET C A M.
PA (CATT/) CATTERTON E.
PA (MILL/) MILLER C E.
PA (SHEN/) SHENOY S G.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (TCHE/) TCHERNEV V T.
PA (PADI/) PADIGARU M.
PA (GUSE/) GUSEV V Y.
PA (MALY/) MALYANKAR U M.
PA (BURG/) BURGESS C E.
PA (GERL/) GERLACH V.
PA (CASM/) CASMAN S J.
PA (RIEG/) RIEGER D K.
PA (GROS/) GROSSE W M.
PA (SMIT/) SMITHSON G.
PA (PEYM/) PEYMAN J A.
PA (STAR/) STARLING G.
PA (ROTH/) ROTHENBERG M E.
PA (LARO/) LAROCHELLE W J.
PA (SHIM/) SHIMKETS R A.
PA (CRAB/) CRABTREE J.
PA (RAST/) RASTELLI L.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (MACD/) MACDOUGALL J R.
PA (ELLE/) ELLERMAN K.
PA (CHAP/) CHAPOVAL A.
Query Match 15.1%; Score 68; DB 8; Length 2199;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
RESULT 699
ID AAB36935 standard; protein; 2201 AA.
DE Human tenascin-C.
PN WO200066628-A1.
PD 09-NOV-2000.
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
Query Match 15.1%; Score 68; DB 4; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
RESULT 700
ID ABP97745 standard; protein; 2201 AA.
DE Amino acid sequence of human HXB polypeptide.
PN WO2003010205-A1.
PD 06-FEB-2003.
PA (UYDU-) UNIV DUKE MEDICAL CENT.
Query Match 15.1%; Score 68; DB 6; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
RESULT 701
ID ABM78955 standard; protein; 2201 AA.
DE Breast cancer specific marker under-expressed in breast cancer.
PN WO2003073911-A2.
PD 12-SEP-2003.
PA (GEOU) UNIV GEORGETOWN.
Query Match 15.1%; Score 68; DB 7; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
RESULT 702
ID ADD69400 standard; protein; 2201 AA.
DE Human tenascin protein - SEQ ID 136.
PN WO2003048185-A2.
PD 12-JUN-2003.
PA (GENV-) GENVEC INC.
Query Match 15.1%; Score 68; DB 7; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
RESULT 703
ID ADD47935 standard; protein; 2201 AA.
DE Human Protein XP_005348, SEQ ID NO 13631.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 15.1%; Score 68; DB 7; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
RESULT 704
ID ADE62224 standard; protein; 2201 AA.
DE Human Protein P24821, SEQ ID NO 8153.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 15.1%; Score 68; DB 7; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
RESULT 705
ID ADO17766 standard; protein; 2201 AA.
DE Differentially expressed protein Lu1, SEQ ID 1.
PN WO2004015390-A2.
PD 19-FEB-2004.
PA (APPL-) APPLERA CORP.
Query Match 15.1%; Score 68; DB 8; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
RESULT 706
ID ADQ19756 standard; protein; 2201 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2575.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.

Query Match 15.1%; Score 68; DB 8; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
RESULT 707
ID ADU06359 standard; protein; 2201 AA.
DE Novel bronchial cancer-associated human protein SeqID583.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 15.1%; Score 68; DB 8; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
RESULT 708
ID ADV70208 standard; protein; 2201 AA.
DE Tumor-associated antigenic target polypeptide TAT450.
PN WO2004112829-A2.
PD 29-DEC-2004.
PA (GETH) GENENTECH INC.
Query Match 15.1%; Score 68; DB 9; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
RESULT 709
ID ADW88533 standard; peptide; 2201 AA.
DE Human tenascin-C.
PN WO2005009366-A2.
PD 03-FEB-2005.
PA (CORR) CORNELL RES FOUND INC.
Query Match 15.1%; Score 68; DB 9; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
RESULT 710
ID AED07152 standard; protein; 2201 AA.
DE Respiratory disease-associated protein, TNC.
PN WO2005092383-A1.
PD 06-OCT-2005.
PA (TAKE) TAKEDA PHARM CO LTD.
Query Match 15.1%; Score 68; DB 9; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
RESULT 711
ID AEE80566 standard; protein; 2201 AA.
DE Human ovarian cancer marker fragment SEQ ID NO 933.
PN WO2005116850-A2.
PD 08-DEC-2005.
PA (COMP-) COMPUGEN LTD.
Query Match 15.1%; Score 68; DB 10; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
RESULT 712
ID AEE80565 standard; protein; 2201 AA.
DE Human ovarian cancer marker fragment SEQ ID NO 932.
PN WO2005116850-A2.
PD 08-DEC-2005.
PA (COMP-) COMPUGEN LTD.
Query Match 15.1%; Score 68; DB 10; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
RESULT 713
ID ABM83294 standard; protein; 2207 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3543.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 15.1%; Score 68; DB 8; Length 2207;
Best Local Similarity 66.7%; Pred. No. 4.9e+02;
RESULT 714
ID ABM83293 standard; protein; 2207 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3542.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 15.1%; Score 68; DB 8; Length 2207;
Best Local Similarity 66.7%; Pred. No. 4.9e+02;
RESULT 715
ID ABM83295 standard; protein; 2207 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3544.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 15.1%; Score 68; DB 8; Length 2207;
Best Local Similarity 66.7%; Pred. No. 4.9e+02;
RESULT 716
ID AEE80567 standard; protein; 2293 AA.
DE Human ovarian cancer marker fragment SEQ ID NO 934.
PN WO2005116850-A2.
PD 08-DEC-2005.
PA (COMP-) COMPUGEN LTD.
Query Match 15.1%; Score 68; DB 10; Length 2293;
Best Local Similarity 66.7%; Pred. No. 5.1e+02;
RESULT 717
ID ABB49395 standard; protein; 296 AA.
DE Listeria monocytogenes protein #2099.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 14.9%; Score 67; DB 5; Length 296;
Best Local Similarity 28.4%; Pred. No. 51;
RESULT 718
ID ABR41213 standard; protein; 337 AA.
DE Human DITHP receptor.
PN WO200297031-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 14.9%; Score 67; DB 6; Length 337;
Best Local Similarity 24.0%; Pred. No. 60;
RESULT 719
ID AAE10579 standard; protein; 500 AA.
DE Human macrophage-expressed protein #4.
PN WO200164839-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 14.9%; Score 67; DB 4; Length 500;
Best Local Similarity 24.0%; Pred. No. 98;
RESULT 720
ID ABG10535 standard; protein; 500 AA.
DE Novel human diagnostic protein #10526.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 14.9%; Score 67; DB 4; Length 500;
Best Local Similarity 24.0%; Pred. No. 98;
RESULT 721
ID ADE62222 standard; protein; 619 AA.
DE Rat Protein AAA50761, SEQ ID NO 8151.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 14.9%; Score 67; DB 7; Length 619;
Best Local Similarity 40.0%; Pred. No. 1.3e+02;
RESULT 722
ID ABU11229 standard; protein; 631 AA.
DE Human monocyte inhibitory receptor precursor protein.
PN WO200280968-A1.
PD 17-OCT-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 14.9%; Score 67; DB 6; Length 631;
Best Local Similarity 24.0%; Pred. No. 1.3e+02;
RESULT 723
ID ABU12086 standard; protein; 632 AA.
DE Human NOV27a CG93884-01 protein SEQ ID 92.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 14.9%; Score 67; DB 6; Length 632;
Best Local Similarity 24.0%; Pred. No. 1.3e+02;
RESULT 724
ID ABG01737 standard; protein; 161 AA.
DE Novel human diagnostic protein #1728.
PN WO200175067-A2.
PD 11-OCT-2001.

PA (HYSE-) HYSEQ INC.
Query Match 14.8%; Score 66.5; DB 4; Length 161;
Best Local Similarity 29.5%; Pred. No. 27;
RESULT 725
ID ABR82240 standard; protein; 677 AA.
DE Human nucleic acid-associated protein (NAAP)-Id 2848827CD1.
PN WO2003052048-A2.
PD 26-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 14.8%; Score 66.5; DB 6; Length 677;
Best Local Similarity 31.6%; Pred. No. 1.6e+02;
RESULT 726
ID ADQ66763 standard; protein; 926 AA.
DE Novel human protein sequence #1736.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 14.8%; Score 66.5; DB 8; Length 926;
Best Local Similarity 31.6%; Pred. No. 2.4e+02;
RESULT 727
ID ABM92081 standard; protein; 1627 AA.
DE M. xanthus protein sequence, seq id 11280.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 14.8%; Score 66.5; DB 9; Length 1627;
Best Local Similarity 28.6%; Pred. No. 4.9e+02;
RESULT 728
ID ADU82617 standard; protein; 1725 AA.
DE Human MDDT polypeptide (ID 7526175CD1).
PN WO2004099390-A2.
PD 18-NOV-2004.
PA (INCY-) INCYTE CORP.
Query Match 14.8%; Score 66.5; DB 8; Length 1725;
Best Local Similarity 31.6%; Pred. No. 5.3e+02;
RESULT 729
ID ADT77471 standard; protein; 2046 AA.
DE Human nucleic acid-associated protein 7526176CD1.
PN WO2004087875-A2.
PD 14-OCT-2004.
PA (INCY-) INCYTE CORP.
Query Match 14.8%; Score 66.5; DB 8; Length 2046;
Best Local Similarity 31.6%; Pred. No. 6.6e+02;
RESULT 730
ID ADD47933 standard; protein; 575 AA.
DE Rat Protein AAA56909, SEQ ID NO 13629.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 14.7%; Score 66; DB 7; Length 575;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
RESULT 731
ID ADP09773 standard; protein; 1217 AA.
DE JNK3 human KIAA0569 protein.
PN WO2003086462-A1.
PD 23-OCT-2003.
PA (CELE-) CELESTAR LEXICO SCI INC.
PA (DAUC) DAIICHI PHARM CO LTD.
Query Match 14.7%; Score 66; DB 7; Length 1217;
Best Local Similarity 27.5%; Pred. No. 3.9e+02;
RESULT 732
ID ABG12658 standard; protein; 1219 AA.
DE Novel human diagnostic protein #12649.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 14.7%; Score 66; DB 4; Length 1219;
Best Local Similarity 27.5%; Pred. No. 3.9e+02;
RESULT 733
ID AAM78969 standard; protein; 1279 AA.
DE Human protein SEQ ID NO 1631.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 14.7%; Score 66; DB 4; Length 1279;
Best Local Similarity 27.5%; Pred. No. 4.2e+02;
RESULT 734
ID AAM79953 standard; protein; 1301 AA.
DE Human protein SEQ ID NO 3599.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 14.7%; Score 66; DB 4; Length 1301;
Best Local Similarity 27.5%; Pred. No. 4.3e+02;
RESULT 735
ID AAR71382 standard; protein; 650 AA.
DE Drosophila semaphorin I protein.
PN WO9507706-A1.
PD 23-MAR-1995.
PA (REGC) UNIV CALIFORNIA.
Query Match 14.6%; Score 65.5; DB 2; Length 650;
Best Local Similarity 31.8%; Pred. No. 2e+02;
RESULT 736
ID ABB64331 standard; protein; 771 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 19785.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 14.6%; Score 65.5; DB 4; Length 771;
Best Local Similarity 31.8%; Pred. No. 2.5e+02;
RESULT 737
ID ABB68283 standard; protein; 905 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 31641.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 14.6%; Score 65.5; DB 4; Length 905;
Best Local Similarity 27.3%; Pred. No. 3.1e+02;
RESULT 738
ID ABM84660 standard; protein; 452 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4909.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 14.5%; Score 65; DB 8; Length 452;
Best Local Similarity 24.0%; Pred. No. 1.5e+02;
RESULT 739
ID ABM84659 standard; protein; 481 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4908.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 14.5%; Score 65; DB 8; Length 481;
Best Local Similarity 24.0%; Pred. No. 1.6e+02;
RESULT 740
ID ADN99607 standard; protein; 512 AA.
DE Novel human protein sequence #423.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 14.5%; Score 65; DB 8; Length 512;
Best Local Similarity 24.0%; Pred. No. 1.7e+02;
RESULT 741
ID AAM20306 standard; protein; 79 AA.
DE Peptide #6740 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.4%; Score 64.5; DB 4; Length 79;
Best Local Similarity 32.8%; Pred. No. 19;
RESULT 742
ID ABB40757 standard; peptide; 79 AA.
DE Peptide #8263 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.4%; Score 64.5; DB 4; Length 79;
Best Local Similarity 32.8%; Pred. No. 19;
RESULT 743
ID AAM34523 standard; protein; 79 AA.
DE Peptide #8560 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.4%; Score 64.5; DB 4; Length 79;
Best Local Similarity 32.8%; Pred. No. 19;
RESULT 744
ID ABB24972 standard; protein; 79 AA.
DE Protein #6971 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.4%; Score 64.5; DB 4; Length 79;
Best Local Similarity 32.8%; Pred. No. 19;
RESULT 745
ID AAM74409 standard; protein; 79 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34715.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.4%; Score 64.5; DB 4; Length 79;
Best Local Similarity 32.8%; Pred. No. 19;
RESULT 746
ID AAM61617 standard; protein; 79 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 33722.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.4%; Score 64.5; DB 4; Length 79;
Best Local Similarity 32.8%; Pred. No. 19;
RESULT 747
ID ABG56204 standard; peptide; 79 AA.
DE Human liver peptide, SEQ ID No 34852.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.4%; Score 64.5; DB 4; Length 79;
Best Local Similarity 32.8%; Pred. No. 19;
RESULT 748
ID ABG44311 standard; peptide; 79 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 33976.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.4%; Score 64.5; DB 5; Length 79;
Best Local Similarity 32.8%; Pred. No. 19;
RESULT 749
ID ADN22431 standard; protein; 461 AA.
DE Bacterial polypeptide #5084.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.4%; Score 64.5; DB 8; Length 461;
Best Local Similarity 26.5%; Pred. No. 1.7e+02;
RESULT 750
ID ADI45315 standard; protein; 1185 AA.
DE Rice isoprenoid biosynthesis-associated protein #123.
PN US2004010815-A1.
PD 15-JAN-2004.
PA (LANG/) LANGE B M.
PA (GHAS/) GHASSEMIAN M.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Query Match 14.4%; Score 64.5; DB 8; Length 1185;
Best Local Similarity 27.8%; Pred. No. 5.6e+02;
RESULT 751
ID ADN24041 standard; protein; 228 AA.
DE Bacterial polypeptide #6694.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.3%; Score 64; DB 8; Length 228;
Best Local Similarity 31.9%; Pred. No. 81;
RESULT 752
ID ABM87753 standard; protein; 959 AA.
DE Rice abiotic stress responsive polypeptide SEQ ID NO:5999.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 14.3%; Score 64; DB 7; Length 959;
Best Local Similarity 26.6%; Pred. No. 4.9e+02;
RESULT 753
ID ADR43499 standard; protein; 3056 AA.
DE CSA-binding malarial variant surface antigen.
PN WO2004067559-A1.
PD 12-AUG-2004.
PA (UYKO-) UNIV KOBENHAVNS.
Query Match 14.3%; Score 64; DB 8; Length 3056;
Best Local Similarity 29.7%; Pred. No. 2.1e+03;
RESULT 754
ID AAB11524 standard; protein; 166 AA.
DE SEN virus protein fragment SEQ ID NO: 70.
PN WO200028039-A2.
PD 18-MAY-2000.
PA (DIAS-) DIASORIN SRL.
Query Match 14.1%; Score 63.5; DB 3; Length 166;
Best Local Similarity 24.2%; Pred. No. 62;
RESULT 755
ID AEB27727 standard; protein; 155 AA.
DE Humanized 2H7 antibody light chain sequence.
PN WO2005060999-A2.
PD 07-JUL-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 155;
Best Local Similarity 29.9%; Pred. No. 65;
RESULT 756
ID ADS33303 standard; protein; 213 AA.
DE Anti-CD20 humanised antibody hu2H7v16, light chain.
PN US2004202658-A1.
PD 14-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 8; Length 213;
Best Local Similarity 29.9%; Pred. No. 97;
RESULT 757
ID ADW03409 standard; protein; 213 AA.
DE Humanized anti-CD20 antibody (hu2H7.v16) light chain - SEQ ID 15.
PN WO2005000351-A2.
PD 06-JAN-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 213;
Best Local Similarity 29.9%; Pred. No. 97;
RESULT 758
ID AEB17637 standard; peptide; 213 AA.
DE Light chain peptide sequence of intact humanized 2H7 antibody.
PN WO2005061542-A2.

PD 07-JUL-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 213;
Best Local Similarity 29.9%; Pred. No. 97;
RESULT 759
ID AEE18959 standard; protein; 213 AA.
DE Humanized antibody light chain variable region #10.
PN WO2005108989-A2.
PD 17-NOV-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 213;
Best Local Similarity 29.9%; Pred. No. 97;
RESULT 760
ID AEE18926 standard; protein; 213 AA.
DE Humanized antibody light chain #1.
PN WO2005108989-A2.
PD 17-NOV-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 213;
Best Local Similarity 29.9%; Pred. No. 97;
RESULT 761
ID AEE18956 standard; protein; 213 AA.
DE Humanized antibody light chain variable region #8.
PN WO2005108989-A2.
PD 17-NOV-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 213;
Best Local Similarity 29.9%; Pred. No. 97;
RESULT 762
ID AEE18962 standard; protein; 213 AA.
DE Humanized antibody light chain variable region #11.
PN WO2005108989-A2.
PD 17-NOV-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 213;
Best Local Similarity 29.9%; Pred. No. 97;
RESULT 763
ID AEE18944 standard; protein; 213 AA.
DE Humanized antibody light chain variable region #5.
PN WO2005108989-A2.
PD 17-NOV-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 213;
Best Local Similarity 29.9%; Pred. No. 97;
RESULT 764
ID AEE18958 standard; protein; 213 AA.
DE Humanized antibody light chain variable region #9.
PN WO2005108989-A2.
PD 17-NOV-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 213;
Best Local Similarity 29.9%; Pred. No. 97;
RESULT 765
ID AEE18953 standard; protein; 213 AA.
DE Humanized antibody light chain variable region #6.
PN WO2005108989-A2.
PD 17-NOV-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 213;
Best Local Similarity 29.9%; Pred. No. 97;
RESULT 766
ID AEE18963 standard; protein; 213 AA.
DE Humanized antibody light chain variable region #12.
PN WO2005108989-A2.
PD 17-NOV-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 213;
Best Local Similarity 29.9%; Pred. No. 97;
RESULT 767
ID AEE26264 standard; protein; 213 AA.
DE Humanized 2H7.v511 antibody light chain variable region.
PN WO2005115453-A2.
PD 08-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 10; Length 213;
Best Local Similarity 29.9%; Pred. No. 97;
RESULT 768
ID AEE26249 standard; protein; 213 AA.
DE Humanized hu2H7.v138 antibody light chain.
PN WO2005115453-A2.
PD 08-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 10; Length 213;
Best Local Similarity 29.9%; Pred. No. 97;
RESULT 769
ID AEE26244 standard; protein; 213 AA.
DE Humanized hu2H7.v16 antibody mature light chain.
PN WO2005115453-A2.
PD 08-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 10; Length 213;
Best Local Similarity 29.9%; Pred. No. 97;
RESULT 770
ID AEE64956 standard; protein; 213 AA.
DE Mature 2H7.v16 light chain.
PN WO2005117978-A2.
PD 15-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 10; Length 213;
Best Local Similarity 29.9%; Pred. No. 97;
RESULT 771
ID AEE64959 standard; protein; 213 AA.
DE Mature 2H7.v511 light chain.
PN WO2005117978-A2.
PD 15-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 10; Length 213;
Best Local Similarity 29.9%; Pred. No. 97;
RESULT 772
ID AEE10477 standard; protein; 213 AA.
DE Humanized 2H7.v16 light chain amino acid sequence SEQ ID NO:13.
PN US2005271658-A1.
PD 08-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 10; Length 213;
Best Local Similarity 29.9%; Pred. No. 97;
RESULT 773
ID AEE10480 standard; protein; 213 AA.
DE Humanized 2H7.v511 light chain amino acid sequence SEQ ID NO:16.
PN US2005271658-A1.
PD 08-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 10; Length 213;
Best Local Similarity 29.9%; Pred. No. 97;
RESULT 774
ID AEE70763 standard; protein; 213 AA.
DE Humanized anti-CD20 antibody 2H7v.16, light chain.
PN WO2005113003-A2.
PD 01-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 10; Length 213;
Best Local Similarity 29.9%; Pred. No. 97;
RESULT 775
ID AEE70776 standard; protein; 213 AA.
DE Humanized anti-CD20 antibody, light chain mutant 2H7v.138.
PN WO2005113003-A2.
PD 01-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 10; Length 213;
Best Local Similarity 29.9%; Pred. No. 97;
RESULT 776
ID AEF05019 standard; protein; 213 AA.
DE Humanized 2H7.v16 variant antibody, mature light chain.
PN WO2005120437-A2.
PD 22-DEC-2005.
PA (GETH) GENENTECH INC.

Query Match 14.0%; Score 63; DB 10; Length 213;
Best Local Similarity 29.9%; Pred. No. 97;
RESULT 777
ID AEF05022 standard; protein; 213 AA.
DE Humanized 2H7.v511 variant antibody, mature light chain.
PN WO2005120437-A2.
PD 22-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 10; Length 213;
Best Local Similarity 29.9%; Pred. No. 97;
RESULT 778
ID AEF64240 standard; protein; 213 AA.
DE Humanized 2H7.v16 antibody light chain variable region SEQ ID NO:13.
PN WO2006012508-A2.
PD 02-FEB-2006.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 10; Length 213;
Best Local Similarity 29.9%; Pred. No. 97;
RESULT 779
ID ADP79583 standard; protein; 232 AA.
DE 2H7.v16 L chain amino acid sequence SEQ ID NO:21.
PN WO2004056312-A2.
PD 08-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 8; Length 232;
Best Local Similarity 29.9%; Pred. No. 1.1e+02;
RESULT 780
ID ADW03398 standard; protein; 232 AA.
DE Human anti-CD20 antibody (hu2H7.v16) light chain - SEQ ID 3.
PN WO2005000351-A2.
PD 06-JAN-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 232;
Best Local Similarity 29.9%; Pred. No. 1.1e+02;
RESULT 781
ID ADW21318 standard; protein; 232 AA.
DE Mouse anti-CD20 antibody 2H7 humanized clone v16, light chain.
PN WO2005005462-A2.
PD 20-JAN-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 232;
Best Local Similarity 29.9%; Pred. No. 1.1e+02;
RESULT 782
ID ADX00804 standard; protein; 232 AA.
DE Humanized 2H7 v16 antibody light chain variable region, SEQ ID 3.
PN US2005032130-A1.
PD 10-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 232;
Best Local Similarity 29.9%; Pred. No. 1.1e+02;
RESULT 783
ID ADY62624 standard; protein; 232 AA.
DE Humanized 2H7 antibody light chain.
PN US2005053602-A1.
PD 10-MAR-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 232;
Best Local Similarity 29.9%; Pred. No. 1.1e+02;
RESULT 784
ID AEE18943 standard; protein; 232 AA.
DE Humanized antibody light chain variable region #4.
PN WO2005108989-A2.
PD 17-NOV-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 232;
Best Local Similarity 29.9%; Pred. No. 1.1e+02;
RESULT 785
ID AEE26243 standard; protein; 232 AA.
DE Humanized hu2H7.v16 antibody complete light chain.
PN WO2005115453-A2.
PD 08-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 10; Length 232;
Best Local Similarity 29.9%; Pred. No. 1.1e+02;
RESULT 786
ID ADD30256 standard; protein; 418 AA.
DE Plant yield-related protein from clone G1360.
PN WO2003013227-A2.
PD 20-FEB-2003.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 14.0%; Score 63; DB 7; Length 418;
Best Local Similarity 27.3%; Pred. No. 2.3e+02;
RESULT 787
ID ADI44129 standard; protein; 418 AA.
DE Plant transcription factor related polypeptide #1653.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAAK/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
Query Match 14.0%; Score 63; DB 8; Length 418;
Best Local Similarity 27.3%; Pred. No. 2.3e+02;
RESULT 788
ID ABB66230 standard; protein; 816 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 25482.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 14.0%; Score 63; DB 4; Length 816;
Best Local Similarity 28.2%; Pred. No. 5.3e+02;
RESULT 789
ID AEE02551 standard; protein; 830 AA.
DE Human herpesvirus 6A antisense strand protein U87.
PN WO2005108581-A1.
PD 17-NOV-2005.
PA (OSAU) UNIV OSAKA.
Query Match 14.0%; Score 63; DB 9; Length 830;
Best Local Similarity 30.3%; Pred. No. 5.4e+02;
RESULT 790
ID ADS42707 standard; protein; 925 AA.
DE Bacterial polypeptide #21137.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.0%; Score 63; DB 8; Length 925;
Best Local Similarity 29.8%; Pred. No. 6.2e+02;
RESULT 791
ID ADN18779 standard; protein; 1165 AA.
DE Bacterial polypeptide #1432.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.0%; Score 63; DB 8; Length 1165;
Best Local Similarity 28.1%; Pred. No. 8.2e+02;
RESULT 792
ID AAB11504 standard; protein; 379 AA.

DE SEN virus protein fragment SEQ ID NO: 21.
PN WO200028039-A2.
PD 18-MAY-2000.
PA (DIAS-) DIASORIN SRL.
Query Match 13.9%; Score 62.5; DB 3; Length 379;
Best Local Similarity 25.6%; Pred. No. 2.3e+02;
RESULT 793
ID ADW08812 standard; protein; 412 AA.
DE Human protein which is up-regulated in HCV-infected tissue - SEQ ID 149.
PN EP1493750-A2.
PD 05-JAN-2005.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 13.9%; Score 62.5; DB 9; Length 412;
Best Local Similarity 24.0%; Pred. No. 2.5e+02;
RESULT 794
ID ADJ68623 standard; protein; 413 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID429.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 13.9%; Score 62.5; DB 7; Length 413;
Best Local Similarity 24.0%; Pred. No. 2.5e+02;
RESULT 795
ID ADO55165 standard; protein; 413 AA.
DE Protein #67 with increased gene expression in renal cell carcinoma.
PN WO2004032842-A2.
PD 22-APR-2004.
PA (VAND-) VAN ANDEL INST.
Query Match 13.9%; Score 62.5; DB 8; Length 413;
Best Local Similarity 24.0%; Pred. No. 2.5e+02;
RESULT 796
ID ADO19653 standard; protein; 413 AA.
DE Human PRO polypeptide #291.
PN WO2004043361-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 13.9%; Score 62.5; DB 8; Length 413;
Best Local Similarity 24.0%; Pred. No. 2.5e+02;
RESULT 797
ID ABM81188 standard; protein; 413 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO61502, SEQ:3067.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 13.9%; Score 62.5; DB 8; Length 413;
Best Local Similarity 24.0%; Pred. No. 2.5e+02;
RESULT 798
ID ADP54767 standard; protein; 413 AA.
DE Human PRO protein sequence SEQ ID NO:743.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 13.9%; Score 62.5; DB 8; Length 413;
Best Local Similarity 24.0%; Pred. No. 2.5e+02;
RESULT 799
ID ADP24138 standard; protein; 413 AA.
DE PRO polypeptide SEQ ID NO:1316.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 13.9%; Score 62.5; DB 8; Length 413;
Best Local Similarity 24.0%; Pred. No. 2.5e+02;
RESULT 800
ID ADT66598 standard; protein; 413 AA.
DE Human aspartate aminotransferase protein.
PN WO2004070383-A2.
PD 19-AUG-2004.
PA (CHEF) GRUENENTHAL GMBH.
Query Match 13.9%; Score 62.5; DB 8; Length 413;
Best Local Similarity 24.0%; Pred. No. 2.5e+02;
RESULT 801
ID ADY16030 standard; protein; 413 AA.
DE PRO polypeptide SEQ ID NO 1836.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 13.9%; Score 62.5; DB 9; Length 413;
Best Local Similarity 24.0%; Pred. No. 2.5e+02;
RESULT 802
ID ADY23183 standard; protein; 443 AA.
DE Plant full length insert polypeptide seqid 70967.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 13.9%; Score 62.5; DB 8; Length 443;
Best Local Similarity 24.6%; Pred. No. 2.8e+02;
RESULT 803
ID AAB11509 standard; protein; 679 AA.
DE SEN virus protein fragment SEQ ID NO: 36.
PN WO200028039-A2.
PD 18-MAY-2000.
PA (DIAS-) DIASORIN SRL.
Query Match 13.9%; Score 62.5; DB 3; Length 679;
Best Local Similarity 25.6%; Pred. No. 4.8e+02;
RESULT 804
ID ADH87440 standard; protein; 711 AA.
DE Enterococcus faecalis polypeptide #1920.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 13.9%; Score 62.5; DB 7; Length 711;
Best Local Similarity 31.2%; Pred. No. 5e+02;
RESULT 805
ID AAE14710 standard; protein; 734 AA.
DE Mouse beta4 dominant negative protein.
PN WO200230465-A2.
PD 18-APR-2002.
PA (UYRP) UNIV ROCHESTER.
Query Match 13.9%; Score 62.5; DB 5; Length 734;
Best Local Similarity 30.3%; Pred. No. 5.3e+02;
RESULT 806
ID ADJ32529 standard; protein; 734 AA.
DE Mouse beta4 dominant negative protein.
PN US2003224993-A1.
PD 04-DEC-2003.
PA (LAND/) LAND H.
PA (DELE/) DELEU L.
Query Match 13.9%; Score 62.5; DB 8; Length 734;
Best Local Similarity 30.3%; Pred. No. 5.3e+02;
RESULT 807
ID ABB64648 standard; protein; 826 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 20736.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 13.9%; Score 62.5; DB 4; Length 826;
Best Local Similarity 28.1%; Pred. No. 6.1e+02;
RESULT 808
ID AAE14709 standard; protein; 1466 AA.
DE Mouse beta4 integrin.
PN WO200230465-A2.
PD 18-APR-2002.
PA (UYRP) UNIV ROCHESTER.
Query Match 13.9%; Score 62.5; DB 5; Length 1466;
Best Local Similarity 30.3%; Pred. No. 1.3e+03;
RESULT 809
ID ADJ32527 standard; protein; 1466 AA.
DE Mouse integrin beta4 subunit protein.
PN US2003224993-A1.

PD 04-DEC-2003.
PA (LAND/) LAND H.
PA (DELE/) DELEU L.
Query Match 13.9%; Score 62.5; DB 8; Length 1466;
Best Local Similarity 30.3%; Pred. No. 1.3e+03;
RESULT 810
ID ABO69591 standard; protein; 290 AA.
DE Pseudomonas aeruginosa polypeptide #1766.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.8%; Score 62; DB 7; Length 290;
Best Local Similarity 24.6%; Pred. No. 1.9e+02;
RESULT 811
ID ABO77973 standard; protein; 372 AA.
DE Pseudomonas aeruginosa polypeptide #10148.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.8%; Score 62; DB 7; Length 372;
Best Local Similarity 23.9%; Pred. No. 2.6e+02;
RESULT 812
ID AAG70883 standard; protein; 592 AA.
DE C albicans apoptosis associated protein #63.
PN WO200102550-A2.
PD 11-JAN-2001.
PA (JANC) JANSSEN PHARM NV.
Query Match 13.8%; Score 62; DB 4; Length 592;
Best Local Similarity 27.3%; Pred. No. 4.6e+02;
RESULT 813
ID ADX95117 standard; protein; 823 AA.
DE Plant full length insert polypeptide seqid 57781.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 13.8%; Score 62; DB 8; Length 823;
Best Local Similarity 28.6%; Pred. No. 6.9e+02;
RESULT 814
ID ADN18993 standard; protein; 891 AA.
DE Bacterial polypeptide #1646.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 13.8%; Score 62; DB 8; Length 891;
Best Local Similarity 27.1%; Pred. No. 7.7e+02;
RESULT 815
ID ABR53813 standard; protein; 971 AA.
DE Protein sequence #SEQ ID 2491.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 13.8%; Score 62; DB 6; Length 971;
Best Local Similarity 27.1%; Pred. No. 8.5e+02;
RESULT 816
ID ADK65020 standard; protein; 971 AA.
DE Disease treating protein complex-derived protein #1506.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 13.8%; Score 62; DB 7; Length 971;
Best Local Similarity 27.1%; Pred. No. 8.5e+02;
RESULT 817
ID AAB84882 standard; protein; 1530 AA.
DE Human protein, SEQ ID 6.
PN WO200127270-A1.
PD 19-APR-2001.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match 13.8%; Score 62; DB 4; Length 1530;
Best Local Similarity 28.2%; Pred. No. 1.5e+03;
RESULT 818
ID AEB41562 standard; protein; 1921 AA.
DE L. pneumophila protein SEQ ID NO 5894.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 13.8%; Score 62; DB 9; Length 1921;
Best Local Similarity 25.6%; Pred. No. 2e+03;
RESULT 819
ID AEB38280 standard; protein; 1956 AA.
DE L. pneumophila protein SEQ ID NO 2612.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 13.8%; Score 62; DB 9; Length 1956;
Best Local Similarity 25.6%; Pred. No. 2.1e+03;
RESULT 820
ID AAB84885 standard; protein; 2266 AA.
DE Human protein, SEQ ID 14.
PN WO200127270-A1.
PD 19-APR-2001.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match 13.8%; Score 62; DB 4; Length 2266;
Best Local Similarity 28.2%; Pred. No. 2.5e+03;
RESULT 821
ID ADX06502 standard; protein; 2266 AA.
DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 1067.
PN WO2005012875-A2.
PD 10-FEB-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 13.8%; Score 62; DB 9; Length 2266;
Best Local Similarity 28.2%; Pred. No. 2.5e+03;
RESULT 822
ID ABG22400 standard; protein; 102 AA.
DE Novel human diagnostic protein #22391.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.7%; Score 61.5; DB 4; Length 102;
Best Local Similarity 27.3%; Pred. No. 57;
RESULT 823
ID ADM05710 standard; protein; 122 AA.
DE Human protein of the invention SEQ ID NO:4395.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 13.7%; Score 61.5; DB 7; Length 122;
Best Local Similarity 25.6%; Pred. No. 72;
RESULT 824
ID AEC88640 standard; protein; 122 AA.
DE Human cDNA clone protein TESTI20178160, SEQ ID 4395.
PN EP1580263-A1.
PD 28-SEP-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 13.7%; Score 61.5; DB 9; Length 122;
Best Local Similarity 25.6%; Pred. No. 72;
RESULT 825
ID ADO05882 standard; peptide; 130 AA.
DE C. jacchus M3-24 MOG-specific Ig kappa light chain Fab fragment.
PN WO2004034031-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.

Query Match 13.7%; Score 61.5; DB 8; Length 130;
Best Local Similarity 30.3%; Pred. No. 78;
RESULT 826
ID ADC85015 standard; protein; 269 AA.
DE HLA DQB1 protein.
PN WO200283947-A1.
PD 24-OCT-2002.
PA (OGOS/) OGOSHI K.
Query Match 13.7%; Score 61.5; DB 7; Length 269;
Best Local Similarity 21.9%; Pred. No. 1.9e+02;
RESULT 827
ID ADC85018 standard; protein; 269 AA.
DE HLA DQB1 protein.
PN WO200283947-A1.
PD 24-OCT-2002.
PA (OGOS/) OGOSHI K.
Query Match 13.7%; Score 61.5; DB 7; Length 269;
Best Local Similarity 21.9%; Pred. No. 1.9e+02;
RESULT 828
ID ADC85012 standard; protein; 269 AA.
DE HLA DQB1 protein.
PN WO200283947-A1.
PD 24-OCT-2002.
PA (OGOS/) OGOSHI K.
Query Match 13.7%; Score 61.5; DB 7; Length 269;
Best Local Similarity 21.9%; Pred. No. 1.9e+02;
RESULT 829
ID ADY24666 standard; protein; 616 AA.
DE Plant full length insert polypeptide seqid 72450.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 13.7%; Score 61.5; DB 8; Length 616;
Best Local Similarity 25.0%; Pred. No. 5.5e+02;
RESULT 830
ID ADW18493 standard; protein; 1024 AA.
DE Pinus radiata transcription factor protein SBP family Seq 2283.
PN WO2005001050-A2.
PD 06-JAN-2005.
PA (ARBO-) ARBORGEN LLC.
Query Match 13.7%; Score 61.5; DB 9; Length 1024;
Best Local Similarity 27.1%; Pred. No. 1e+03;
RESULT 831
ID ADW17829 standard; protein; 1024 AA.
DE Pinus radiata transcription factor protein SBP family Seq 1606.
PN WO2005001050-A2.
PD 06-JAN-2005.
PA (ARBO-) ARBORGEN LLC.
Query Match 13.7%; Score 61.5; DB 9; Length 1024;
Best Local Similarity 27.1%; Pred. No. 1e+03;
RESULT 832
ID ADS43681 standard; protein; 1034 AA.
DE Bacterial polypeptide #22111.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 13.7%; Score 61.5; DB 8; Length 1034;
Best Local Similarity 28.8%; Pred. No. 1.1e+03;
RESULT 833
ID ADS05365 standard; protein; 45 AA.
DE Staphylococcus epidermis polypeptide seqid 4660.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
Query Match 13.6%; Score 61; DB 8; Length 45;
Best Local Similarity 42.9%; Pred. No. 23;
RESULT 834
ID AAB56760 standard; protein; 187 AA.
DE Human prostate cancer antigen protein sequence SEQ ID NO:1338.
PN WO200055174-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 13.6%; Score 61; DB 3; Length 187;
Best Local Similarity 26.2%; Pred. No. 1.4e+02;
RESULT 835
ID ADZ59470 standard; protein; 283 AA.
DE L19 antibody protein with N-terminal linker & C-terminal tagged peptide.
PN WO2005037312-A2.
PD 28-APR-2005.
PA (SCHD) SCHERING AG.
Query Match 13.6%; Score 61; DB 9; Length 283;
Best Local Similarity 27.5%; Pred. No. 2.4e+02;
RESULT 836
ID AAR20807 standard; protein; 311 AA.
DE Human CDw32 antigen.
PN WO9201049-A.
PD 23-JAN-1992.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 13.6%; Score 61; DB 2; Length 311;
Best Local Similarity 40.6%; Pred. No. 2.7e+02;
RESULT 837
ID AAM48902 standard; protein; 365 AA.
DE Aminotransferase related human protein.
PN WO200192490-A2.
PD 06-DEC-2001.
PA (APPL-) APPLERA CORP.
Query Match 13.6%; Score 61; DB 5; Length 365;
Best Local Similarity 25.0%; Pred. No. 3.3e+02;
RESULT 838
ID ADB85178 standard; protein; 413 AA.
DE Rat aspartate aminotransferase SEQ ID NO:59.
PN EP1284297-A2.
PD 19-FEB-2003.
PA (WARN) WARNER LAMBERT CO.
Query Match 13.6%; Score 61; DB 7; Length 413;
Best Local Similarity 25.0%; Pred. No. 3.8e+02;
RESULT 839
ID ADT66600 standard; protein; 413 AA.
DE Rat aspartate aminotransferase protein.
PN WO2004070383-A2.
PD 19-AUG-2004.
PA (CHEF) GRUENENTHAL GMBH.
Query Match 13.6%; Score 61; DB 8; Length 413;
Best Local Similarity 25.0%; Pred. No. 3.8e+02;
RESULT 840
ID AAU15075 standard; protein; 715 AA.
DE Protein encoded by C. albicans essential gene CaYJL090C (DPB11).
PN WO200160975-A2.
PD 23-AUG-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 13.6%; Score 61; DB 4; Length 715;
Best Local Similarity 35.9%; Pred. No. 7.6e+02;
RESULT 841
ID ABP73165 standard; protein; 715 AA.
DE Candida albicans essential protein SEQ ID NO 7002.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 13.6%; Score 61; DB 5; Length 715;
Best Local Similarity 35.9%; Pred. No. 7.6e+02;
RESULT 842
ID ABB62311 standard; protein; 788 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 13725.
PN WO200171042-A2.
PD 27-SEP-2001.

PA (PEKE) PE CORP NY.
Query Match 13.6%; Score 61; DB 4; Length 788;
Best Local Similarity 26.6%; Pred. No. 8.6e+02;
RESULT 843
ID AAR94563 standard; protein; 1810 AA.
DE Chicken cytotactin.
PN WO9608513-A1.
PD 21-MAR-1996.
PA (SCRI) SCRIPPS RES INST.
Query Match 13.6%; Score 61; DB 2; Length 1810;
Best Local Similarity 46.2%; Pred. No. 2.4e+03;
RESULT 844
ID ADS85087 standard; protein; 2019 AA.
DE Mouse atopic dermatitis-related protein sequence SeqID89.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.
Query Match 13.6%; Score 61; DB 8; Length 2019;
Best Local Similarity 55.6%; Pred. No. 2.8e+03;
RESULT 845
ID ADY24980 standard; protein; 436 AA.
DE Plant full length insert polypeptide seqid 72764.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 13.5%; Score 60.5; DB 8; Length 436;
Best Local Similarity 26.0%; Pred. No. 4.6e+02;
RESULT 846
ID ABU24178 standard; protein; 444 AA.
DE Protein encoded by Prokaryotic essential gene #9705.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 13.5%; Score 60.5; DB 6; Length 444;
Best Local Similarity 29.3%; Pred. No. 4.8e+02;
RESULT 847
ID ABG92810 standard; protein; 588 AA.
DE Protein encoded by fungal peptide synthetase gene cluster ORF16.
PN WO200242444-A2.
PD 30-MAY-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (CORR) CORNELL RES FOUND INC.
PA (YODE/) YODER O.
PA (TURG/) TURGEON B G.
PA (LUSS/) LU S.
Query Match 13.5%; Score 60.5; DB 5; Length 588;
Best Local Similarity 25.0%; Pred. No. 6.8e+02;
RESULT 848
ID AAU96804 standard; protein; 890 AA.
DE Human immunodeficiency virus type 2 derived polypeptide #4.
PN US2002051967-A1.
PD 02-MAY-2002.
PA (INSP) INST PASTEUR.
Query Match 13.5%; Score 60.5; DB 5; Length 890;
Best Local Similarity 22.9%; Pred. No. 1.1e+03;
RESULT 849
ID ADO00996 standard; protein; 937 AA.
DE Mouse homologue of Fruit fly AD-related protein CG10198.
PN US2004067535-A1.
PD 08-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
Query Match 13.5%; Score 60.5; DB 8; Length 937;
Best Local Similarity 30.7%; Pred. No. 1.2e+03;
RESULT 850
ID ADO07917 standard; protein; 937 AA.
DE Rat polypeptide.
PN US2004071700-A1.
PD 15-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
Query Match 13.5%; Score 60.5; DB 8; Length 937;
Best Local Similarity 30.7%; Pred. No. 1.2e+03;
RESULT 851
ID ABR53184 standard; protein; 992 AA.
DE Protein sequence #SEQ ID 1233.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 13.5%; Score 60.5; DB 6; Length 992;
Best Local Similarity 19.8%; Pred. No. 1.3e+03;
RESULT 852
ID ADK63220 standard; protein; 992 AA.
DE Disease treating protein complex-derived protein #736.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 13.5%; Score 60.5; DB 7; Length 992;
Best Local Similarity 19.8%; Pred. No. 1.3e+03;
RESULT 853
ID ADI27180 standard; protein; 1611 AA.
DE Human LRP binding family protein #11.
PN WO2003106657-A2.
PD 24-DEC-2003.
PA (STOW-) STOWERS INST MEDICAL RES.
Query Match 13.5%; Score 60.5; DB 8; Length 1611;
Best Local Similarity 28.1%; Pred. No. 2.4e+03;
RESULT 854
ID ABP31105 standard; protein; 116 AA.
DE Human ORF78 protein, SEQ ID NO:156.
PN WO200190366-A2.
PD 29-NOV-2001.
PA (CURA-) CURAGEN CORP.
Query Match 13.4%; Score 60; DB 5; Length 116;
Best Local Similarity 26.5%; Pred. No. 1e+02;
RESULT 855
ID AAO03609 standard; protein; 141 AA.
DE Human polypeptide SEQ ID NO 17501.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.4%; Score 60; DB 4; Length 141;
Best Local Similarity 24.2%; Pred. No. 1.3e+02;
RESULT 856
ID AAE35326 standard; protein; 213 AA.
DE Humanised murine antibody BIWA4 light chain protein.
PN EP1258255-A1.
PD 20-NOV-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 13.4%; Score 60; DB 6; Length 213;
Best Local Similarity 29.9%; Pred. No. 2.2e+02;
RESULT 857
ID AAE34878 standard; protein; 213 AA.
DE BIWA4/8 antibody light chain mature protein.
PN WO200294879-A1.
PD 28-NOV-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
Query Match 13.4%; Score 60; DB 6; Length 213;
Best Local Similarity 29.9%; Pred. No. 2.2e+02;
RESULT 858
ID AAE34877 standard; protein; 213 AA.
DE BIWA4 antibody light chain mature protein.
PN WO200294879-A1.
PD 28-NOV-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
Query Match 13.4%; Score 60; DB 6; Length 213;
Best Local Similarity 29.9%; Pred. No. 2.2e+02;
RESULT 859
ID ADL15441 standard; protein; 213 AA.
DE Humanised murine antibody BIWA4 light chain protein.

PN EP1391213-A1.
PD 25-FEB-2004.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 13.4%; Score 60; DB 8; Length 213;
Best Local Similarity 29.9%; Pred. No. 2.2e+02;
RESULT 860
ID ADL15445 standard; protein; 213 AA.
DE Humanised murine antibody BIWA8 light chain protein.
PN EP1391213-A1.
PD 25-FEB-2004.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 13.4%; Score 60; DB 8; Length 213;
Best Local Similarity 29.9%; Pred. No. 2.2e+02;
RESULT 861
ID ADO00849 standard; protein; 213 AA.
DE Humanised murine antibody BIWA 4 light chain protein SEQ ID NO:4.
PN EP1417974-A1.
PD 12-MAY-2004.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 13.4%; Score 60; DB 8; Length 213;
Best Local Similarity 29.9%; Pred. No. 2.2e+02;
RESULT 862
ID ADO00853 standard; protein; 213 AA.
DE Humanised murine antibody BIWA 8 light chain protein SEQ ID NO:8.
PN EP1417974-A1.
PD 12-MAY-2004.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 13.4%; Score 60; DB 8; Length 213;
Best Local Similarity 29.9%; Pred. No. 2.2e+02;
RESULT 863
ID AEB29787 standard; protein; 213 AA.
DE Humanized anti-CD44 antibody light chain A.
PN WO2005065717-A2.
PD 21-JUL-2005.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
PA (BOEH) BOEHRINGER INGELHEIM PHARMA GMBH & CO KG.
Query Match 13.4%; Score 60; DB 9; Length 213;
Best Local Similarity 29.9%; Pred. No. 2.2e+02;
RESULT 864
ID AEB29791 standard; protein; 213 AA.
DE Humanized anti-CD44 antibody light chain B.
PN WO2005065717-A2.
PD 21-JUL-2005.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
PA (BOEH) BOEHRINGER INGELHEIM PHARMA GMBH & CO KG.
Query Match 13.4%; Score 60; DB 9; Length 213;
Best Local Similarity 29.9%; Pred. No. 2.2e+02;
RESULT 865
ID AEB29782 standard; protein; 213 AA.
DE Humanized anti-CD44 antibody light chain B.
PN WO2005065709-A2.
PD 21-JUL-2005.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
PA (BOEH) BOEHRINGER INGELHEIM PHARMA GMBH & CO KG.
Query Match 13.4%; Score 60; DB 9; Length 213;
Best Local Similarity 29.9%; Pred. No. 2.2e+02;
RESULT 866
ID AEB29778 standard; protein; 213 AA.
DE Humanized anti-CD44 antibody light chain A.
PN WO2005065709-A2.
PD 21-JUL-2005.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
PA (BOEH) BOEHRINGER INGELHEIM PHARMA GMBH & CO KG.
Query Match 13.4%; Score 60; DB 9; Length 213;
Best Local Similarity 29.9%; Pred. No. 2.2e+02;
RESULT 867
ID ADY70960 standard; protein; 214 AA.
DE Human monoclonal antibody CRJA light chain.
PN WO2005023849-A2.
PD 17-MAR-2005.
PA (CRUC-) CRUCELL HOLLAND BV.
Query Match 13.4%; Score 60; DB 9; Length 214;
Best Local Similarity 28.4%; Pred. No. 2.2e+02;

RESULT 868
ID ABR01492 standard; protein; 215 AA.
DE Human anti-TIMP-1 antibody light chain #33.
PN WO200286085-A2.
PD 31-OCT-2002.
PA (FARB) BAYER CORP.
PA (MORP-) MORPHOSYS AG.
Query Match 13.4%; Score 60; DB 6; Length 215;
Best Local Similarity 29.9%; Pred. No. 2.2e+02;
RESULT 869
ID AAO14066 standard; protein; 234 AA.
DE Light chain protein of the monoclonal antibody from clone JA.
PN WO200188132-A2.
PD 22-NOV-2001.
PA (UYJE-) UNIV JEFFERSON THOMAS.
Query Match 13.4%; Score 60; DB 5; Length 234;
Best Local Similarity 28.4%; Pred. No. 2.4e+02;
RESULT 870
ID ABU08018 standard; protein; 234 AA.
DE Human monoclonal rabies virus antibody light chain, clone JH, protein.
PN WO2003016501-A2.
PD 27-FEB-2003.
PA (UYJE-) UNIV JEFFERSON THOMAS.
Query Match 13.4%; Score 60; DB 6; Length 234;
Best Local Similarity 28.4%; Pred. No. 2.4e+02;
RESULT 871
ID ADF65776 standard; protein; 234 AA.
DE Human monoclonal rabies virus antibody light chain.
PN US2003157112-A1.
PD 21-AUG-2003.
PA (HOOP/) HOOPER D C.
PA (DIET/) DIETZSCHOLD B.
Query Match 13.4%; Score 60; DB 7; Length 234;
Best Local Similarity 28.4%; Pred. No. 2.4e+02;
RESULT 872
ID ADJ92516 standard; protein; 234 AA.
DE Human SOJA monoclonal antibody light chain protein.
PN US2004013672-A1.
PD 22-JAN-2004.
PA (UYJE-) UNIV JEFFERSON THOMAS.
Query Match 13.4%; Score 60; DB 8; Length 234;
Best Local Similarity 28.4%; Pred. No. 2.4e+02;
RESULT 873
ID AAB82912 standard; protein; 241 AA.
DE Human immune response protein HIRP1.
PN WO200168696-A1.
PD 20-SEP-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 13.4%; Score 60; DB 4; Length 241;
Best Local Similarity 28.4%; Pred. No. 2.5e+02;
RESULT 874
ID ADV86419 standard; protein; 482 AA.
DE Novel C1q domain-containing protein #40.
PN US2004248156-A1.
PD 09-DEC-2004.
PA (HUTT/) HU T.
PA (TANG/) TANG Y T.
PA (GHOS/) GHOSH M J.
PA (WANG/) WANG J.
PA (WANG/) WANG Z.
PA (ZHAO/) ZHAO Q.
PA (XUCC/) XU C.
PA (MULE/) MULERO J.
Query Match 13.4%; Score 60; DB 9; Length 482;
Best Local Similarity 29.3%; Pred. No. 6e+02;
RESULT 875
ID ABM68541 standard; protein; 920 AA.
DE Photorhabdus luminescens protein sequence #1638.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 13.4%; Score 60; DB 6; Length 920;

Best Local Similarity 29.8%; Pred. No. 1.4e+03;
RESULT 876
ID AAU30825 standard; protein; 962 AA.
DE Novel human secreted protein #1316.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.4%; Score 60; DB 4; Length 962;
Best Local Similarity 24.6%; Pred. No. 1.4e+03;
RESULT 877
ID AAU48592 standard; protein; 1341 AA.
DE Propionibacterium acnes immunogenic protein #9488.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 13.4%; Score 60; DB 4; Length 1341;
Best Local Similarity 26.5%; Pred. No. 2.2e+03;
RESULT 878
ID ABM45111 standard; protein; 1341 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #9787.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 13.4%; Score 60; DB 6; Length 1341;
Best Local Similarity 26.5%; Pred. No. 2.2e+03;
RESULT 879
ID ADL70800 standard; protein; 213 AA.
DE Anti-TNFalpha antibody VL region, SEQ ID 73.
PN WO2004020588-A2.
PD 11-MAR-2004.
PA (BIOR-) BIOREXIS PHARM CORP.
Query Match 13.3%; Score 59.5; DB 8; Length 213;
Best Local Similarity 28.8%; Pred. No. 2.5e+02;
RESULT 880
ID ABM84937 standard; protein; 225 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5186.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 13.3%; Score 59.5; DB 8; Length 225;
Best Local Similarity 32.1%; Pred. No. 2.6e+02;
RESULT 881
ID ABP63108 standard; protein; 384 AA.
DE FLO11 gene expression regulator At27.
PN WO200257456-A2.
PD 25-JUL-2002.
PA (MICR-) MICROBIA.
Query Match 13.3%; Score 59.5; DB 5; Length 384;
Best Local Similarity 57.1%; Pred. No. 5.2e+02;
RESULT 882
ID ABM85836 standard; protein; 393 AA.
DE Mouse protein sequence mCP13663.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 13.3%; Score 59.5; DB 7; Length 393;
Best Local Similarity 27.7%; Pred. No. 5.3e+02;
RESULT 883
ID AAB42218 standard; protein; 436 AA.
DE Human ORFX ORF1982 polypeptide sequence SEQ ID NO:3964.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 13.3%; Score 59.5; DB 3; Length 436;
Best Local Similarity 28.4%; Pred. No. 6.1e+02;
RESULT 884
ID AEA20121 standard; protein; 650 AA.
DE Novel human polypeptide SEQ ID NO 815.
PN WO2005049806-A2.
PD 02-JUN-2005.
PA (NUVE-) NUVELO INC.
Query Match 13.3%; Score 59.5; DB 9; Length 650;
Best Local Similarity 28.4%; Pred. No. 1e+03;
RESULT 885
ID ADZ84991 standard; protein; 668 AA.
DE Partial FHOS interacting protein, mAK044679(668).
PN US2005100966-A1.
PD 12-MAY-2005.
PA (SAKA/) SAKAMOTO T.
PA (TAKE/) TAKEDA S.
Query Match 13.3%; Score 59.5; DB 9; Length 668;
Best Local Similarity 28.4%; Pred. No. 1e+03;
RESULT 886
ID AEA20120 standard; protein; 725 AA.
DE Novel human polypeptide SEQ ID NO 814.
PN WO2005049806-A2.
PD 02-JUN-2005.
PA (NUVE-) NUVELO INC.
Query Match 13.3%; Score 59.5; DB 9; Length 725;
Best Local Similarity 28.4%; Pred. No. 1.1e+03;
RESULT 887
ID ADS44222 standard; protein; 821 AA.
DE Bacterial polypeptide #22652.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 13.3%; Score 59.5; DB 8; Length 821;
Best Local Similarity 28.9%; Pred. No. 1.3e+03;
RESULT 888
ID ABG79353 standard; protein; 884 AA.
DE Human GPCR15 protein.
PN WO200264793-A2.
PD 22-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 13.3%; Score 59.5; DB 5; Length 884;
Best Local Similarity 30.0%; Pred. No. 1.5e+03;
RESULT 889
ID AAM40399 standard; protein; 1150 AA.
DE Human polypeptide SEQ ID NO 3544.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.3%; Score 59.5; DB 4; Length 1150;
Best Local Similarity 28.4%; Pred. No. 2.1e+03;
RESULT 890
ID ADE59446 standard; protein; 1152 AA.
DE Human Protein XP_047123, SEQ ID NO 5341.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.3%; Score 59.5; DB 7; Length 1152;
Best Local Similarity 28.4%; Pred. No. 2.1e+03;
RESULT 891
ID AAY81947 standard; protein; 1330 AA.
DE Heterosigma akashiwo Na+-ATPase protein.
PN JP2000050874-A.
PD 22-FEB-2000.
PA (NORQ) NORINSUISANSHO KOKUSAI NORIN SUISANGYO.
Query Match 13.3%; Score 59.5; DB 3; Length 1330;
Best Local Similarity 25.9%; Pred. No. 2.5e+03;
RESULT 892
ID AEA20119 standard; protein; 1709 AA.
DE Novel human polypeptide SEQ ID NO 813.
PN WO2005049806-A2.
PD 02-JUN-2005.
PA (NUVE-) NUVELO INC.
Query Match 13.3%; Score 59.5; DB 9; Length 1709;
Best Local Similarity 28.4%; Pred. No. 3.4e+03;
RESULT 893
ID AEF41876 standard; protein; 1709 AA.
DE Human modifier of IGF (MIGF) trinucleotide repeat containing 6.

PN WO2006009947-A2.
PD 26-JAN-2006.
PA (EXEL-) EXELIXIS INC.
Query Match 13.3%; Score 59.5; DB 10; Length 1709;
Best Local Similarity 28.4%; Pred. No. 3.4e+03;
RESULT 894
ID ABU00419 standard; protein; 105 AA.
DE Human novel polypeptide #512.
PN WO200274961-A1.
PD 26-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 13.1%; Score 59; DB 6; Length 105;
Best Local Similarity 26.8%; Pred. No. 1.2e+02;
RESULT 895
ID ADD14077 standard; protein; 146 AA.
DE Human src biomarker polypeptide SEQ ID NO:266.
PN WO2003062395-A2.
PD 31-JUL-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 13.1%; Score 59; DB 7; Length 146;
Best Local Similarity 34.2%; Pred. No. 1.7e+02;
RESULT 896
ID ADD44869 standard; protein; 146 AA.
DE Human Protein O43169, SEQ ID NO 10300.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.1%; Score 59; DB 7; Length 146;
Best Local Similarity 34.2%; Pred. No. 1.7e+02;
RESULT 897
ID ADD47797 standard; protein; 146 AA.
DE Human Protein O43169, SEQ ID NO 13493.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.1%; Score 59; DB 7; Length 146;
Best Local Similarity 34.2%; Pred. No. 1.7e+02;
RESULT 898
ID ADD48851 standard; protein; 146 AA.
DE Human Protein O43169, SEQ ID NO 14562.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.1%; Score 59; DB 7; Length 146;
Best Local Similarity 34.2%; Pred. No. 1.7e+02;
RESULT 899
ID ADJ69511 standard; protein; 146 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1317.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 13.1%; Score 59; DB 7; Length 146;
Best Local Similarity 34.2%; Pred. No. 1.7e+02;
RESULT 900
ID ABM81767 standard; protein; 146 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO82609, SEQ:4554.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 59; DB 8; Length 146;
Best Local Similarity 34.2%; Pred. No. 1.7e+02;
RESULT 901
ID ADY14610 standard; protein; 146 AA.
DE PRO polypeptide SEQ ID NO 416.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 59; DB 9; Length 146;
Best Local Similarity 34.2%; Pred. No. 1.7e+02;
RESULT 902
ID AAB32861 standard; protein; 153 AA.
DE Eucalyptus grandis transcription factor protein sequence #319.
PN WO200053724-A2.
PD 14-SEP-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 13.1%; Score 59; DB 3; Length 153;
Best Local Similarity 31.9%; Pred. No. 1.9e+02;
RESULT 903
ID AAW74475 standard; protein; 155 AA.
DE Amino acid sequence of human Cytochrome B5.
PN WO9836071-A1.
PD 20-AUG-1998.
PA (INCY-) INCYTE PHARM INC.
Query Match 13.1%; Score 59; DB 2; Length 155;
Best Local Similarity 34.2%; Pred. No. 1.9e+02;
RESULT 904
ID AAG73876 standard; protein; 155 AA.
DE Human colon cancer antigen protein SEQ ID NO:4640.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.1%; Score 59; DB 4; Length 155;
Best Local Similarity 34.2%; Pred. No. 1.9e+02;
RESULT 905
ID ABP41469 standard; protein; 155 AA.
DE Human ovarian antigen HPDOC39, SEQ ID NO:2601.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.1%; Score 59; DB 5; Length 155;
Best Local Similarity 34.2%; Pred. No. 1.9e+02;
RESULT 906
ID ABR41609 standard; protein; 155 AA.
DE Human DITHP electron transfer-associated protein.
PN WO200297031-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 13.1%; Score 59; DB 6; Length 155;
Best Local Similarity 34.2%; Pred. No. 1.9e+02;
RESULT 907
ID AAB43457 standard; protein; 169 AA.
DE Human cancer associated protein sequence SEQ ID NO:902.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.1%; Score 59; DB 3; Length 169;
Best Local Similarity 34.2%; Pred. No. 2.1e+02;
RESULT 908
ID AAY08599 standard; protein; 214 AA.
DE Anti-human TNF-alpha monoclonal antibody L-chain protein.
PN JP11127855-A.
PD 18-MAY-1999.
PA (NIHA) JAPAN ENERGY CORP.
Query Match 13.1%; Score 59; DB 2; Length 214;
Best Local Similarity 28.4%; Pred. No. 2.8e+02;
RESULT 909
ID ADL70799 standard; protein; 214 AA.
DE Anti-TNFalpha antibody VL region, SEQ ID 72.
PN WO2004020588-A2.
PD 11-MAR-2004.
PA (BIOR-) BIOREXIS PHARM CORP.
Query Match 13.1%; Score 59; DB 8; Length 214;
Best Local Similarity 28.4%; Pred. No. 2.8e+02;
RESULT 910
ID AAB75036 standard; protein; 224 AA.
DE TRO005 HuMab kappa chain protein sequence 1CC8K.
PN WO200125492-A1.
PD 12-APR-2001.
PA (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
Query Match 13.1%; Score 59; DB 4; Length 224;

Best Local Similarity 28.4%; Pred. No. 3e+02;
RESULT 911
ID AAB75038 standard; protein; 224 AA.
DE TRO005 HuMab kappa chain protein sequence 1CE8K.
PN WO200125492-A1.
PD 12-APR-2001.
PA (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
Query Match 13.1%; Score 59; DB 4; Length 224;
Best Local Similarity 28.4%; Pred. No. 3e+02;
RESULT 912
ID AAB75034 standard; protein; 224 AA.
DE TRO005 HuMab kappa chain protein sequence 1CC2K.
PN WO200125492-A1.
PD 12-APR-2001.
PA (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
Query Match 13.1%; Score 59; DB 4; Length 224;
Best Local Similarity 28.4%; Pred. No. 3e+02;
RESULT 913
ID AAB75037 standard; protein; 224 AA.
DE TRO005 HuMab kappa chain protein sequence 1CD7K.
PN WO200125492-A1.
PD 12-APR-2001.
PA (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
Query Match 13.1%; Score 59; DB 4; Length 224;
Best Local Similarity 28.4%; Pred. No. 3e+02;
RESULT 914
ID AAB75039 standard; protein; 224 AA.
DE TRO005 HuMab kappa chain protein sequence 1CC6K.
PN WO200125492-A1.
PD 12-APR-2001.
PA (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
Query Match 13.1%; Score 59; DB 4; Length 224;
Best Local Similarity 28.4%; Pred. No. 3e+02;
RESULT 915
ID ADN04732 standard; protein; 227 AA.
DE Antipsoriatic protein sequence #547.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 59; DB 8; Length 227;
Best Local Similarity 33.3%; Pred. No. 3e+02;
RESULT 916
ID ADW18317 standard; protein; 246 AA.
DE Eucalyptus grandis transcription factor protein MYB family Seq 2104.
PN WO2005001050-A2.
PD 06-JAN-2005.
PA (ARBO-) ARBORGEN LLC.
Query Match 13.1%; Score 59; DB 9; Length 246;
Best Local Similarity 31.9%; Pred. No. 3.4e+02;
RESULT 917
ID ABB59849 standard; protein; 600 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 6339.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 13.1%; Score 59; DB 4; Length 600;
Best Local Similarity 21.9%; Pred. No. 1e+03;
RESULT 918
ID ABO78248 standard; protein; 641 AA.
DE Pseudomonas aeruginosa polypeptide #10423.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.1%; Score 59; DB 7; Length 641;
Best Local Similarity 31.6%; Pred. No. 1.1e+03;
RESULT 919
ID AAU74519 standard; protein; 1781 AA.
DE Lactobacillus reuteri glucosyltransferase A (gtfA) polypeptide.
PN WO200190372-A1.
PD 29-NOV-2001.
PA (NEDE) NEDERLANDSE ORG TOEGEPAST.
Query Match 13.1%; Score 59; DB 5; Length 1781;
Best Local Similarity 23.7%; Pred. No. 4.1e+03;
RESULT 920
ID ABG14083 standard; protein; 104 AA.
DE Novel human diagnostic protein #14074.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.0%; Score 58.5; DB 4; Length 104;
Best Local Similarity 30.0%; Pred. No. 1.3e+02;
RESULT 921
ID ADP74724 standard; protein; 137 AA.
DE Human porimin protein SEQ ID NO: 6.
PN WO2004047762-A2.
PD 10-JUN-2004.
PA (CHIR) CHIRON CORP.
Query Match 13.0%; Score 58.5; DB 8; Length 137;
Best Local Similarity 28.0%; Pred. No. 1.8e+02;
RESULT 922
ID AAB11523 standard; protein; 166 AA.
DE SEN virus protein fragment SEQ ID NO: 69.
PN WO200028039-A2.
PD 18-MAY-2000.
PA (DIAS-) DIASORIN SRL.
Query Match 13.0%; Score 58.5; DB 3; Length 166;
Best Local Similarity 24.4%; Pred. No. 2.3e+02;
RESULT 923
ID AAU14973 standard; protein; 177 AA.
DE Novel bone marrow polypeptide #179.
PN WO200155442-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.0%; Score 58.5; DB 4; Length 177;
Best Local Similarity 28.0%; Pred. No. 2.5e+02;
RESULT 924
ID AAG68168 standard; protein; 207 AA.
DE Zmax1 signaling pathway analysis bait protein.
PN WO200177327-A1.
PD 18-OCT-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.0%; Score 58.5; DB 4; Length 207;
Best Local Similarity 26.2%; Pred. No. 3.1e+02;
RESULT 925
ID ABR41135 standard; protein; 207 AA.
DE LRP5 related yeast two hybrid protein.
PN WO200292764-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 13.0%; Score 58.5; DB 6; Length 207;
Best Local Similarity 26.2%; Pred. No. 3.1e+02;
RESULT 926
ID ADB98802 standard; protein; 207 AA.
DE LRP5-related protein #9.
PN WO200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 13.0%; Score 58.5; DB 7; Length 207;
Best Local Similarity 26.2%; Pred. No. 3.1e+02;
RESULT 927
ID AAY66761 standard; protein; 208 AA.
DE Membrane-bound protein PRO1271.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 3; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 928
ID AAY94908 standard; protein; 208 AA.
DE Human secreted protein clone ci52_2 protein sequence SEQ ID NO:22.

PN WO200009552-A1.
PD 24-FEB-2000.
PA (GEMY) GENETICS INST INC.
Query Match 13.0%; Score 58.5; DB 3; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 929
ID AAE06585 standard; protein; 208 AA.
DE Human protein having hydrophobic domain, HP10753.
PN WO200149728-A2.
PD 12-JUL-2001.
PA (PROT-) PROTEGENE INC.
PA (SAGA) SAGAMI CHEM RES CENT.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 930
ID AAU12426 standard; protein; 208 AA.
DE Human PRO1271 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 931
ID AAU14891 standard; protein; 208 AA.
DE Novel bone marrow polypeptide #97.
PN WO200155442-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 932
ID AAE01725 standard; protein; 208 AA.
DE Human gene 12 encoded secreted protein HNTAC64, SEQ ID NO:137.
PN WO200134767-A2.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 933
ID AAE01683 standard; protein; 208 AA.
DE Human gene 12 encoded secreted protein HNTAC64, SEQ ID NO:95.
PN WO200134767-A2.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 934
ID AAE01724 standard; protein; 208 AA.
DE Human gene 12 encoded secreted protein HNTAC64, SEQ ID NO:136.
PN WO200134767-A2.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 935
ID AAE01723 standard; protein; 208 AA.
DE Human gene 12 encoded secreted protein HNTAC64, SEQ ID NO:135.
PN WO200134767-A2.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 936
ID AAE03766 standard; protein; 208 AA.
DE Human gene 3 encoded secreted protein HNTAC64, SEQ ID NO:36.
PN WO200132837-A1.
PD 10-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 937
ID AAB88375 standard; protein; 208 AA.
DE Human membrane or secretory protein clone PSEC0111.
PN EP1067182-A2.
PD 10-JAN-2001.
PA (HELI-) HELIX RES INST.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 938
ID AAG81329 standard; protein; 208 AA.
DE Human AFP protein sequence SEQ ID NO:176.
PN WO200129221-A2.
PD 26-APR-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 939
ID AAB50924 standard; protein; 208 AA.
DE Human PRO1271 protein.
PN WO200073452-A2.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 940
ID AAB65284 standard; protein; 208 AA.
DE Human PRO1271 (UNQ641) protein sequence SEQ ID NO:416.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 941
ID ABG63986 standard; protein; 208 AA.
DE Human albumin fusion protein #661.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 5; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 942
ID ABG63987 standard; protein; 208 AA.
DE Human albumin fusion protein #662.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 5; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 943
ID ABG63985 standard; protein; 208 AA.
DE Human albumin fusion protein #660.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 5; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 944
ID ABG65496 standard; protein; 208 AA.
DE Human albumin fusion protein #2171.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 5; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 945
ID ABG63988 standard; protein; 208 AA.
DE Human albumin fusion protein #663.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 5; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 946
ID ABU58099 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2003027163-A1.

PD 06-FEB-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 947
ID ABU59177 standard; protein; 208 AA.
DE Novel human secreted or transmembrane protein PRO1271.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 948
ID ABU82689 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 949
ID ABO17870 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 950
ID ABU60608 standard; protein; 208 AA.
DE Human secreted/transmembrane protein, #167.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 951
ID ABU13990 standard; protein; 208 AA.
DE Human PRO1271 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 952
ID ABU81124 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 953
ID ABU72575 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 954
ID ABU66824 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 955
ID ABU59905 standard; protein; 208 AA.
DE Novel secreted and transmembrane protein PRO1271.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 956
ID ABU59324 standard; protein; 208 AA.
DE Human secreted/transmembrane protein, #167.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 957
ID ABO26021 standard; protein; 208 AA.
DE Human PRO1271 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 958
ID ABO25095 standard; protein; 208 AA.
DE Human secreted/transmembrane protein (PRO) #255.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 959
ID ABU59030 standard; protein; 208 AA.
DE Human sectreted/transmembrane protein, #167.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 960
ID ABU92408 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 961
ID ABU59473 standard; protein; 208 AA.
DE Novel human secreted or transmembrane protein PRO1375.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 962
ID ABU67100 standard; protein; 208 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 510.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 963
ID ABU92239 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 964
ID ABU10945 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 965
ID ABU81697 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2002177164-A1.

PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 966
ID ABU88636 standard; protein; 208 AA.
DE Human secreted and transmembrane polypeptide PRO1271.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 967
ID ABO34150 standard; protein; 208 AA.
DE Human PRO1271 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 968
ID ADA46029 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 969
ID ADA76460 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 970
ID ADA19110 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 971
ID ADA61733 standard; protein; 208 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 972
ID ADB19518 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 973
ID ADB28059 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 974
ID ADA86538 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 975
ID ADB16102 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 976
ID ADA37927 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 977
ID ADA47888 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 978
ID ADA21613 standard; protein; 208 AA.
DE Human secreted/transmembrane polypeptide PRO1271.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 979
ID ADA10400 standard; protein; 208 AA.
DE Human secreted/transmembrane protein, PRO1271.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 980
ID ADA67683 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 981
ID ADB30690 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 982
ID ADA85986 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 983
ID ADA17944 standard; protein; 208 AA.
DE Human PRO1271 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 984
ID ADA97198 standard; protein; 208 AA.

DE Human PRO polypeptide #255.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 985
ID ADA79502 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 986
ID ADA87641 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 987
ID ADB16843 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 988
ID ADA28052 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 989
ID ADA91935 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 990
ID ADB14998 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 991
ID ADB18959 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 992
ID ADA94174 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 993
ID ADB20070 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 994
ID ADB13382 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 995
ID ABO43403 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 996
ID ADA94632 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 997
ID ADA74636 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 998
ID ADB24869 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 999
ID ADA82393 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1000
ID ADA75356 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1001
ID ADA85434 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1002
ID ADA84882 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;

RESULT 1003
ID ADB30138 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;

RESULT 1004
ID ADA80666 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;

RESULT 1005
ID ADA75908 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;

RESULT 1006
ID ADA38857 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;

RESULT 1007
ID ADA47133 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;

RESULT 1008
ID ADB25429 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;

RESULT 1009
ID ADA93605 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;

RESULT 1010
ID ADB26955 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;

RESULT 1011
ID ADB31242 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;

RESULT 1012
ID ADA92978 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;

RESULT 1013
ID ADA61170 standard; protein; 208 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;

RESULT 1014
ID ADB24317 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;

RESULT 1015
ID ADA96646 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;

RESULT 1016
ID ADA81218 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;

RESULT 1017
ID ADA96094 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;

RESULT 1018
ID ADB26403 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;

RESULT 1019
ID ADB21888 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;

RESULT 1020
ID ADA77667 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;

RESULT 1021
ID ADB18407 standard; protein; 208 AA.

DE Human PRO polypeptide #255.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1022
ID ADA87090 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1023
ID ADA88193 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1024
ID ADA46581 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1025
ID ADB28611 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1026
ID ADB29163 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1027
ID ABO53236 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1028
ID ADA77115 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1029
ID ADA22539 standard; protein; 208 AA.
DE Human secreted/transmembrane polypeptide PRO1271.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1030
ID ADA88745 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1031
ID ADA97750 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1032
ID ADB27507 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1033
ID ADB22440 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1034
ID ABO22606 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1035
ID ADA06705 standard; protein; 208 AA.
DE Human secreted/transmembrane PRO polypeptide #131.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1036
ID ADA39398 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1037
ID ADA67131 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1038
ID ADB22992 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1039
ID ADB23765 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1040
ID ADA92487 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.

PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1041
ID ADB15550 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1042
ID ADB38802 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1043
ID ADB96424 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1044
ID ADB38250 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1045
ID ADB66722 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1046
ID ADB89802 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1047
ID ADB90534 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1048
ID ADB39635 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1049
ID ADB47258 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1050
ID ADB86865 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1051
ID ADB77470 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1052
ID ADB34627 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1053
ID ADB35731 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1054
ID ADB34075 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1055
ID ADB35179 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1056
ID ADB36283 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1057
ID ADB46678 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1058
ID ADC57896 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;

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  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1059
ID   ADC55260 standard; protein; 208 AA.
DE   Human PRO polypeptide #131.
PN   US2003045463-A1.
PD   06-MAR-2003.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1060
ID   ADC12127 standard; protein; 208 AA.
DE   Human secreted/transmembrane protein PRO1271.
PN   US2003049681-A1.
PD   13-MAR-2003.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1061
ID   ADC56549 standard; protein; 208 AA.
DE   Human PRO polypeptide #131.
PN   US2003064375-A1.
PD   03-APR-2003.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1062
ID   ADC07604 standard; protein; 208 AA.
DE   Human secreted/transmembrane protein PRO1271.
PN   US2003068647-A1.
PD   10-APR-2003.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1063
ID   ADC11594 standard; protein; 208 AA.
DE   Human secreted/transmembrane protein PRO1271.
PN   US2003069403-A1.
PD   10-APR-2003.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1064
ID   ADC50551 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003092106-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1065
ID   ADC72098 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003092107-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1066
ID   ADC60077 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003092105-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1067
ID   ADC53084 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein Seq ID510.
PN   US2003087365-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1068
ID   ADC57438 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein Seq ID510.
PN   US2003087366-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1069
ID   ADC60629 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003087367-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1070
ID   ADC51104 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003087361-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1071
ID   ADC65631 standard; protein; 208 AA.
DE   Human PRO polypeptide #255.
PN   US2003087362-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1072
ID   ADC54729 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein Seq ID510.
PN   US2003087363-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1073
ID   ADC53690 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein Seq ID510.
PN   US2003087364-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1074
ID   ADC59213 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein Seq ID510.
PN   US2003087359-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1075
ID   ADC56091 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein Seq ID510.
PN   US2003087360-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1076
ID   ADC58661 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein Seq ID510.
PN   US2003087346-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1077
ID   ADC14716 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003082546-A1.
PD   01-MAY-2003.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
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  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1078
ID   ADD08248 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003068623-A1.
PD   10-APR-2003.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1079
ID   ADD03335 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003092104-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1080
ID   ADC90327 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003087348-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1081
ID   ADC82073 standard; protein; 208 AA.
DE   Human PRO polypeptide #131.
PN   US2003083461-A1.
PD   01-MAY-2003.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1082
ID   ADC69746 standard; protein; 208 AA.
DE   Human PRO polypeptide #255.
PN   US2003194770-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1083
ID   ADC48635 standard; protein; 208 AA.
DE   Human PRO polypeptide #255.
PN   US2003194773-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1084
ID   ADD10164 standard; protein; 208 AA.
DE   Human PRO polypeptide #255.
PN   US2003194776-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1085
ID   ADD07715 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2002193299-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1086
ID   ADD04739 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003087354-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1087
ID   ADC82606 standard; protein; 208 AA.
DE   Human PRO polypeptide #131.
PN   US2003059833-A1.
PD   27-MAR-2003.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1088
ID   ADC80695 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003092103-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1089
ID   ADD11202 standard; protein; 208 AA.
DE   Human PRO polypeptide #255.
PN   US2003194774-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1090
ID   ADC48083 standard; protein; 208 AA.
DE   Human PRO polypeptide #255.
PN   US2003194771-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1091
ID   ADD08786 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003073090-A1.
PD   17-APR-2003.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1092
ID   ADC80143 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003087358-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1093
ID   ADD07035 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2002193300-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1094
ID   ADD09612 standard; protein; 208 AA.
DE   Human PRO polypeptide #255.
PN   US2003194775-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1095
ID   ADC83282 standard; protein; 208 AA.
DE   Human PRO polypeptide #131.
PN   US2003059783-A1.
PD   27-MAR-2003.
  Query Match             13.0%;  Score 58.5;  DB 7;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1096
ID   ADD41325 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003203438-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
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Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1097
ID ADD52464 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1098
ID ADD53204 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1099
ID ADD53756 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1100
ID ADD55389 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1101
ID ADD56347 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1102
ID ADD51912 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1103
ID ADD02711 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1104
ID ADD02145 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1105
ID ADD54327 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1106
ID ADD54785 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1107
ID ADD92644 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1108
ID ADD91540 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1109
ID ADE04154 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1110
ID ADE26939 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1111
ID ADE32451 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1112
ID ADE22383 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1113
ID ADD79607 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1114
ID ADE42143 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1115
ID ADE17960 standard; protein; 208 AA.
DE Human PRO polypeptide #255.

PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1116
ID ADD92092 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1117
ID ADE33555 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1118
ID ADE34107 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1119
ID ADD80159 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1120
ID ADD93196 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1121
ID ADE19616 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1122
ID ADE19064 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1123
ID ADE43260 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1124
ID ADD96049 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1125
ID ADE22935 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1126
ID ADD79053 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1127
ID ADE26406 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1128
ID ADE33003 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1129
ID ADE42695 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1130
ID ADD80711 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1131
ID ADD89739 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1132
ID ADE41023 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1133
ID ADE04822 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1134
ID ADF60236 standard; protein; 208 AA.
DE Human contig polypeptide sequence SEQ ID NO:2603.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1135
ID ADE92951 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1136
ID ADF67343 standard; protein; 208 AA.
DE Human PRO1271 amino acid sequence SEQ ID NO:416.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1137
ID ADG21660 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1138
ID ADG23301 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1139
ID ADF97636 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1140
ID ADG80700 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1141
ID ADG80148 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1142
ID ADH55440 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1143
ID ADH55992 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1144
ID ADI35597 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1145
ID ADI64211 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1146
ID ADI65160 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1147
ID ADI63659 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1148
ID ADH82073 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1149
ID ADI00090 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1150
ID ADH81521 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1151
ID ADM82690 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1152
ID ADN16089 standard; protein; 208 AA.

DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1153
ID ADN16718 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1154
ID ADN15537 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1155
ID ADN14985 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1156
ID ADC81247 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1157
ID ADD76695 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1158
ID ADD88059 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1159
ID ADD86463 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1160
ID ADE75911 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1161
ID ADE23487 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1162
ID ADE24039 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1163
ID ADE24682 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1164
ID ADD87507 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1165
ID ADE89373 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1166
ID ADE18512 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1167
ID ADE88821 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1168
ID ADE94841 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1169
ID ADE91252 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1170
ID ADF35542 standard; protein; 208 AA.
DE Human PRO1271 polypeptide.
PN US2003194760-A1.

PD 16-OCT-2003.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1171
ID ADE95393 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1172
ID ADE93503 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1173
ID ADF35084 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1174
ID ADE92399 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1175
ID ADE90700 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1176
ID ADE91847 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1177
ID ADG11792 standard; protein; 208 AA.
DE Human PRO1271 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1178
ID ADG02426 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1179
ID ADG22212 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1180
ID ADG20282 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1181
ID ADF98188 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1182
ID ADG24405 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1183
ID ADF98759 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1184
ID ADG03590 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1185
ID ADF99311 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1186
ID ADG16896 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1187
ID ADG05355 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1188
ID ADG19622 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;

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  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1189
ID   ADG13459 standard; protein; 208 AA.
DE   Human PRO polypeptide #255.
PN   US2003207357-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1190
ID   ADG08516 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003207424-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1191
ID   ADG15686 standard; protein; 208 AA.
DE   Human PRO polypeptide #255.
PN   US2003219885-A1.
PD   27-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1192
ID   ADF97084 standard; protein; 208 AA.
DE   Human PRO polypeptide #255.
PN   US2003207371-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1193
ID   ADG06269 standard; protein; 208 AA.
DE   Human PRO polypeptide #255.
PN   US2003207374-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1194
ID   ADG23853 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003207389-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1195
ID   ADG04142 standard; protein; 208 AA.
DE   Human PRO polypeptide #255.
PN   US2003207423-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1196
ID   ADG25043 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003207427-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1197
ID   ADG07340 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003207350-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1198
ID   ADG07892 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003207356-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1199
ID   ADG55387 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003194778-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1200
ID   ADG61051 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003207390-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1201
ID   ADG62155 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003207428-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1202
ID   ADG82356 standard; protein; 208 AA.
DE   Human PRO polypeptide #255.
PN   US2003207358-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1203
ID   ADG57595 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003207362-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1204
ID   ADG57043 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003207364-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1205
ID   ADG55939 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003207365-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1206
ID   ADG58699 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003207368-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1207
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ID   ADG71065 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003207420-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1208
ID   ADG58147 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003207363-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1209
ID   ADG53731 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003207415-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1210
ID   ADG71617 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003207421-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1211
ID   ADG81804 standard; protein; 208 AA.
DE   Human PRO polypeptide #255.
PN   US2003207805-A1.
PD   06-NOV-2003.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1212
ID   ADH19662 standard; protein; 208 AA.
DE   Human secreted/transmembrane protein PRO1271.
PN   US2003228656-A1.
PD   11-DEC-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1213
ID   ADH30766 standard; protein; 208 AA.
DE   Human PRO polypeptide #255.
PN   US2003077723-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1214
ID   ADH12133 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003207419-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1215
ID   ADG52555 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003207414-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1216
ID   ADG54283 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003207416-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1217
ID   ADG81252 standard; protein; 208 AA.
DE   Human PRO polypeptide #255.
PN   US2003194793-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1218
ID   ADG56491 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003207366-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1219
ID   ADH12757 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003207378-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1220
ID   ADH21155 standard; protein; 208 AA.
DE   Human secreted/transmembrane protein PRO1271.
PN   US2003224358-A1.
PD   04-DEC-2003.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1221
ID   ADG61603 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003207429-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1222
ID   ADH20195 standard; protein; 208 AA.
DE   Human secreted/transmembrane protein PRO1271.
PN   US2003219856-A1.
PD   27-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1223
ID   ADH28690 standard; protein; 208 AA.
DE   Human PRO polypeptide #255.
PN   US2003022331-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1224
ID   ADG54835 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003207367-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           13.0%;  Score 58.5;  DB 8;  Length 208;
  Best Local Similarity   28.0%;  Pred. No. 3.1e+02;
RESULT 1225
ID   ADG59875 standard; protein; 208 AA.
DE   Novel human secreted and transmembrane protein PRO1271.
PN   US2003207369-A1.
PD   06-NOV-2003.
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PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1226
ID ADI81299 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1227
ID ADG10042 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1228
ID ADI15513 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1229
ID ADG09390 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1230
ID ADI14845 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1231
ID ADI18440 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1232
ID ADJ63721 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1233
ID ADL77250 standard; protein; 208 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 732.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1234
ID ADL77251 standard; protein; 208 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 733.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1235
ID ADL77253 standard; protein; 208 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 735.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1236
ID ADL77252 standard; protein; 208 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 734.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1237
ID ADL78763 standard; protein; 208 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 2245.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1238
ID ADJ77616 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1239
ID ADJ65738 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1240
ID ADM27874 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1241
ID ADM42598 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1242
ID ADM28460 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1243
ID ADP07778 standard; protein; 208 AA.

DE Human secreted protein, seq id 261.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1244
ID ADP74722 standard; protein; 208 AA.
DE Human porimin protein SEQ ID NO: 4.
PN WO2004047762-A2.
PD 10-JUN-2004.
PA (CHIR) CHIRON CORP.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1245
ID ADI95942 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1246
ID ADI96494 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1247
ID ADS32446 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1248
ID ADT03430 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1249
ID ADY63115 standard; protein; 208 AA.
DE Human clone PSEC0111 protein, SEQ ID 118.
PN EP1514933-A1.
PD 16-MAR-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 13.0%; Score 58.5; DB 9; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1250
ID ADZ03481 standard; protein; 208 AA.
DE Human secreted/transmembrane PRO1271 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 9; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1251
ID AEA38633 standard; protein; 208 AA.
DE Human secreted/transmembrane protein, #199.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 9; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1252
ID AEB14227 standard; protein; 208 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 510.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 13.0%; Score 58.5; DB 9; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1253
ID AED86425 standard; protein; 208 AA.
DE Human PRO amino acid sequence, seq id 510.
PN US2005245730-A1.
PD 03-NOV-2005.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 9; Length 208;
Best Local Similarity 28.0%; Pred. No. 3.1e+02;
RESULT 1254
ID ABM84936 standard; protein; 225 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5185.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 13.0%; Score 58.5; DB 8; Length 225;
Best Local Similarity 30.4%; Pred. No. 3.4e+02;
RESULT 1255
ID ABM84934 standard; protein; 225 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5183.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 13.0%; Score 58.5; DB 8; Length 225;
Best Local Similarity 30.4%; Pred. No. 3.4e+02;
RESULT 1256
ID ADI17268 standard; protein; 230 AA.
DE Polypeptide homologous to a human NOVX domain SeqID 804.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 13.0%; Score 58.5; DB 5; Length 230;
Best Local Similarity 24.6%; Pred. No. 3.5e+02;
RESULT 1257
ID ADI17276 standard; protein; 230 AA.
DE Polypeptide homologous to a human NOVX domain SeqID 812.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 13.0%; Score 58.5; DB 5; Length 230;
Best Local Similarity 24.6%; Pred. No. 3.5e+02;
RESULT 1258
ID ADJ83075 standard; protein; 230 AA.
DE Trypsin-like serine protease protein - SEQ ID 66.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (LEPL/) LEPLEY D M.

PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match 13.0%; Score 58.5; DB 7; Length 230;
Best Local Similarity 24.6%; Pred. No. 3.5e+02;
RESULT 1259
ID AEF27705 standard; protein; 230 AA.
DE Trypsin-like serine protease consensus sequence, SEQ:135.
PN US2006009634-A1.
PD 12-JAN-2006.
PA (KEKU/) KEKUDA R.
PA (ALSO/) ALSOBROOK J.
PA (TCHE/) TCHERNEV V.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K.
PA (PATT/) PATTURAJAN M.
PA (GROS/) GROSSE W.
PA (LEPL/) LEPLEY D.
PA (BURG/) BURGESS C.
PA (VERN/) VERNET C.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (EDIN/) EDINGER S.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U.
PA (ROTH/) ROTHENBERG M.
PA (STON/) STONE D.
PA (BOLD/) BOLDOG F.
PA (GUOX/) GUO X.
PA (SHEN/) SHENOY S.
PA (ANDE/) ANDERSON D.
PA (PADI/) PADIGARU M.
PA (TAUP/) TAUPIER R.
PA (MILL/) MILLER C.
PA (EISE/) EISEN A.
Query Match 13.0%; Score 58.5; DB 10; Length 230;
Best Local Similarity 24.6%; Pred. No. 3.5e+02;
RESULT 1260
ID ABB69469 standard; protein; 276 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 35199.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 13.0%; Score 58.5; DB 4; Length 276;
Best Local Similarity 26.1%; Pred. No. 4.4e+02;
RESULT 1261
ID ADW17748 standard; protein; 288 AA.
DE Pinus radiata transcription factor protein MYB family Seq 1522.
PN WO2005001050-A2.
PD 06-JAN-2005.
PA (ARBO-) ARBORGEN LLC.
Query Match 13.0%; Score 58.5; DB 9; Length 288;
Best Local Similarity 25.3%; Pred. No. 4.7e+02;
RESULT 1262
ID ADM03974 standard; protein; 302 AA.
DE Human protein of the invention SEQ ID NO:2659.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 13.0%; Score 58.5; DB 7; Length 302;
Best Local Similarity 29.4%; Pred. No. 5e+02;
RESULT 1263
ID AEC86904 standard; protein; 302 AA.
DE Human cDNA clone protein BRAMY10001570, SEQ ID 2659.
PN EP1580263-A1.
PD 28-SEP-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 13.0%; Score 58.5; DB 9; Length 302;
Best Local Similarity 29.4%; Pred. No. 5e+02;
RESULT 1264
ID ADE55614 standard; protein; 328 AA.
DE Rat Protein CAA08796, SEQ ID NO 1433.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.0%; Score 58.5; DB 7; Length 328;
Best Local Similarity 30.5%; Pred. No. 5.5e+02;
RESULT 1265
ID ADE55610 standard; protein; 328 AA.
DE Rat Protein CAA08796, SEQ ID NO 1429.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.0%; Score 58.5; DB 7; Length 328;
Best Local Similarity 30.5%; Pred. No. 5.5e+02;
RESULT 1266
ID AAG47665 standard; protein; 330 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 60101.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 13.0%; Score 58.5; DB 3; Length 330;
Best Local Similarity 36.0%; Pred. No. 5.6e+02;
RESULT 1267
ID ABB63026 standard; protein; 357 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15870.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 13.0%; Score 58.5; DB 4; Length 357;
Best Local Similarity 29.3%; Pred. No. 6.1e+02;
RESULT 1268
ID ADR20443 standard; protein; 374 AA.
DE Trichinella spiralis serine protease protein fragment 1.
PN JP2004229599-A.
PD 19-AUG-2004.
PA (GIFU-) UNIV GIFU.
Query Match 13.0%; Score 58.5; DB 8; Length 374;
Best Local Similarity 25.0%; Pred. No. 6.5e+02;
RESULT 1269
ID ADR20442 standard; protein; 421 AA.
DE Full length Trichinella spiralis serine protease protein.
PN JP2004229599-A.
PD 19-AUG-2004.
PA (GIFU-) UNIV GIFU.
Query Match 13.0%; Score 58.5; DB 8; Length 421;
Best Local Similarity 25.0%; Pred. No. 7.6e+02;
RESULT 1270
ID ADW17284 standard; protein; 494 AA.
DE Eucalyptus grandis transcription factor protein GRAS family Seq 1035.
PN WO2005001050-A2.
PD 06-JAN-2005.
PA (ARBO-) ARBORGEN LLC.
Query Match 13.0%; Score 58.5; DB 9; Length 494;
Best Local Similarity 25.0%; Pred. No. 9.2e+02;
RESULT 1271
ID ABM88793 standard; protein; 1161 AA.
DE Rice abiotic stress responsive polypeptide SEQ ID NO:7039.

PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 13.0%; Score 58.5; DB 7; Length 1161;
Best Local Similarity 27.7%; Pred. No. 2.7e+03;
RESULT 1272
ID AAW83310 standard; protein; 1451 AA.
DE LRP5 protein from isoform 2 (also isoform 4,5,6).
PN WO9846743-A1.
PD 22-OCT-1998.
PA (WELL) WELLCOME TRUST LTD.
PA (MERI) MERCK & CO INC.
Query Match 13.0%; Score 58.5; DB 2; Length 1451;
Best Local Similarity 26.2%; Pred. No. 3.6e+03;
RESULT 1273
ID ADC86833 standard; protein; 1494 AA.
DE Human GPCR protein SEQ ID NO:1286.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 13.0%; Score 58.5; DB 7; Length 1494;
Best Local Similarity 26.2%; Pred. No. 3.7e+03;
RESULT 1274
ID AAW83308 standard; protein; 1591 AA.
DE Mature LRP5 protein.
PN WO9846743-A1.
PD 22-OCT-1998.
PA (WELL) WELLCOME TRUST LTD.
PA (MERI) MERCK & CO INC.
Query Match 13.0%; Score 58.5; DB 2; Length 1591;
Best Local Similarity 26.2%; Pred. No. 4e+03;
RESULT 1275
ID AAW83309 standard; protein; 1615 AA.
DE LRP5 protein from the longest open reading frame.
PN WO9846743-A1.
PD 22-OCT-1998.
PA (WELL) WELLCOME TRUST LTD.
PA (MERI) MERCK & CO INC.
Query Match 13.0%; Score 58.5; DB 2; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1276
ID AAG68169 standard; protein; 1615 AA.
DE Human Zmax1 protein SEQ ID NO:3.
PN WO200177327-A1.
PD 18-OCT-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.0%; Score 58.5; DB 4; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1277
ID AAG68170 standard; protein; 1615 AA.
DE Human HBM protein SEQ ID NO:4.
PN WO200177327-A1.
PD 18-OCT-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.0%; Score 58.5; DB 4; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1278
ID AAE21740 standard; protein; 1615 AA.
DE Human BSMR protein mutant, R494Q.
PN WO200216553-A2.
PD 28-FEB-2002.
PA (AVET) AVENTIS PHARMA SA.
PA (HARD) HARVARD COLLEGE.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 13.0%; Score 58.5; DB 5; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1279
ID AAE21741 standard; protein; 1615 AA.
DE Human BSMR protein mutant, A1330L.
PN WO200216553-A2.
PD 28-FEB-2002.
PA (AVET) AVENTIS PHARMA SA.
PA (HARD) HARVARD COLLEGE.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 13.0%; Score 58.5; DB 5; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1280
ID AAE21730 standard; protein; 1615 AA.
DE Human bone strength and mineralisation regulatory protein (BSMR).
PN WO200216553-A2.
PD 28-FEB-2002.
PA (AVET) AVENTIS PHARMA SA.
PA (HARD) HARVARD COLLEGE.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 13.0%; Score 58.5; DB 5; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1281
ID AAU80879 standard; protein; 1615 AA.
DE Human Zmax1 polypeptide.
PN WO200192891-A2.
PD 06-DEC-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
Query Match 13.0%; Score 58.5; DB 5; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1282
ID AAU80880 standard; protein; 1615 AA.
DE Human high bone mass (HBM) polypeptide.
PN WO200192891-A2.
PD 06-DEC-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
Query Match 13.0%; Score 58.5; DB 5; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1283
ID ABR41093 standard; protein; 1615 AA.
DE Human wild-type LRP5.
PN WO200292764-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 13.0%; Score 58.5; DB 6; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1284
ID ABR41094 standard; protein; 1615 AA.
DE Human LRP5 allelic variant HBM.
PN WO200292764-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 13.0%; Score 58.5; DB 6; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1285
ID ABR41131 standard; protein; 1615 AA.
DE Human LRP5 protein.
PN WO200292764-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 13.0%; Score 58.5; DB 6; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1286
ID ADB98058 standard; protein; 1615 AA.
DE Human LRP5.
PN WO200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 13.0%; Score 58.5; DB 7; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1287
ID ADB98798 standard; protein; 1615 AA.
DE Human Zmax1(LRP5).
PN WO200292000-A2.
PD 21-NOV-2002.

PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 13.0%; Score 58.5; DB 7; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1288
ID ADB98059 standard; protein; 1615 AA.
DE LRP5 mutein.
PN WO200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 13.0%; Score 58.5; DB 7; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1289
ID ADE82428 standard; protein; 1615 AA.
DE Human HBM gene.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 13.0%; Score 58.5; DB 7; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1290
ID ADE82427 standard; protein; 1615 AA.
DE Human Zmax1 gene.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 13.0%; Score 58.5; DB 7; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1291
ID ADI27181 standard; protein; 1615 AA.
DE Human LRP binding family protein #12.
PN WO2003106657-A2.
PD 24-DEC-2003.
PA (STOW-) STOWERS INST MEDICAL RES.
Query Match 13.0%; Score 58.5; DB 8; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1292
ID ADQ20524 standard; protein; 1615 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3344.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 13.0%; Score 58.5; DB 8; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1293
ID ADR17561 standard; protein; 1615 AA.
DE Human high bone mass gene, HBM allele, protein #2.
PN US6780609-B1.
PD 24-AUG-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.0%; Score 58.5; DB 8; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1294
ID ADR16921 standard; protein; 1615 AA.
DE Human high bone mass gene, wild type allele Zmax1, protein #1.
PN US6780609-B1.
PD 24-AUG-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.0%; Score 58.5; DB 8; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1295
ID ADR17560 standard; protein; 1615 AA.
DE Human high bone mass gene, wild type allele Zmax1, protein #2.
PN US6780609-B1.
PD 24-AUG-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.0%; Score 58.5; DB 8; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1296
ID ADR16922 standard; protein; 1615 AA.
DE Human high bone mass gene, HBM allele, protein #1.
PN US6780609-B1.
PD 24-AUG-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.0%; Score 58.5; DB 8; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1297
ID ABO84659 standard; protein; 1615 AA.
DE Human cancer-associated protein HP20-001.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 13.0%; Score 58.5; DB 8; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1298
ID ADR47572 standard; protein; 1615 AA.
DE Human high bone mass gene, wild type allele Zmax1, protein #1.
PN US2004176582-A1.
PD 09-SEP-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON.
Query Match 13.0%; Score 58.5; DB 8; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1299
ID ADR48212 standard; protein; 1615 AA.
DE Human high bone mass gene, HBM allele, protein #2.
PN US2004176582-A1.
PD 09-SEP-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON.
Query Match 13.0%; Score 58.5; DB 8; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1300
ID ADR47573 standard; protein; 1615 AA.
DE Human high bone mass gene, HBM allele, protein #1.
PN US2004176582-A1.
PD 09-SEP-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON.
Query Match 13.0%; Score 58.5; DB 8; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1301
ID ADR48211 standard; protein; 1615 AA.
DE Human high bone mass gene, wild type allele Zmax1, protein #2.
PN US2004176582-A1.
PD 09-SEP-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON.
Query Match 13.0%; Score 58.5; DB 8; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1302
ID ADR73482 standard; protein; 1615 AA.
DE Human low density lipoprotein receptor-related protein 5, LRP5, protein.
PN WO2004076682-A2.
PD 10-SEP-2004.
PA (SURR-) SURROMED INC.
Query Match 13.0%; Score 58.5; DB 8; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1303
ID ADV97195 standard; protein; 1615 AA.
DE Human low density lipoprotein receptor-related protein 5 (LRP5), SEQ:50.
PN US2005003390-A1.
PD 06-JAN-2005.
PA (AXEN/) AXENOVICH S A.
PA (STUL/) STULL R.
PA (GELM/) GELMAN M.
PA (CHUI/) CHUI K.
PA (NGDD/) NG D.
Query Match 13.0%; Score 58.5; DB 9; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1304
ID AEB69940 standard; protein; 1615 AA.
DE Human High Bone Mass gene, wild type allele Zmax1 protein.

PN US2005142617-A1.
PD 30-JUN-2005.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
Query Match 13.0%; Score 58.5; DB 9; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1305
ID AEB69301 standard; protein; 1615 AA.
DE Human High Bone Mass gene, wild type allele Zmax1 protein, SEQ ID 3.
PN US2005142617-A1.
PD 30-JUN-2005.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
Query Match 13.0%; Score 58.5; DB 9; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1306
ID AEB69302 standard; protein; 1615 AA.
DE Human High Bone Mass gene, mutant allele HBM protein, SEQ ID 4.
PN US2005142617-A1.
PD 30-JUN-2005.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
Query Match 13.0%; Score 58.5; DB 9; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1307
ID AED95409 standard; protein; 1615 AA.
DE Human LRP5 protein SEQ ID NO:80.
PN US2005261189-A1.
PD 24-NOV-2005.
PA (HYDR-) HYDRA BIOSCIENCES INC.
Query Match 13.0%; Score 58.5; DB 10; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1308
ID AEF80276 standard; protein; 1615 AA.
DE Human LRP5 protein sequence.
PN WO2006015373-A2.
PD 09-FEB-2006.
PA (AMGE-) AMGEN INC.
Query Match 13.0%; Score 58.5; DB 10; Length 1615;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1309
ID ABM85665 standard; protein; 1627 AA.
DE Human protein sequence hCP1690976.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 13.0%; Score 58.5; DB 7; Length 1627;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1310
ID ABO84660 standard; protein; 1627 AA.
DE Human cancer-associated protein HP20-001.2.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 13.0%; Score 58.5; DB 8; Length 1627;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1311
ID AAW83311 standard; protein; 1639 AA.
DE LRP5 isoform 3 protein.
PN WO9846743-A1.
PD 22-OCT-1998.
PA (WELL) WELLCOME TRUST LTD.
PA (MERI) MERCK & CO INC.
Query Match 13.0%; Score 58.5; DB 2; Length 1639;
Best Local Similarity 26.2%; Pred. No. 4.2e+03;
RESULT 1312
ID ABR41133 standard; protein; 1665 AA.
DE Human LRP5 protein.
PN WO200292764-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 13.0%; Score 58.5; DB 6; Length 1665;
Best Local Similarity 26.2%; Pred. No. 4.3e+03;
RESULT 1313
ID ADB98800 standard; protein; 1665 AA.
DE Human Zmax1(LRP5).
PN WO200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 13.0%; Score 58.5; DB 7; Length 1665;
Best Local Similarity 26.2%; Pred. No. 4.3e+03;
RESULT 1314
ID ABG77164 standard; protein; 236 AA.
DE Germline protein sequence of anti-IGF-1R antibody AJ30/Jk1.
PN WO200253596-A2.
PD 11-JUL-2002.
PA (PFIZ) PFIZER INC.
PA (ABGE-) ABGENIX INC.
Query Match 12.9%; Score 58; DB 5; Length 236;
Best Local Similarity 28.4%; Pred. No. 4.2e+02;
RESULT 1315
ID ADR28586 standard; protein; 236 AA.
DE Human anti-IGF-IR antibody heavy chain A30/Jk1 protein SEQ ID NO:52.
PN WO2004071529-A2.
PD 26-AUG-2004.
PA (PFIZ) PFIZER PROD INC.
Query Match 12.9%; Score 58; DB 8; Length 236;
Best Local Similarity 28.4%; Pred. No. 4.2e+02;
RESULT 1316
ID ADX57906 standard; protein; 236 AA.
DE Human germline A30/Jk1 protein sequence SeqID6.
PN WO2005016967-A2.
PD 24-FEB-2005.
PA (PFIZ) PFIZER PROD INC.
Query Match 12.9%; Score 58; DB 9; Length 236;
Best Local Similarity 28.4%; Pred. No. 4.2e+02;
RESULT 1317
ID AEF54350 standard; protein; 236 AA.
DE Human light chain region germline A30/Jk1 sequence.
PN US2006018910-A1.
PD 26-JAN-2006.
PA (PFIZ) PFIZER INC.
Query Match 12.9%; Score 58; DB 10; Length 236;
Best Local Similarity 28.4%; Pred. No. 4.2e+02;
RESULT 1318
ID AEF34922 standard; protein; 236 AA.
DE Human germline A30/Jk1 light chain sequence.
PN WO2006008639-A1.
PD 26-JAN-2006.
PA (PFIZ) PFIZER PROD INC.
Query Match 12.9%; Score 58; DB 10; Length 236;
Best Local Similarity 28.4%; Pred. No. 4.2e+02;
RESULT 1319
ID ADS43001 standard; protein; 375 AA.
DE Bacterial polypeptide #21431.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.9%; Score 58; DB 8; Length 375;
Best Local Similarity 24.2%; Pred. No. 7.5e+02;
RESULT 1320
ID ADS15092 standard; protein; 405 AA.
DE Pseudomonas aeruginosa quorum sensing controlled protein, SEQ ID 647.
PN WO2004083385-A2.
PD 30-SEP-2004.
PA (IOWA) UNIV IOWA RES FOUND.
Query Match 12.9%; Score 58; DB 8; Length 405;
Best Local Similarity 38.6%; Pred. No. 8.2e+02;
RESULT 1321
ID ADX90494 standard; protein; 418 AA.

DE Plant full length insert polypeptide seqid 53158.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 12.9%; Score 58; DB 8; Length 418;
Best Local Similarity 31.7%; Pred. No. 8.6e+02;
RESULT 1322
ID AAU31533 standard; protein; 450 AA.
DE Novel human secreted protein #2024.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.9%; Score 58; DB 4; Length 450;
Best Local Similarity 29.5%; Pred. No. 9.4e+02;
RESULT 1323
ID ABO78245 standard; protein; 469 AA.
DE Pseudomonas aeruginosa polypeptide #10420.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.9%; Score 58; DB 7; Length 469;
Best Local Similarity 38.6%; Pred. No. 9.9e+02;
RESULT 1324
ID AAW05408 standard; protein; 486 AA.
DE Mouse HS1 protein.
PN WO9631625-A1.
PD 10-OCT-1996.
PA (CYTO-) CYTOGEN CORP.
PA (UYNC-) UNIV NORTH CAROLINA.
Query Match 12.9%; Score 58; DB 2; Length 486;
Best Local Similarity 36.6%; Pred. No. 1e+03;
RESULT 1325
ID AAY03795 standard; protein; 486 AA.
DE Murine Lck binding protein, LckBP1.
PN US5891673-A.
PD 06-APR-1999.
PA (SYNT) SYNTEX USA INC.
Query Match 12.9%; Score 58; DB 2; Length 486;
Best Local Similarity 36.6%; Pred. No. 1e+03;
RESULT 1326
ID ABR44110 standard; protein; 486 AA.
DE Human protein expressed in haematopoietic cells.
PN EP1295895-A1.
PD 26-MAR-2003.
PA (INSR) INST ROUSSY GUSTAVE.
PA (UYPA-) UNIV PARIS SUD.
Query Match 12.9%; Score 58; DB 6; Length 486;
Best Local Similarity 36.6%; Pred. No. 1e+03;
RESULT 1327
ID ABO07214 standard; protein; 486 AA.
DE Human p53 modifying protein, SEQ ID 174.
PN WO200299122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 12.9%; Score 58; DB 6; Length 486;
Best Local Similarity 36.6%; Pred. No. 1e+03;
RESULT 1328
ID ADD67624 standard; protein; 486 AA.
DE Human Ly1729P protein SEQ ID NO:101.
PN WO2003062401-A2.
PD 31-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 12.9%; Score 58; DB 7; Length 486;
Best Local Similarity 36.6%; Pred. No. 1e+03;
RESULT 1329
ID ADM67192 standard; protein; 486 AA.
DE Human haematopoietic cell specific Lyn substrate 1 protein SeqID 546.
PN WO2004011618-A2.
PD 05-FEB-2004.
PA (HMGE-) HMGENE INC.
Query Match 12.9%; Score 58; DB 8; Length 486;
Best Local Similarity 36.6%; Pred. No. 1e+03;
RESULT 1330
ID ADM67191 standard; protein; 486 AA.
DE Murine haematopoietic cell specific Lyn substrate 1 protein SeqID 545.
PN WO2004011618-A2.
PD 05-FEB-2004.
PA (HMGE-) HMGENE INC.
Query Match 12.9%; Score 58; DB 8; Length 486;
Best Local Similarity 36.6%; Pred. No. 1e+03;
RESULT 1331
ID ADN25984 standard; protein; 496 AA.
DE Bacterial polypeptide #8637.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.9%; Score 58; DB 8; Length 496;
Best Local Similarity 30.0%; Pred. No. 1.1e+03;
RESULT 1332
ID AEB41830 standard; protein; 499 AA.
DE L. pneumophila protein SEQ ID NO 6162.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 12.9%; Score 58; DB 9; Length 499;
Best Local Similarity 38.7%; Pred. No. 1.1e+03;
RESULT 1333
ID ABO58685 standard; protein; 501 AA.
DE Human genome derived single exon protein #4919.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 12.9%; Score 58; DB 8; Length 501;
Best Local Similarity 28.0%; Pred. No. 1.1e+03;
RESULT 1334
ID AEB38588 standard; protein; 507 AA.
DE L. pneumophila protein SEQ ID NO 2920.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 12.9%; Score 58; DB 9; Length 507;
Best Local Similarity 38.7%; Pred. No. 1.1e+03;
RESULT 1335
ID AAW90945 standard; protein; 540 AA.
DE Comamonas testosterroni R5 phenol hydroxylase protein #4.
PN JP2000069968-A.
PD 07-MAR-2000.
PA (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
Query Match 12.9%; Score 58; DB 3; Length 540;
Best Local Similarity 22.6%; Pred. No. 1.2e+03;
RESULT 1336
ID ADJ49107 standard; protein; 628 AA.
DE Oil-associated gene related protein #607.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.

PA (ROGE/) ROGERS J A.
Query Match 12.9%; Score 58; DB 8; Length 628;
Best Local Similarity 26.9%; Pred. No. 1.4e+03;
RESULT 1337
ID ADJ49064 standard; protein; 628 AA.
DE Oil-associated gene related protein #564.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 12.9%; Score 58; DB 8; Length 628;
Best Local Similarity 26.9%; Pred. No. 1.4e+03;
RESULT 1338
ID AAM78503 standard; protein; 797 AA.
DE Human protein SEQ ID NO 1165.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.9%; Score 58; DB 4; Length 797;
Best Local Similarity 28.0%; Pred. No. 1.9e+03;
RESULT 1339
ID AAM40565 standard; protein; 801 AA.
DE Human polypeptide SEQ ID NO 5496.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.9%; Score 58; DB 4; Length 801;
Best Local Similarity 28.0%; Pred. No. 1.9e+03;
RESULT 1340
ID ABB11940 standard; peptide; 973 AA.
DE Human secreted protein homologue, SEQ ID NO:2310.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.9%; Score 58; DB 4; Length 973;
Best Local Similarity 28.0%; Pred. No. 2.5e+03;
RESULT 1341
ID AAM79487 standard; protein; 973 AA.
DE Human protein SEQ ID NO 3133.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.9%; Score 58; DB 4; Length 973;
Best Local Similarity 28.0%; Pred. No. 2.5e+03;
RESULT 1342
ID ADC31585 standard; protein; 1094 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1667.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 12.9%; Score 58; DB 7; Length 1094;
Best Local Similarity 28.0%; Pred. No. 2.9e+03;
RESULT 1343
ID ADC31584 standard; protein; 1114 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1666.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 12.9%; Score 58; DB 7; Length 1114;
Best Local Similarity 28.0%; Pred. No. 2.9e+03;
RESULT 1344
ID ADQ66563 standard; protein; 1139 AA.
DE Novel human protein sequence #1536.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 12.9%; Score 58; DB 8; Length 1139;
Best Local Similarity 28.0%; Pred. No. 3e+03;
RESULT 1345
ID ABP74029 standard; protein; 1177 AA.
DE Candida albicans essential protein SEQ ID NO 7866.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.9%; Score 58; DB 5; Length 1177;
Best Local Similarity 23.3%; Pred. No. 3.1e+03;
RESULT 1346
ID AAE29358 standard; protein; 1331 AA.
DE Plasmodium falciparum BBP-5 protein.
PN WO200270542-A2.
PD 12-SEP-2002.
PA (SELI-) ST ELIZABETH'S MEDICAL CENT INC.
Query Match 12.9%; Score 58; DB 5; Length 1331;
Best Local Similarity 23.8%; Pred. No. 3.7e+03;
RESULT 1347
ID AAM84121 standard; protein; 95 AA.
DE Human immune/haematopoietic antigen SEQ ID NO:11714.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.8%; Score 57.5; DB 4; Length 95;
Best Local Similarity 28.0%; Pred. No. 1.5e+02;
RESULT 1348
ID AAU31789 standard; protein; 213 AA.
DE Novel human secreted protein #2280.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.8%; Score 57.5; DB 4; Length 213;
Best Local Similarity 26.3%; Pred. No. 4.2e+02;
RESULT 1349
ID ADL70801 standard; protein; 213 AA.
DE Anti-TNFalpha antibody VL region, SEQ ID 74.
PN WO2004020588-A2.
PD 11-MAR-2004.
PA (BIOR-) BIOREXIS PHARM CORP.
Query Match 12.8%; Score 57.5; DB 8; Length 213;
Best Local Similarity 28.8%; Pred. No. 4.2e+02;
RESULT 1350
ID ABM83745 standard; protein; 221 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3994.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.8%; Score 57.5; DB 8; Length 221;
Best Local Similarity 30.8%; Pred. No. 4.4e+02;
RESULT 1351
ID ADE34554 standard; protein; 269 AA.
DE Human MHC class II HLA-DR2/Dw12 #SEQ ID 38.
PN WO2003048323-A2.
PD 12-JUN-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (CARM/) CARMAN J.
PA (NADL/) NADLER S G.
PA (BOWE/) BOWEN M.
PA (NEUB/) NEUBAUER M.
PA (LUPP/) LU P.
Query Match 12.8%; Score 57.5; DB 7; Length 269;
Best Local Similarity 21.0%; Pred. No. 5.6e+02;
RESULT 1352
ID ADX91260 standard; protein; 273 AA.
DE Plant full length insert polypeptide seqid 53924.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 12.8%; Score 57.5; DB 8; Length 273;
Best Local Similarity 26.6%; Pred. No. 5.7e+02;
RESULT 1353

ID ABU15131 standard; protein; 275 AA.
DE Protein encoded by Prokaryotic essential gene #658.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.8%; Score 57.5; DB 6; Length 275;
Best Local Similarity 35.6%; Pred. No. 5.8e+02;
RESULT 1354
ID ABO62158 standard; protein; 281 AA.
DE Klebsiella pneumoniae polypeptide seqid 8675.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.8%; Score 57.5; DB 7; Length 281;
Best Local Similarity 22.2%; Pred. No. 5.9e+02;
RESULT 1355
ID AEA26355 standard; protein; 286 AA.
DE Stress tolerant plant-related transcription factor protein SeqID196.
PN WO2005047516-A2.
PD 26-MAY-2005.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 12.8%; Score 57.5; DB 9; Length 286;
Best Local Similarity 32.3%; Pred. No. 6.1e+02;
RESULT 1356
ID ABU31908 standard; protein; 308 AA.
DE Protein encoded by Prokaryotic essential gene #17435.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.8%; Score 57.5; DB 6; Length 308;
Best Local Similarity 28.6%; Pred. No. 6.7e+02;
RESULT 1357
ID ADN22689 standard; protein; 546 AA.
DE Bacterial polypeptide #5342.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.8%; Score 57.5; DB 8; Length 546;
Best Local Similarity 33.8%; Pred. No. 1.4e+03;
RESULT 1358
ID ABB48487 standard; protein; 574 AA.
DE Listeria monocytogenes protein #1191.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 12.8%; Score 57.5; DB 5; Length 574;
Best Local Similarity 27.9%; Pred. No. 1.5e+03;
RESULT 1359
ID ADY09430 standard; protein; 715 AA.
DE Plant full length insert polypeptide seqid 65245.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 12.8%; Score 57.5; DB 8; Length 715;
Best Local Similarity 25.3%; Pred. No. 1.9e+03;
RESULT 1360
ID ABB60747 standard; protein; 722 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 9033.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.8%; Score 57.5; DB 4; Length 722;
Best Local Similarity 21.0%; Pred. No. 1.9e+03;
RESULT 1361
ID AAW34501 standard; protein; 804 AA.
DE Obesity receptor protein splice variant.
PN WO9725424-A1.
PD 17-JUL-1997.
PA (AMGE-) AMGEN INC.
Query Match 12.8%; Score 57.5; DB 2; Length 804;
Best Local Similarity 26.9%; Pred. No. 2.2e+03;
RESULT 1362
ID ADB12853 standard; protein; 804 AA.
DE Human leptin receptor, OB-RE , splice variant protein.
PN US2003073829-A1.
PD 17-APR-2003.
PA (ADHA/) ADHAM N.
PA (BORO/) BOROWSKY B.
PA (LEVE/) LEVENS N.
PA (SKOD/) SKODA R C.
Query Match 12.8%; Score 57.5; DB 7; Length 804;
Best Local Similarity 26.9%; Pred. No. 2.2e+03;
RESULT 1363
ID AAW34502 standard; protein; 839 AA.
DE Obesity receptor protein.
PN WO9725424-A1.
PD 17-JUL-1997.
PA (AMGE-) AMGEN INC.
Query Match 12.8%; Score 57.5; DB 2; Length 839;
Best Local Similarity 26.9%; Pred. No. 2.3e+03;
RESULT 1364
ID ADG63038 standard; protein; 867 AA.
DE Human ObR truncated protein.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 867;
Best Local Similarity 26.9%; Pred. No. 2.4e+03;
RESULT 1365
ID ADG63030 standard; protein; 868 AA.
DE Human ObR truncated protein, delta 868.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 868;
Best Local Similarity 26.9%; Pred. No. 2.5e+03;
RESULT 1366
ID AAW50003 standard; protein; 896 AA.
DE Human OB-R variant Form 3.
PN WO9741263-A1.
PD 06-NOV-1997.
PA (PROG-) PROGENITOR INC.
Query Match 12.8%; Score 57.5; DB 2; Length 896;
Best Local Similarity 26.9%; Pred. No. 2.6e+03;
RESULT 1367
ID AAW24052 standard; protein; 896 AA.
DE Human WSX receptor variant 6.4.
PN WO9725425-A1.
PD 17-JUL-1997.
PA (GETH) GENENTECH INC.
Query Match 12.8%; Score 57.5; DB 2; Length 896;
Best Local Similarity 26.9%; Pred. No. 2.6e+03;
RESULT 1368
ID AAW14841 standard; protein; 896 AA.
DE Human haemopoietin receptor NR2.
PN WO9712037-A1.
PD 03-APR-1997.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
Query Match 12.8%; Score 57.5; DB 2; Length 896;
Best Local Similarity 26.9%; Pred. No. 2.6e+03;
RESULT 1369
ID ABU87939 standard; protein; 896 AA.
DE Human WSX receptor splice variant 6.4.
PN US2003004109-A1.
PD 02-JAN-2003.
PA (BENN/) BENNETT B.
PA (MATT/) MATTHEWS W.

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  Query Match             12.8%;  Score 57.5;  DB 6;  Length 896;
  Best Local Similarity   26.9%;  Pred. No. 2.6e+03;
RESULT 1370
ID   ABO53758 standard; protein; 896 AA.
DE   Human WSX receptor variant 6.4.
PN   US6541604-B1.
PD   01-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             12.8%;  Score 57.5;  DB 6;  Length 896;
  Best Local Similarity   26.9%;  Pred. No. 2.6e+03;
RESULT 1371
ID   ADC08904 standard; protein; 896 AA.
DE   Human WSX receptor variant 6.4.
PN   US2002193571-A1.
PD   19-DEC-2002.
PA   (CART/) CARTER P J.
PA   (CHIA/) CHIANG N Y.
PA   (KIMK/) KIM K J.
PA   (MATT/) MATTHEWS W.
PA   (RODR/) RODRIGUES M L.
  Query Match             12.8%;  Score 57.5;  DB 7;  Length 896;
  Best Local Similarity   26.9%;  Pred. No. 2.6e+03;
RESULT 1372
ID   ADD95274 standard; protein; 896 AA.
DE   Human leptin receptor OBR1.
PN   WO2003072787-A2.
PD   04-SEP-2003.
PA   (AVET ) AVENTIS PHARMA SA.
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (CNRS ) CENT NAT RECH SCI.
  Query Match             12.8%;  Score 57.5;  DB 7;  Length 896;
  Best Local Similarity   26.9%;  Pred. No. 2.6e+03;
RESULT 1373
ID   ADN04458 standard; protein; 896 AA.
DE   Antipsoriatic protein sequence #422.
PN   WO2004028479-A2.
PD   08-APR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             12.8%;  Score 57.5;  DB 8;  Length 896;
  Best Local Similarity   26.9%;  Pred. No. 2.6e+03;
RESULT 1374
ID   ADR27661 standard; protein; 896 AA.
DE   Human leptin receptor related protein OB-RGRP related sequence SEQ ID 10.
PN   FR2850971-A1.
PD   13-AUG-2004.
PA   (AVET ) AVENTIS PHARMA SA.
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
  Query Match             12.8%;  Score 57.5;  DB 8;  Length 896;
  Best Local Similarity   26.9%;  Pred. No. 2.6e+03;
RESULT 1375
ID   ADW88112 standard; protein; 896 AA.
DE   Human WSX receptor variant 6.4 protein.
PN   US2005019325-A1.
PD   27-JAN-2005.
PA   (CART/) CARTER P J.
PA   (CHIA/) CHIANG N Y.
PA   (KIMK/) KIM K J.
PA   (MATT/) MATTHEWS W.
PA   (RODR/) RODRIGUES M L.
  Query Match             12.8%;  Score 57.5;  DB 9;  Length 896;
  Best Local Similarity   26.9%;  Pred. No. 2.6e+03;
RESULT 1376
ID   AEE64731 standard; protein; 896 AA.
DE   Human WSX receptor variant 6.4 protein, SEQ ID : 3.
PN   US2005272656-A1.
PD   08-DEC-2005.
PA   (MATT/) MATTHEWS W.
  Query Match             12.8%;  Score 57.5;  DB 10;  Length 896;
  Best Local Similarity   26.9%;  Pred. No. 2.6e+03;
RESULT 1377
ID   AAR88912 standard; protein; 898 AA.
DE   Haematopoietin receptor Hu-B1.219 Form 3 protein.
PN   WO9608510-A1.
PD   21-MAR-1996.
PA   (PROG-) PROGENITOR INC.
  Query Match             12.8%;  Score 57.5;  DB 2;  Length 898;
  Best Local Similarity   26.9%;  Pred. No. 2.6e+03;
RESULT 1378
ID   AAW50002 standard; protein; 904 AA.
DE   Human OB-R variant Form 2.
PN   WO9741263-A1.
PD   06-NOV-1997.
PA   (PROG-) PROGENITOR INC.
  Query Match             12.8%;  Score 57.5;  DB 2;  Length 904;
  Best Local Similarity   26.9%;  Pred. No. 2.6e+03;
RESULT 1379
ID   AAR88911 standard; protein; 908 AA.
DE   Haematopoietin receptor Hu-B1.219 Form 2 protein.
PN   WO9608510-A1.
PD   21-MAR-1996.
PA   (PROG-) PROGENITOR INC.
  Query Match             12.8%;  Score 57.5;  DB 2;  Length 908;
  Best Local Similarity   26.9%;  Pred. No. 2.6e+03;
RESULT 1380
ID   AAW19536 standard; protein; 908 AA.
DE   Variant form of human leptin receptor OB-R.
PN   WO9726523-A2.
PD   24-JUL-1997.
PA   (PROG-) PROGENITOR INC.
  Query Match             12.8%;  Score 57.5;  DB 2;  Length 908;
  Best Local Similarity   26.9%;  Pred. No. 2.6e+03;
RESULT 1381
ID   AAW24053 standard; protein; 923 AA.
DE   Human WSX receptor variant 12.1.
PN   WO9725425-A1.
PD   17-JUL-1997.
PA   (GETH ) GENENTECH INC.
  Query Match             12.8%;  Score 57.5;  DB 2;  Length 923;
  Best Local Similarity   26.9%;  Pred. No. 2.6e+03;
RESULT 1382
ID   ABU87940 standard; protein; 923 AA.
DE   Human WSX receptor splice variant 12.1.
PN   US2003004109-A1.
PD   02-JAN-2003.
PA   (BENN/) BENNETT B.
PA   (MATT/) MATTHEWS W.
  Query Match             12.8%;  Score 57.5;  DB 6;  Length 923;
  Best Local Similarity   26.9%;  Pred. No. 2.6e+03;
RESULT 1383
ID   ABO53759 standard; protein; 923 AA.
DE   Human WSX receptor variant 12.1.
PN   US6541604-B1.
PD   01-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             12.8%;  Score 57.5;  DB 6;  Length 923;
  Best Local Similarity   26.9%;  Pred. No. 2.6e+03;
RESULT 1384
ID   ADC08905 standard; protein; 923 AA.
DE   Human WSX receptor variant 12.1.
PN   US2002193571-A1.
PD   19-DEC-2002.
PA   (CART/) CARTER P J.
PA   (CHIA/) CHIANG N Y.
PA   (KIMK/) KIM K J.
PA   (MATT/) MATTHEWS W.
PA   (RODR/) RODRIGUES M L.
  Query Match             12.8%;  Score 57.5;  DB 7;  Length 923;
  Best Local Similarity   26.9%;  Pred. No. 2.6e+03;
RESULT 1385
ID   ADW88113 standard; protein; 923 AA.
DE   Human WSX receptor variant 12.1 protein.
PN   US2005019325-A1.
PD   27-JAN-2005.
PA   (CART/) CARTER P J.
PA   (CHIA/) CHIANG N Y.
PA   (KIMK/) KIM K J.
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PA (MATT/) MATTHEWS W.
PA (RODR/) RODRIGUES M L.
Query Match 12.8%; Score 57.5; DB 9; Length 923;
Best Local Similarity 26.9%; Pred. No. 2.6e+03;
RESULT 1386
ID AEE64732 standard; protein; 923 AA.
DE Human WSX receptor variant 12.1 protein, SEQ ID : 4.
PN US2005272656-A1.
PD 08-DEC-2005.
PA (MATT/) MATTHEWS W.
Query Match 12.8%; Score 57.5; DB 10; Length 923;
Best Local Similarity 26.9%; Pred. No. 2.6e+03;
RESULT 1387
ID ADO23831 standard; protein; 925 AA.
DE Leptin receptor extracellular domain-GPI fusion protein.
PN WO2003034275-A2.
PD 24-APR-2003.
PA (ASTE-) ASTERION LTD.
Query Match 12.8%; Score 57.5; DB 7; Length 925;
Best Local Similarity 26.9%; Pred. No. 2.7e+03;
RESULT 1388
ID AAW38214 standard; protein; 958 AA.
DE Human OB-R variant Form 1.
PN WO9741263-A1.
PD 06-NOV-1997.
PA (PROG-) PROGENITOR INC.
Query Match 12.8%; Score 57.5; DB 2; Length 958;
Best Local Similarity 26.9%; Pred. No. 2.8e+03;
RESULT 1389
ID AAW31911 standard; protein; 958 AA.
DE Human OB-R leptin receptor variant.
PN WO9726370-A1.
PD 24-JUL-1997.
PA (PROG-) PROGENITOR INC.
Query Match 12.8%; Score 57.5; DB 2; Length 958;
Best Local Similarity 26.9%; Pred. No. 2.8e+03;
RESULT 1390
ID AAW19535 standard; protein; 958 AA.
DE Human OB-R leptin receptor variant.
PN WO9726272-A1.
PD 24-JUL-1997.
PA (PROG-) PROGENITOR INC.
Query Match 12.8%; Score 57.5; DB 2; Length 958;
Best Local Similarity 26.9%; Pred. No. 2.8e+03;
RESULT 1391
ID AAW22773 standard; protein; 958 AA.
DE Human haematopoietin receptor variant Hu-B1.219 form 1.
PN WO9727286-A1.
PD 31-JUL-1997.
PA (PROG-) PROGENITOR INC.
Query Match 12.8%; Score 57.5; DB 2; Length 958;
Best Local Similarity 26.9%; Pred. No. 2.8e+03;
RESULT 1392
ID AAR88910 standard; protein; 960 AA.
DE Haematopoietin receptor Hu-B1.219 Form 1 protein.
PN WO9608510-A1.
PD 21-MAR-1996.
PA (PROG-) PROGENITOR INC.
Query Match 12.8%; Score 57.5; DB 2; Length 960;
Best Local Similarity 26.9%; Pred. No. 2.8e+03;
RESULT 1393
ID ADG63037 standard; protein; 964 AA.
DE Human ObR truncated protein.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 964;
Best Local Similarity 26.9%; Pred. No. 2.8e+03;
RESULT 1394
ID ADG63031 standard; protein; 965 AA.
DE Human ObR truncated protein, delta 965.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 965;
Best Local Similarity 26.9%; Pred. No. 2.8e+03;
RESULT 1395
ID AAW34499 standard; protein; 970 AA.
DE Obesity receptor C protein.
PN WO9725424-A1.
PD 17-JUL-1997.
PA (AMGE-) AMGEN INC.
Query Match 12.8%; Score 57.5; DB 2; Length 970;
Best Local Similarity 26.9%; Pred. No. 2.8e+03;
RESULT 1396
ID AAW34497 standard; protein; 972 AA.
DE Obesity receptor A protein.
PN WO9725424-A1.
PD 17-JUL-1997.
PA (AMGE-) AMGEN INC.
Query Match 12.8%; Score 57.5; DB 2; Length 972;
Best Local Similarity 26.9%; Pred. No. 2.8e+03;
RESULT 1397
ID AAW34498 standard; protein; 999 AA.
DE Obesity receptor B protein.
PN WO9725424-A1.
PD 17-JUL-1997.
PA (AMGE-) AMGEN INC.
Query Match 12.8%; Score 57.5; DB 2; Length 999;
Best Local Similarity 26.9%; Pred. No. 2.9e+03;
RESULT 1398
ID ADG63032 standard; protein; 1065 AA.
DE Human ObR truncated protein, delta 1065.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 1065;
Best Local Similarity 26.9%; Pred. No. 3.2e+03;
RESULT 1399
ID ADG63039 standard; protein; 1067 AA.
DE Human ObR truncated protein.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 1067;
Best Local Similarity 26.9%; Pred. No. 3.2e+03;
RESULT 1400
ID ADG63033 standard; protein; 1115 AA.
DE Human ObR truncated protein, delta 1115.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 1115;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1401
ID AEA19287 standard; protein; 1152 AA.
DE Mouse B220.
PN WO2005049865-A2.
PD 02-JUN-2005.
PA (REPR-) REPROCELL INC.
Query Match 12.8%; Score 57.5; DB 9; Length 1152;
Best Local Similarity 21.7%; Pred. No. 3.5e+03;
RESULT 1402
ID ADG63040 standard; protein; 1155 AA.
DE Human ObR truncated protein.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 1155;
Best Local Similarity 26.9%; Pred. No. 3.5e+03;
RESULT 1403
ID ABO84453 standard; protein; 1157 AA.
DE Mouse cancer-associated protein MP13-011.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.

Query Match 12.8%; Score 57.5; DB 8; Length 1157;
Best Local Similarity 21.7%; Pred. No. 3.5e+03;
RESULT 1404
ID ADG63041 standard; protein; 1161 AA.
DE Human ObR truncated protein.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 1161;
Best Local Similarity 26.9%; Pred. No. 3.5e+03;
RESULT 1405
ID AAW24051 standard; protein; 1165 AA.
DE Human WSX receptor variant 13.2.
PN WO9725425-A1.
PD 17-JUL-1997.
PA (GETH) GENENTECH INC.
Query Match 12.8%; Score 57.5; DB 2; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.5e+03;
RESULT 1406
ID AAW19116 standard; protein; 1165 AA.
DE Human Ob receptor.
PN WO9719952-A1.
PD 05-JUN-1997.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 2; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.5e+03;
RESULT 1407
ID AAY13474 standard; protein; 1165 AA.
DE Peptide Seq ID No: 4 of WO9923493.
PN WO9923493-A1.
PD 14-MAY-1999.
PA (UYRQ) UNIV ROCKEFELLER.
Query Match 12.8%; Score 57.5; DB 2; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.5e+03;
RESULT 1408
ID AAE12551 standard; protein; 1165 AA.
DE Human Ob receptor (ObR) protein mutant (Y1141F).
PN US6287782-B1.
PD 11-SEP-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 4; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.5e+03;
RESULT 1409
ID AAE12609 standard; protein; 1165 AA.
DE Human Ob receptor (ObR) protein.
PN US6287782-B1.
PD 11-SEP-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 4; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.5e+03;
RESULT 1410
ID AAE25455 standard; protein; 1165 AA.
DE Human Ob receptor (ObR) protein.
PN US6395498-B1.
PD 28-MAY-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 5; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.5e+03;
RESULT 1411
ID AAE25774 standard; protein; 1165 AA.
DE Human obesity receptor (ObR) mutant protein, Y1079F.
PN US6403552-B1.
PD 11-JUN-2002.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 5; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.5e+03;
RESULT 1412
ID AAE25765 standard; protein; 1165 AA.
DE Human obesity receptor (ObR) protein.
PN US6403552-B1.
PD 11-JUN-2002.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 5; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.5e+03;
RESULT 1413
ID AAE25772 standard; protein; 1165 AA.
DE Human obesity receptor (ObR) mutant protein, Y1141F.
PN US6403552-B1.
PD 11-JUN-2002.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 5; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.5e+03;
RESULT 1414
ID AAE25773 standard; protein; 1165 AA.
DE Human obesity receptor (ObR) mutant protein, Y986F.
PN US6403552-B1.
PD 11-JUN-2002.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 5; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.5e+03;
RESULT 1415
ID AAE23859 standard; protein; 1165 AA.
DE Human Ob receptor (obR) protein.
PN US6380363-B1.
PD 30-APR-2002.
PA (TART/) TARTAGLIA L A.
PA (TEPP/) TEPPER R I.
PA (CULP/) CULPEPPER J A.
PA (WHIT/) WHITE D W.
Query Match 12.8%; Score 57.5; DB 5; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.5e+03;
RESULT 1416
ID ABU87938 standard; protein; 1165 AA.
DE Human DNA full length WSX receptor.
PN US2003004109-A1.
PD 02-JAN-2003.
PA (BENN/) BENNETT B.
PA (MATT/) MATTHEWS W.
Query Match 12.8%; Score 57.5; DB 6; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.5e+03;
RESULT 1417
ID ABP72720 standard; protein; 1165 AA.
DE Human leptin receptor long form.
PN WO2003017825-A2.
PD 06-MAR-2003.
PA (JOSL-) JOSLIN DIABETES CENT INC.
Query Match 12.8%; Score 57.5; DB 6; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.5e+03;
RESULT 1418
ID ABO53757 standard; protein; 1165 AA.
DE Human full length WSX receptor variant 13.2.
PN US6541604-B1.
PD 01-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.8%; Score 57.5; DB 6; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.5e+03;
RESULT 1419
ID ADC08903 standard; protein; 1165 AA.
DE Human WSX receptor variant 13.2.
PN US2002193571-A1.
PD 19-DEC-2002.
PA (CART/) CARTER P J.
PA (CHIA/) CHIANG N Y.
PA (KIMK/) KIM K J.
PA (MATT/) MATTHEWS W.
PA (RODR/) RODRIGUES M L.
Query Match 12.8%; Score 57.5; DB 7; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.5e+03;
RESULT 1420
ID ADE62888 standard; protein; 1165 AA.
DE Human Protein P48357, SEQ ID NO 8822.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 12.8%; Score 57.5; DB 7; Length 1165;

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  Best Local Similarity   26.9%;  Pred. No. 3.5e+03;
RESULT 1421
ID   ADD46275 standard; protein; 1165 AA.
DE   Human Protein P48357, SEQ ID NO 11950.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
  Query Match           12.8%;  Score 57.5;  DB 7;  Length 1165;
  Best Local Similarity   26.9%;  Pred. No. 3.5e+03;
RESULT 1422
ID   ADG63035 standard; protein; 1165 AA.
DE   Human ObR mutant protein, Y986F.
PN   US2002182676-A1.
PD   05-DEC-2002.
PA   (MILL-) MILLENNIUM PHARM INC.
  Query Match           12.8%;  Score 57.5;  DB 8;  Length 1165;
  Best Local Similarity   26.9%;  Pred. No. 3.5e+03;
RESULT 1423
ID   ADG62979 standard; protein; 1165 AA.
DE   Human ObR protein from clone famj5312.
PN   US2002182676-A1.
PD   05-DEC-2002.
PA   (MILL-) MILLENNIUM PHARM INC.
  Query Match           12.8%;  Score 57.5;  DB 8;  Length 1165;
  Best Local Similarity   26.9%;  Pred. No. 3.5e+03;
RESULT 1424
ID   ADG63036 standard; protein; 1165 AA.
DE   Human ObR mutant protein, Y1141F.
PN   US2002182676-A1.
PD   05-DEC-2002.
PA   (MILL-) MILLENNIUM PHARM INC.
  Query Match           12.8%;  Score 57.5;  DB 8;  Length 1165;
  Best Local Similarity   26.9%;  Pred. No. 3.5e+03;
RESULT 1425
ID   ADG63034 standard; protein; 1165 AA.
DE   Human ObR mutant protein, Y1079F.
PN   US2002182676-A1.
PD   05-DEC-2002.
PA   (MILL-) MILLENNIUM PHARM INC.
  Query Match           12.8%;  Score 57.5;  DB 8;  Length 1165;
  Best Local Similarity   26.9%;  Pred. No. 3.5e+03;
RESULT 1426
ID   ADW88111 standard; protein; 1165 AA.
DE   Human WSX receptor variant 13.2 protein.
PN   US2005019325-A1.
PD   27-JAN-2005.
PA   (CART/) CARTER P J.
PA   (CHIA/) CHIANG N Y.
PA   (KIMK/) KIM K J.
PA   (MATT/) MATTHEWS W.
PA   (RODR/) RODRIGUES M L.
  Query Match           12.8%;  Score 57.5;  DB 9;  Length 1165;
  Best Local Similarity   26.9%;  Pred. No. 3.5e+03;
RESULT 1427
ID   AEB32310 standard; protein; 1165 AA.
DE   Human protein #12.
PN   US2005147987-A1.
PD   07-JUL-2005.
PA   (APPL-) APPLERA CORP NY.
  Query Match           12.8%;  Score 57.5;  DB 9;  Length 1165;
  Best Local Similarity   26.9%;  Pred. No. 3.5e+03;
RESULT 1428
ID   AEE64730 standard; protein; 1165 AA.
DE   Human WSX receptor variant 13.2 protein, SEQ ID : 2.
PN   US2005272656-A1.
PD   08-DEC-2005.
PA   (MATT/) MATTHEWS W.
  Query Match           12.8%;  Score 57.5;  DB 10;  Length 1165;
  Best Local Similarity   26.9%;  Pred. No. 3.5e+03;
RESULT 1429
ID   AEE75688 standard; protein; 1165 AA.
DE   Human Ob receptor protein SEQ ID NO:4.
PN   US6977240-B1.
PD   20-DEC-2005.
PA   (MILL-) MILLENIUM PHARM INC.
  Query Match           12.8%;  Score 57.5;  DB 10;  Length 1165;
  Best Local Similarity   26.9%;  Pred. No. 3.5e+03;
RESULT 1430
ID   AEF92921 standard; protein; 1165 AA.
DE   Human obesity receptor (obR) protein.
PN   US2006029964-A1.
PD   09-FEB-2006.
PA   (MILL-) MILLENNIUM PHARM INC.
  Query Match           12.8%;  Score 57.5;  DB 10;  Length 1165;
  Best Local Similarity   26.9%;  Pred. No. 3.5e+03;
RESULT 1431
ID   AEF92925 standard; protein; 1165 AA.
DE   Human obesity receptor (obR) long form protein.
PN   US2006029964-A1.
PD   09-FEB-2006.
PA   (MILL-) MILLENNIUM PHARM INC.
  Query Match           12.8%;  Score 57.5;  DB 10;  Length 1165;
  Best Local Similarity   26.9%;  Pred. No. 3.5e+03;
RESULT 1432
ID   AEF92872 standard; protein; 1165 AA.
DE   Human obesity receptor (obR) long form protein, SEQ ID: 4.
PN   US2006029964-A1.
PD   09-FEB-2006.
PA   (MILL-) MILLENNIUM PHARM INC.
  Query Match           12.8%;  Score 57.5;  DB 10;  Length 1165;
  Best Local Similarity   26.9%;  Pred. No. 3.5e+03;
RESULT 1433
ID   AEB32324 standard; protein; 1167 AA.
DE   Human protein #26.
PN   US2005147987-A1.
PD   07-JUL-2005.
PA   (APPL-) APPLERA CORP NY.
  Query Match           12.8%;  Score 57.5;  DB 9;  Length 1167;
  Best Local Similarity   26.9%;  Pred. No. 3.6e+03;
RESULT 1434
ID   AAW34500 standard; protein; 1220 AA.
DE   Obesity receptor D protein.
PN   WO9725424-A1.
PD   17-JUL-1997.
PA   (AMGE-) AMGEN INC.
  Query Match           12.8%;  Score 57.5;  DB 2;  Length 1220;
  Best Local Similarity   26.9%;  Pred. No. 3.8e+03;
RESULT 1435
ID   AAW62544 standard; protein; 1221 AA.
DE   Human ob-receptor replacement mutant.
PN   WO9824881-A1.
PD   11-JUN-1998.
PA   (MERI ) MERCK & CO INC.
  Query Match           12.8%;  Score 57.5;  DB 2;  Length 1221;
  Best Local Similarity   26.9%;  Pred. No. 3.8e+03;
RESULT 1436
ID   ADL16234 standard; protein; 1291 AA.
DE   Mouse protein tyrosine phosphatase #7.
PN   WO2003068984-A2.
PD   21-AUG-2003.
PA   (COLD-) COLD SPRING HARBOR LAB.
PA   (CEPT-) CEPTYR INC.
  Query Match           12.8%;  Score 57.5;  DB 7;  Length 1291;
  Best Local Similarity   21.7%;  Pred. No. 4e+03;
RESULT 1437
ID   ADM67208 standard; protein; 1343 AA.
DE   Murine adipocyte specific leukocyte common antigen protein SeqID 562.
PN   WO2004011618-A2.
PD   05-FEB-2004.
PA   (HMGE-) HMGENE INC.
  Query Match           12.8%;  Score 57.5;  DB 8;  Length 1343;
  Best Local Similarity   21.7%;  Pred. No. 4.2e+03;
RESULT 1438
ID   AAW52217 standard; protein; 105 AA.
DE   Antibody LD1-84-VL chain sequence.
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PN WO9749809-A1.
PD 31-DEC-1997.
PA (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
Query Match 12.7%; Score 57; DB 2; Length 105;
Best Local Similarity 35.6%; Pred. No. 2e+02;
RESULT 1439
ID ADY66220 standard; protein; 135 AA.
DE S. mansoni protein SEQ ID 1638.
PN WO2005023979-A2.
PD 17-MAR-2005.
PA (AMPA-) FUNDACAO AMPARO A PESQUISA DO ESTADO.
Query Match 12.7%; Score 57; DB 9; Length 135;
Best Local Similarity 33.3%; Pred. No. 2.7e+02;
RESULT 1440
ID AAB16367 standard; protein; 136 AA.
DE Eucalyptus grandis diphenol oxidase protein sequence SEQ ID NO:293.
PN WO200022099-A1.
PD 20-APR-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 12.7%; Score 57; DB 3; Length 136;
Best Local Similarity 31.7%; Pred. No. 2.7e+02;
RESULT 1441
ID ADD41543 standard; protein; 136 AA.
DE Diphenol oxidase #4.
PN US2003131373-A1.
PD 10-JUL-2003.
PA (BLOK/) BLOKSBERG L N.
PA (HAVU/) HAVUKKALA I.
Query Match 12.7%; Score 57; DB 7; Length 136;
Best Local Similarity 31.7%; Pred. No. 2.7e+02;
RESULT 1442
ID AAY34312 standard; protein; 147 AA.
DE IgM antibody CEM 10.12 G5 kappa chain sequence.
PN WO9945031-A2.
PD 10-SEP-1999.
PA (ABGE-) ABGENIX INC.
Query Match 12.7%; Score 57; DB 2; Length 147;
Best Local Similarity 28.4%; Pred. No. 3e+02;
RESULT 1443
ID ADP44641 standard; protein; 213 AA.
DE Human anti-CD20 light chain protein.
PN WO2004050041-A2.
PD 17-JUN-2004.
PA (MOLE-) APPLIED MOLECULAR EVOLUTION INC.
Query Match 12.7%; Score 57; DB 8; Length 213;
Best Local Similarity 28.4%; Pred. No. 4.8e+02;
RESULT 1444
ID ADU80277 standard; protein; 213 AA.
DE CD20 binding AME 33 complete light chain variable protein.
PN WO2004103404-A1.
PD 02-DEC-2004.
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
Query Match 12.7%; Score 57; DB 8; Length 213;
Best Local Similarity 28.4%; Pred. No. 4.8e+02;
RESULT 1445
ID AEA60641 standard; protein; 213 AA.
DE Human butyrylcholinesterase variant protein SEQ ID NO:198.
PN US2005136044-A1.
PD 23-JUN-2005.
PA (WATK/) WATKINS J D.
PA (PANC/) PANCOOK J D.
Query Match 12.7%; Score 57; DB 9; Length 213;
Best Local Similarity 28.4%; Pred. No. 4.8e+02;
RESULT 1446
ID AEG04996 standard; protein; 213 AA.
DE Anti-CD20 antibody light chain variable region SEQ ID NO:29.
PN WO2006020114-A2.
PD 23-FEB-2006.
PA (MOLE-) APPLIED MOLECULAR EVOLUTION INC.
Query Match 12.7%; Score 57; DB 10; Length 213;
Best Local Similarity 28.4%; Pred. No. 4.8e+02;
RESULT 1447
ID AEF65405 standard; protein; 214 AA.
DE Anti-RhD Fab clone RhD243.109A05 Lc region sequence.
PN WO2006007850-A1.
PD 26-JAN-2006.
PA (SYMP-) SYMPHOGEN AS.
Query Match 12.7%; Score 57; DB 10; Length 214;
Best Local Similarity 28.4%; Pred. No. 4.8e+02;
RESULT 1448
ID AEF65392 standard; protein; 214 AA.
DE Anti-RhD Fab clone RhD200.164G10 Lc region sequence.
PN WO2006007850-A1.
PD 26-JAN-2006.
PA (SYMP-) SYMPHOGEN AS.
Query Match 12.7%; Score 57; DB 10; Length 214;
Best Local Similarity 26.9%; Pred. No. 4.8e+02;
RESULT 1449
ID ABO73390 standard; protein; 218 AA.
DE Pseudomonas aeruginosa polypeptide #5565.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.7%; Score 57; DB 7; Length 218;
Best Local Similarity 24.5%; Pred. No. 4.9e+02;
RESULT 1450
ID AAR59416 standard; protein; 219 AA.
DE 6D9 antibody light chain.
PN JP06220072-A.
PD 09-AUG-1994.
PA (TANP-) TANPAKU KOGAKU KENKYUSHO KK.
Query Match 12.7%; Score 57; DB 2; Length 219;
Best Local Similarity 28.4%; Pred. No. 4.9e+02;
RESULT 1451
ID AEB08093 standard; protein; 220 AA.
DE Murine Ig kappa light chain constant domain, SEQ ID NO: 55.
PN WO2005058251-A2.
PD 30-JUN-2005.
PA (DEND-) DENDREON CORP.
Query Match 12.7%; Score 57; DB 9; Length 220;
Best Local Similarity 28.4%; Pred. No. 5e+02;
RESULT 1452
ID ADZ57707 standard; protein; 236 AA.
DE Anti-cMet antibody 8.90.3 light chain protein.
PN GB2404660-A.
PD 09-FEB-2005.
PA (PFIZ) PFIZER PROD INC..
PA (ABGE-) ABGENIX INC.
Query Match 12.7%; Score 57; DB 9; Length 236;
Best Local Similarity 26.9%; Pred. No. 5.4e+02;
RESULT 1453
ID ADX95267 standard; protein; 321 AA.
DE Plant full length insert polypeptide seqid 57931.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 12.7%; Score 57; DB 8; Length 321;
Best Local Similarity 29.7%; Pred. No. 8e+02;
RESULT 1454
ID ADT57341 standard; protein; 370 AA.
DE Plant polypeptide, SEQ ID 7418.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 12.7%; Score 57; DB 8; Length 370;
Best Local Similarity 29.7%; Pred. No. 9.6e+02;
RESULT 1455
ID ADG83832 standard; protein; 454 AA.
DE Red belly black snake venom protease.
PN WO2003082914-A1.

PD 09-OCT-2003.
PA (UYQU) UNIV QUEENSLAND.
Query Match 12.7%; Score 57; DB 8; Length 454;
Best Local Similarity 32.8%; Pred. No. 1.2e+03;
RESULT 1456
ID AAG64459 standard; protein; 573 AA.
DE Mouse 6D9 catalytic antibody.
PN JP2001128681-A.
PD 15-MAY-2001.
PA (NISB) JAPAN TOBACCO INC.
PA (SEIB-) SEIBUTSU BUNSHI KOGAKU KENKYUSHO KK.
PA (TANP-) TANPAKU KOGAKU KENKYUSHO KK.
Query Match 12.7%; Score 57; DB 4; Length 573;
Best Local Similarity 28.4%; Pred. No. 1.7e+03;
RESULT 1457
ID ABO77277 standard; protein; 576 AA.
DE Pseudomonas aeruginosa polypeptide #9452.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.7%; Score 57; DB 7; Length 576;
Best Local Similarity 38.2%; Pred. No. 1.7e+03;
RESULT 1458
ID ADC08221 standard; protein; 676 AA.
DE Rice protein sequence Seq ID526 related to grain filling.
PN WO2003000905-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 12.7%; Score 57; DB 7; Length 676;
Best Local Similarity 45.5%; Pred. No. 2e+03;
RESULT 1459
ID ADC07938 standard; protein; 729 AA.
DE Rice protein sequence Seq ID204 related to grain filling.
PN WO2003000905-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 12.7%; Score 57; DB 7; Length 729;
Best Local Similarity 45.5%; Pred. No. 2.2e+03;
RESULT 1460
ID AAO15273 standard; protein; 757 AA.
DE Human nervous serine protease inhibitor (PI12) 83-27.
PN CN1333249-A.
PD 30-JAN-2002.
PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
Query Match 12.7%; Score 57; DB 5; Length 757;
Best Local Similarity 28.0%; Pred. No. 2.4e+03;
RESULT 1461
ID ABB64716 standard; protein; 971 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 20940.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.7%; Score 57; DB 4; Length 971;
Best Local Similarity 35.2%; Pred. No. 3.2e+03;
RESULT 1462
ID ADR18920 standard; protein; 1225 AA.
DE Human tracheobronchial mucin protein, MUC5A.
PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match 12.7%; Score 57; DB 8; Length 1225;
Best Local Similarity 27.7%; Pred. No. 4.3e+03;
RESULT 1463
ID ADD93316 standard; protein; 1302 AA.
DE Zebrafish Flt1 protein required for angiogenesis.
PN WO2003079776-A2.
PD 02-OCT-2003.
PA (ARTE-) ARTEMIS PHARM GMBH.
Query Match 12.7%; Score 57; DB 7; Length 1302;
Best Local Similarity 30.0%; Pred. No. 4.7e+03;
RESULT 1464
ID ABR53378 standard; protein; 1411 AA.
DE Protein sequence #SEQ ID 1621.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 12.7%; Score 57; DB 6; Length 1411;
Best Local Similarity 36.4%; Pred. No. 5.2e+03;
RESULT 1465
ID ADK63342 standard; protein; 1411 AA.
DE Disease treating protein complex-derived protein #982.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 12.7%; Score 57; DB 7; Length 1411;
Best Local Similarity 36.4%; Pred. No. 5.2e+03;
RESULT 1466
ID ADR18918 standard; protein; 2202 AA.
DE Mature Human mucin-like protein, SCS0005, SEQ ID 8.
PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match 12.7%; Score 57; DB 8; Length 2202;
Best Local Similarity 27.7%; Pred. No. 9e+03;
RESULT 1467
ID ADR18917 standard; protein; 2227 AA.
DE Human mucin-like protein, SCS0005, SEQ ID 7.
PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match 12.7%; Score 57; DB 8; Length 2227;
Best Local Similarity 27.7%; Pred. No. 9.2e+03;
RESULT 1468
ID ADR18919 standard; protein; 2233 AA.
DE His-tagged Human mucin-like protein, SCS0005, SEQ ID 9.
PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match 12.7%; Score 57; DB 8; Length 2233;
Best Local Similarity 27.7%; Pred. No. 9.2e+03;
RESULT 1469
ID ADV24899 standard; protein; 3869 AA.
DE Anabaena microcystin polyketide synthase mcyD protein.
PN WO2004104211-A2.
PD 02-DEC-2004.
PA (HELS-) HELSINGIN YLIOPISTO.
PA (UYLI-) UNIV LIEGE.
PA (CNDR) CONSIGLIO NAZ DELLE RICERCHE.
Query Match 12.7%; Score 57; DB 9; Length 3869;
Best Local Similarity 35.4%; Pred. No. 1.8e+04;
RESULT 1470
ID ADP79571 standard; protein; 107 AA.
DE Humanised 2H7.v16 variant light chain variable domain SEQ ID NO:2.
PN WO2004056312-A2.
PD 08-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 8; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
RESULT 1471
ID ADS33301 standard; protein; 107 AA.
DE Anti-CD20 humanised antibody hu2H7v16, light chain variable domain.
PN US2004202658-A1.
PD 14-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 8; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
RESULT 1472
ID ADW03407 standard; protein; 107 AA.
DE Humanized anti-CD20 antibody light chain variable region - SEQ ID 13.
PN WO2005000351-A2.
PD 06-JAN-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 9; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
RESULT 1473
ID ADW21304 standard; protein; 107 AA.

DE Mouse anti-CD20 antibody 2H7 VL, humanized clone v16.
PN WO2005005462-A2.
PD 20-JAN-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 9; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
RESULT 1474
ID ADX00802 standard; protein; 107 AA.
DE Humanized 2H7 v16 antibody light chain variable region, SEQ ID 1.
PN US2005032130-A1.
PD 10-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 9; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
RESULT 1475
ID ADY62622 standard; protein; 107 AA.
DE Humanized 2H7 antibody variable light chain.
PN US2005053602-A1.
PD 10-MAR-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 9; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
RESULT 1476
ID AEB27725 standard; protein; 107 AA.
DE Humanized 2H7 antibody light chain variable region sequence.
PN WO2005060999-A2.
PD 07-JUL-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 9; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
RESULT 1477
ID AEB17635 standard; peptide; 107 AA.
DE Variable light peptide sequence of humanized 2H7 antibody.
PN WO2005061542-A2.
PD 07-JUL-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 9; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
RESULT 1478
ID AEE18955 standard; protein; 107 AA.
DE Humanized antibody light chain variable region #7.
PN WO2005108989-A2.
PD 17-NOV-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 9; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
RESULT 1479
ID AEE18935 standard; protein; 107 AA.
DE Humanized antibody light chain variable region #2.
PN WO2005108989-A2.
PD 17-NOV-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 9; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
RESULT 1480
ID AEE18924 standard; protein; 107 AA.
DE Humanized antibody light chain variable region #1.
PN WO2005108989-A2.
PD 17-NOV-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 9; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
RESULT 1481
ID AEE26263 standard; protein; 107 AA.
DE Humanized 2H7 antibody light chain variable region.
PN WO2005115453-A2.
PD 08-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 10; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
RESULT 1482
ID AEE26230 standard; protein; 107 AA.
DE Humanized hu2H7.v16 antibody variable light chain.
PN WO2005115453-A2.
PD 08-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 10; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
RESULT 1483
ID AEE64951 standard; protein; 107 AA.
DE Humanised antibody 2H7.v16 light chain variable domain.
PN WO2005117978-A2.
PD 15-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 10; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
RESULT 1484
ID AEE64966 standard; protein; 107 AA.
DE Humanised antibody 2H7.v511 light chain variable domain.
PN WO2005117978-A2.
PD 15-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 10; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
RESULT 1485
ID AEE10466 standard; protein; 107 AA.
DE Humanized 2H7.v16 variant light chain variable region SEQ ID NO:2.
PN US2005271658-A1.
PD 08-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 10; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
RESULT 1486
ID AEE10487 standard; protein; 107 AA.
DE Humanized 2H7 variable domain amino acid sequence SEQ ID NO:23.
PN US2005271658-A1.
PD 08-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 10; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
RESULT 1487
ID AEE70761 standard; protein; 107 AA.
DE Humanized anti-CD20 antibody 2H7v.16, light chain variable region.
PN WO2005113003-A2.
PD 01-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 10; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
RESULT 1488
ID AEE70780 standard; protein; 107 AA.
DE Humanized anti-CD20 antibody 2H7v.16, mutant VL.
PN WO2005113003-A2.
PD 01-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 10; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
RESULT 1489
ID AEF05029 standard; protein; 107 AA.
DE Humanized 2H7.v511 variant antibody, light chain variable domain.
PN WO2005120437-A2.
PD 22-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 10; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
RESULT 1490
ID AEF05014 standard; protein; 107 AA.
DE Light chain variable domain (VL) of humanized 2H7.v16 variant antibody.
PN WO2005120437-A2.
PD 22-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 10; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
RESULT 1491
ID AEF64255 standard; protein; 107 AA.
DE Humanized 2H7.v511 antibody light chain variable region SEQ ID NO:23.
PN WO2006012508-A2.

PD 02-FEB-2006.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 10; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
RESULT 1492
ID AEF64229 standard; protein; 107 AA.
DE Humanized 2H7.v16 antibody light chain variable region.
PN WO2006012508-A2.
PD 02-FEB-2006.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 10; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
RESULT 1493
ID ADA89110 standard; protein; 109 AA.
DE MS-Pro-28-VL amino acid sequence SEQ ID NO:98.
PN WO2002102973-A2.
PD 27-DEC-2002.
PA (PROC-) PROCHON BIOTECH LTD.
Query Match 12.6%; Score 56.5; DB 6; Length 109;
Best Local Similarity 36.1%; Pred. No. 2.3e+02;
RESULT 1494
ID ADG74361 standard; protein; 109 AA.
DE MSPRO light chain variable region protein, SEQ ID No 98.
PN WO2002102972-A2.
PD 27-DEC-2002.
PA (PROC-) PROCHON BIOTECH LTD.
PA (MORP-) MORPHOSYS AG.
Query Match 12.6%; Score 56.5; DB 7; Length 109;
Best Local Similarity 36.1%; Pred. No. 2.3e+02;
RESULT 1495
ID ADI26478 standard; protein; 114 AA.
DE H. pylori HpU-18-L SEQ ID NO:14.
PN WO2004009805-A1.
PD 29-JAN-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 12.6%; Score 56.5; DB 8; Length 114;
Best Local Similarity 38.9%; Pred. No. 2.5e+02;
RESULT 1496
ID ABO58078 standard; protein; 169 AA.
DE Human genome derived single exon protein #4312.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 12.6%; Score 56.5; DB 8; Length 169;
Best Local Similarity 24.2%; Pred. No. 4.1e+02;
RESULT 1497
ID ADP55680 standard; protein; 175 AA.
DE Human PRO protein sequence SEQ ID NO:1656.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 8; Length 175;
Best Local Similarity 29.3%; Pred. No. 4.3e+02;
RESULT 1498
ID ADY22634 standard; protein; 186 AA.
DE Plant full length insert polypeptide seqid 70418.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 12.6%; Score 56.5; DB 8; Length 186;
Best Local Similarity 29.1%; Pred. No. 4.6e+02;
RESULT 1499
ID AEF65397 standard; protein; 215 AA.
DE Anti-RhD Fab clone RhD205.160B12 Lc region sequence.
PN WO2006007850-A1.
PD 26-JAN-2006.
PA (SYMP-) SYMPHOGEN AS.
Query Match 12.6%; Score 56.5; DB 10; Length 215;
Best Local Similarity 27.9%; Pred. No. 5.5e+02;
RESULT 1500
ID ABM84939 standard; protein; 221 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5188.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.6%; Score 56.5; DB 8; Length 221;
Best Local Similarity 32.7%; Pred. No. 5.7e+02;

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: November 21, 2006, 20:09:55 ; Search time 23.4862 Seconds
(without alignments)
298.151 Million cell updates/sec

Title: US-10-063-553-48_COPY_111_190
Perfect score: 449
Sequence: 1 KGPLMCNSPSNSNANCEFSL.....RASSFHFDSEENKHRLIHFS 80

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	449	100.0	229	2	US-09-991-181-258	Sequence 258, App
2	449	100.0	229	2	US-09-990-444-258	Sequence 258, App
3	449	100.0	229	2	US-09-997-333-258	Sequence 258, App
4	449	100.0	229	2	US-09-992-598-258	Sequence 258, App
5	449	100.0	229	2	US-09-989-735-258	Sequence 258, App
6	449	100.0	229	3	US-09-989-726-258	Sequence 258, App
7	449	100.0	229	3	US-09-997-514-258	Sequence 258, App
8	449	100.0	229	3	US-09-989-728-258	Sequence 258, App
9	449	100.0	229	3	US-09-997-349-258	Sequence 258, App
10	449	100.0	229	3	US-09-997-653-258	Sequence 258, App
11	449	100.0	229	3	US-09-989-293A-258	Sequence 258, App
12	68	15.1	2199	2	US-08-793-273C-2	Sequence 2, Appli
13	68	15.1	2199	5	PCT-US95-11684-2	Sequence 2, Appli
14	68	15.1	2200	2	US-09-796-575-2	Sequence 2, Appli
15	67	14.9	345	2	US-09-248-796A-26951	Sequence 26951, A
16	67	14.9	631	2	US-09-345-468-12	Sequence 12, Appl
17	67	14.9	631	2	US-09-414-453A-12	Sequence 12, Appl
18	67	14.9	631	2	US-09-610-118-12	Sequence 12, Appl
19	66.5	14.8	271	2	US-09-248-796A-14877	Sequence 14877, A
20	66.5	14.8	1627	2	US-09-902-540-11280	Sequence 11280, A
21	65.5	14.6	650	1	US-08-121-713D-60	Sequence 60, Appl
22	65.5	14.6	650	1	US-08-835-268-60	Sequence 60, Appl
23	65.5	14.6	650	1	US-09-060-692-60	Sequence 60, Appl
24	65.5	14.6	650	2	US-08-833-391-60	Sequence 60, Appl
25	65.5	14.6	650	2	US-09-060-610-60	Sequence 60, Appl
26	65.5	14.6	650	5	PCT-US94-10151A-60	Sequence 60, Appl
27	64.5	14.4	3177	1	US-08-477-451-4	Sequence 4, Appli
28	63	14.0	216	2	US-09-248-796A-14175	Sequence 14175, A
29	63	14.0	1165	2	US-09-487-558B-76	Sequence 76, Appl
30	62.5	13.9	152	2	US-09-270-767-47052	Sequence 47052, A
31	62.5	13.9	270	2	US-09-270-767-46312	Sequence 46312, A
32	62.5	13.9	416	2	US-09-949-016-7087	Sequence 7087, Ap
33	62.5	13.9	711	2	US-09-134-000C-5325	Sequence 5325, Ap
34	62	13.8	290	2	US-09-252-991A-18337	Sequence 18337, A
35	62	13.8	341	2	US-09-248-796A-20844	Sequence 20844, A
36	62	13.8	372	2	US-09-252-991A-26719	Sequence 26719, A
37	61	13.6	296	2	US-09-270-767-37980	Sequence 37980, A
38	61	13.6	296	2	US-09-270-767-53197	Sequence 53197, A
39	61	13.6	365	2	US-09-801-874-5	Sequence 5, Appli
40	61	13.6	715	2	US-09-792-024-85	Sequence 85, Appl
41	61	13.6	741	2	US-09-248-796A-18963	Sequence 18963, A
42	61	13.6	852	2	US-09-206-551-19	Sequence 19, Appl
43	61	13.6	1810	2	US-08-793-273C-4	Sequence 4, Appli
44	61	13.6	1810	5	PCT-US95-11684-4	Sequence 4, Appli
45	60.5	13.5	172	2	US-09-248-796A-21509	Sequence 21509, A
46	60	13.4	160	2	US-09-248-796A-24377	Sequence 24377, A
47	60	13.4	213	2	US-10-147-849-8	Sequence 8, Appli
48	60	13.4	213	2	US-10-147-849-9	Sequence 9, Appli
49	60	13.4	234	2	US-09-848-832-4	Sequence 4, Appli
50	60	13.4	646	2	US-09-949-016-7344	Sequence 7344, Ap
51	59.5	13.3	384	2	US-10-029-180-50	Sequence 50, Appl
52	59	13.1	153	2	US-09-640-211A-910	Sequence 910, App
53	59	13.1	155	1	US-08-801-972-1	Sequence 1, Appli
54	59	13.1	155	2	US-09-178-881-1	Sequence 1, Appli
55	59	13.1	329	2	US-09-604-957-2	Sequence 2, Appli
56	59	13.1	641	2	US-09-252-991A-26994	Sequence 26994, A
57	59	13.1	1781	2	US-09-995-749A-2	Sequence 2, Appli
58	58.5	13.0	208	2	US-09-991-181-416	Sequence 416, App
59	58.5	13.0	208	2	US-09-990-444-416	Sequence 416, App
60	58.5	13.0	208	2	US-09-832-129-36	Sequence 36, Appl
61	58.5	13.0	208	2	US-09-997-333-416	Sequence 416, App
62	58.5	13.0	208	2	US-09-992-598-416	Sequence 416, App
63	58.5	13.0	208	2	US-09-989-735-416	Sequence 416, App
64	58.5	13.0	208	3	US-09-989-726-416	Sequence 416, App
65	58.5	13.0	208	3	US-09-997-514-416	Sequence 416, App
66	58.5	13.0	208	3	US-09-989-728-416	Sequence 416, App
67	58.5	13.0	208	3	US-09-997-349-416	Sequence 416, App
68	58.5	13.0	208	3	US-09-997-653-416	Sequence 416, App
69	58.5	13.0	208	3	US-09-989-293A-416	Sequence 416, App
70	58.5	13.0	230	2	US-10-037-417-135	Sequence 135, App
71	58.5	13.0	238	2	US-09-270-767-41693	Sequence 41693, A
72	58.5	13.0	1451	2	US-09-060-299-25	Sequence 25, Appl
73	58.5	13.0	1451	2	US-09-402-923A-25	Sequence 25, Appl
74	58.5	13.0	1584	2	US-09-060-299-39	Sequence 39, Appl
75	58.5	13.0	1584	2	US-09-402-923A-39	Sequence 39, Appl
76	58.5	13.0	1591	2	US-09-060-299-4	Sequence 4, Appli
77	58.5	13.0	1591	2	US-09-060-299-43	Sequence 43, Appl
78	58.5	13.0	1591	2	US-09-402-923A-4	Sequence 4, Appli
79	58.5	13.0	1591	2	US-09-402-923A-43	Sequence 43, Appl
80	58.5	13.0	1615	2	US-09-060-299-3	Sequence 3, Appli
81	58.5	13.0	1615	2	US-09-402-923A-3	Sequence 3, Appli
82	58.5	13.0	1615	2	US-09-544-398B-3	Sequence 3, Appli
83	58.5	13.0	1615	2	US-09-544-398B-4	Sequence 4, Appli
84	58.5	13.0	1615	2	US-09-543-771B-3	Sequence 3, Appli
85	58.5	13.0	1615	2	US-09-543-771B-4	Sequence 4, Appli
86	58.5	13.0	1639	2	US-09-060-299-29	Sequence 29, Appl
87	58.5	13.0	1639	2	US-09-402-923A-29	Sequence 29, Appl
88	58	12.9	213	2	US-08-397-411-12	Sequence 12, Appl
89	58	12.9	469	2	US-09-252-991A-26991	Sequence 26991, A
90	58	12.9	486	1	US-08-942-423-2	Sequence 2, Appli
91	58	12.9	486	1	US-08-942-423-3	Sequence 3, Appli
92	58	12.9	486	2	US-08-630-915A-26	Sequence 26, Appl
93	58	12.9	486	2	US-09-879-957-26	Sequence 26, Appl
94	58	12.9	486	2	US-09-538-092-926	Sequence 926, App
95	57.5	12.8	241	2	US-09-270-767-61882	Sequence 61882, A
96	57.5	12.8	281	2	US-09-489-039A-8675	Sequence 8675, Ap
97	57.5	12.8	379	2	US-09-248-796A-22533	Sequence 22533, A
98	57.5	12.8	804	2	US-09-116-676-10	Sequence 10, Appl
99	57.5	12.8	896	1	US-08-640-389A-10	Sequence 10, Appl

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101	57.5	12.8	896	2	US-09-043-816E-13	Sequence 13, Appl
102	57.5	12.8	896	2	US-09-357-914-33	Sequence 33, Appl
103	57.5	12.8	896	2	US-08-780-562-3	Sequence 3, Appli
104	57.5	12.8	896	2	US-10-095-929-10	Sequence 10, Appl
105	57.5	12.8	896	2	US-10-014-156-13	Sequence 13, Appl
106	57.5	12.8	898	1	US-08-693-697-36	Sequence 36, Appl
107	57.5	12.8	898	2	US-08-588-189-3	Sequence 3, Appli
108	57.5	12.8	898	2	US-10-245-616-3	Sequence 3, Appli
109	57.5	12.8	906	1	US-08-640-389A-9	Sequence 9, Appli
110	57.5	12.8	906	2	US-08-618-957A-9	Sequence 9, Appli
111	57.5	12.8	906	2	US-09-357-914-32	Sequence 32, Appl
112	57.5	12.8	906	2	US-10-095-929-9	Sequence 9, Appli
113	57.5	12.8	908	1	US-08-693-697-33	Sequence 33, Appl
114	57.5	12.8	908	1	US-08-588-526-3	Sequence 3, Appli
115	57.5	12.8	923	2	US-08-780-562-4	Sequence 4, Appli
116	57.5	12.8	958	1	US-08-640-389A-8	Sequence 8, Appli
117	57.5	12.8	958	2	US-08-618-957A-8	Sequence 8, Appli
118	57.5	12.8	958	2	US-10-095-929-8	Sequence 8, Appli
119	57.5	12.8	960	1	US-08-355-888A-8	Sequence 8, Appli
120	57.5	12.8	960	1	US-08-588-190-3	Sequence 3, Appli
121	57.5	12.8	960	1	US-08-693-697-8	Sequence 8, Appli
122	57.5	12.8	960	1	US-08-640-389A-3	Sequence 3, Appli
123	57.5	12.8	960	2	US-08-693-696-8	Sequence 8, Appli
124	57.5	12.8	960	2	US-08-618-957A-3	Sequence 3, Appli
125	57.5	12.8	960	2	US-09-357-914-8	Sequence 8, Appli
126	57.5	12.8	960	2	US-10-095-929-3	Sequence 3, Appli
127	57.5	12.8	1165	1	US-08-640-389A-11	Sequence 11, Appl
128	57.5	12.8	1165	1	US-08-599-455B-4	Sequence 4, Appli
129	57.5	12.8	1165	2	US-09-093-814-1	Sequence 1, Appli
130	57.5	12.8	1165	2	US-09-069-781B-4	Sequence 4, Appli
131	57.5	12.8	1165	2	US-08-618-957A-11	Sequence 11, Appl
132	57.5	12.8	1165	2	US-09-137-132-4	Sequence 4, Appli
133	57.5	12.8	1165	2	US-08-864-564A-4	Sequence 4, Appli
134	57.5	12.8	1165	2	US-09-094-410-4	Sequence 4, Appli
135	57.5	12.8	1165	2	US-08-708-123D-4	Sequence 4, Appli
136	57.5	12.8	1165	2	US-08-583-153A-4	Sequence 4, Appli
137	57.5	12.8	1165	2	US-08-570-142D-4	Sequence 4, Appli
138	57.5	12.8	1165	2	US-08-780-562-2	Sequence 2, Appli
139	57.5	12.8	1165	2	US-08-638-524B-4	Sequence 4, Appli
140	57.5	12.8	1165	2	US-10-095-929-11	Sequence 11, Appl
141	57.5	12.8	1165	2	US-09-950-149-4	Sequence 4, Appli
142	57.5	12.8	1221	2	US-08-982-430-2	Sequence 2, Appli
143	57	12.7	136	2	US-09-615-192A-293	Sequence 293, App
144	57	12.7	218	2	US-09-252-991A-22136	Sequence 22136, A
145	57	12.7	576	2	US-09-252-991A-26023	Sequence 26023, A
146	56.5	12.6	198	2	US-09-248-796A-18306	Sequence 18306, A
147	56.5	12.6	235	2	US-09-252-991A-18300	Sequence 18300, A
148	56.5	12.6	412	2	US-10-094-749-3008	Sequence 3008, Ap
149	56.5	12.6	629	2	US-10-104-047-3405	Sequence 3405, Ap
150	56.5	12.6	811	2	US-09-605-703B-1114	Sequence 1114, Ap
151	56.5	12.6	811	2	US-09-605-703B-1116	Sequence 1116, Ap
152	56.5	12.6	1912	1	US-08-409-995-4	Sequence 4, Appli
153	56.5	12.6	1912	2	US-08-685-467-4	Sequence 4, Appli
154	56.5	12.6	2353	2	US-09-377-155-33	Sequence 33, Appl
155	56.5	12.6	2353	2	US-08-913-942-4	Sequence 4, Appli
156	56.5	12.6	2353	2	US-09-669-974-33	Sequence 33, Appl
157	56.5	12.6	2353	2	US-09-797-862-33	Sequence 33, Appl
158	56.5	12.6	2353	2	US-09-684-707-4	Sequence 4, Appli
159	56.5	12.6	2354	2	US-09-268-347-47	Sequence 47, Appl
160	56.5	12.6	2411	2	US-09-268-347-36	Sequence 36, Appl
161	56	12.5	137	2	US-09-252-991A-25510	Sequence 25510, A
162	56	12.5	213	2	US-09-996-288-241	Sequence 241, App
163	56	12.5	213	2	US-09-996-265-241	Sequence 241, App
164	56	12.5	236	2	US-09-859-053-30	Sequence 30, Appl
165	56	12.5	237	2	US-10-020-786-10	Sequence 10, Appl
166	56	12.5	269	1	US-08-484-905-116	Sequence 116, App
167	56	12.5	269	2	US-08-481-985B-116	Sequence 116, App
168	56	12.5	269	2	US-08-370-476-116	Sequence 116, App
169	56	12.5	282	2	US-09-270-767-41535	Sequence 41535, A
170	56	12.5	459	2	US-09-002-361-6	Sequence 6, Appli
171	56	12.5	481	2	US-09-002-361-5	Sequence 5, Appli
172	56	12.5	631	2	US-09-310-463-20	Sequence 20, Appl
173	56	12.5	631	2	US-08-842-248A-20	Sequence 20, Appl
174	56	12.5	631	3	US-10-143-618-20	Sequence 20, Appl
175	56	12.5	694	2	US-09-902-540-10624	Sequence 10624, A
176	55.5	12.4	168	2	US-09-199-637A-425	Sequence 425, App
177	55.5	12.4	302	2	US-09-710-279-2980	Sequence 2980, Ap
178	55.5	12.4	350	2	US-09-134-001C-3383	Sequence 3383, Ap
179	55.5	12.4	441	1	US-08-121-713D-56	Sequence 56, Appl
180	55.5	12.4	441	1	US-08-835-268-56	Sequence 56, Appl
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182	55.5	12.4	441	2	US-08-833-391-56	Sequence 56, Appl
183	55.5	12.4	441	2	US-09-060-610-56	Sequence 56, Appl
184	55.5	12.4	441	5	PCT-US94-10151A-56	Sequence 56, Appl
185	55.5	12.4	704	2	US-09-487-558B-218	Sequence 218, App
186	55.5	12.4	920	2	US-09-538-092-1197	Sequence 1197, Ap
187	55.5	12.4	1068	1	US-08-537-210A-2	Sequence 2, Appli
188	55.5	12.4	1068	2	US-09-113-825-2	Sequence 2, Appli
189	55.5	12.4	1709	2	US-09-949-016-11345	Sequence 11345, A
190	55.5	12.4	2385	2	US-09-543-681A-6304	Sequence 6304, Ap
191	55.5	12.4	2556	1	US-08-185-432-17	Sequence 17, Appl
192	55.5	12.4	2556	2	US-08-899-232-2	Sequence 2, Appli
193	55.5	12.4	2556	2	US-09-121-457-2	Sequence 2, Appli
194	55	12.2	209	2	US-10-135-636-11	Sequence 11, Appl
195	55	12.2	213	2	US-09-996-288-209	Sequence 209, App
196	55	12.2	213	2	US-09-996-288-213	Sequence 213, App
197	55	12.2	213	2	US-09-996-288-215	Sequence 215, App
198	55	12.2	213	2	US-09-996-288-217	Sequence 217, App
199	55	12.2	213	2	US-09-996-288-219	Sequence 219, App
200	55	12.2	213	2	US-09-996-288-221	Sequence 221, App
201	55	12.2	213	2	US-09-996-288-223	Sequence 223, App
202	55	12.2	213	2	US-09-996-288-225	Sequence 225, App
203	55	12.2	213	2	US-09-996-288-227	Sequence 227, App
204	55	12.2	213	2	US-09-996-288-229	Sequence 229, App
205	55	12.2	213	2	US-09-996-288-231	Sequence 231, App
206	55	12.2	213	2	US-09-996-288-233	Sequence 233, App
207	55	12.2	213	2	US-09-996-288-235	Sequence 235, App
208	55	12.2	213	2	US-09-996-288-237	Sequence 237, App
209	55	12.2	213	2	US-09-996-288-239	Sequence 239, App
210	55	12.2	213	2	US-09-996-288-243	Sequence 243, App
211	55	12.2	213	2	US-09-996-288-245	Sequence 245, App
212	55	12.2	213	2	US-09-996-288-247	Sequence 247, App
213	55	12.2	213	2	US-09-996-288-251	Sequence 251, App
214	55	12.2	213	2	US-09-996-288-253	Sequence 253, App
215	55	12.2	213	2	US-09-996-288-255	Sequence 255, App
216	55	12.2	213	2	US-09-996-288-257	Sequence 257, App
217	55	12.2	213	2	US-09-996-265-209	Sequence 209, App
218	55	12.2	213	2	US-09-996-265-213	Sequence 213, App
219	55	12.2	213	2	US-09-996-265-215	Sequence 215, App
220	55	12.2	213	2	US-09-996-265-217	Sequence 217, App
221	55	12.2	213	2	US-09-996-265-219	Sequence 219, App
222	55	12.2	213	2	US-09-996-265-221	Sequence 221, App
223	55	12.2	213	2	US-09-996-265-223	Sequence 223, App
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225	55	12.2	213	2	US-09-996-265-227	Sequence 227, App
226	55	12.2	213	2	US-09-996-265-229	Sequence 229, App
227	55	12.2	213	2	US-09-996-265-231	Sequence 231, App
228	55	12.2	213	2	US-09-996-265-233	Sequence 233, App
229	55	12.2	213	2	US-09-996-265-235	Sequence 235, App
230	55	12.2	213	2	US-09-996-265-237	Sequence 237, App
231	55	12.2	213	2	US-09-996-265-239	Sequence 239, App
232	55	12.2	213	2	US-09-996-265-243	Sequence 243, App
233	55	12.2	213	2	US-09-996-265-245	Sequence 245, App
234	55	12.2	213	2	US-09-996-265-247	Sequence 247, App
235	55	12.2	213	2	US-09-996-265-251	Sequence 251, App
236	55	12.2	213	2	US-09-996-265-253	Sequence 253, App
237	55	12.2	213	2	US-09-996-265-255	Sequence 255, App
238	55	12.2	213	2	US-09-996-265-257	Sequence 257, App
239	55	12.2	213	2	US-10-135-636-7	Sequence 7, Appli
240	55	12.2	214	2	US-09-996-288-249	Sequence 249, App
241	55	12.2	214	2	US-09-996-265-249	Sequence 249, App
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243	55	12.2	253	2	US-09-310-463-36	Sequence 36, Appl
244	55	12.2	265	2	US-09-310-463-34	Sequence 34, Appl
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250	55	12.2	332	2	US-09-170-354-6	Sequence 6, Appli
251	55	12.2	368	1	US-07-977-630-4	Sequence 4, Appli
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257	55	12.2	2842	1	US-08-289-548A-7	Sequence 7, Appli
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273	55	12.2	2843	6	US-09-442-489F-7	Sequence 7, Appli
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275	55	12.2	2973	1	US-09-003-687A-7	Sequence 7, Appli
276	55	12.2	2973	2	US-09-136-605-7	Sequence 7, Appli
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280	54.5	12.1	348	2	US-09-684-254-3	Sequence 3, Appli
281	54.5	12.1	348	2	US-09-409-926-3	Sequence 3, Appli
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286	54.5	12.1	2523	2	US-09-121-457-3	Sequence 3, Appli
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309	54	12.0	984	2	US-08-460-736-120	Sequence 120, App
310	54	12.0	984	2	US-09-535-370-120	Sequence 120, App
311	54	12.0	984	2	US-09-663-667-120	Sequence 120, App
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318	53.5	11.9	226	2	US-09-453-234-72	Sequence 72, Appl
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320	53.5	11.9	235	2	US-08-874-102-6	Sequence 6, Appli
321	53.5	11.9	235	2	US-08-984-919A-6	Sequence 6, Appli
322	53.5	11.9	235	2	US-09-006-595A-6	Sequence 6, Appli
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326	53.5	11.9	359	2	US-09-270-767-43751	Sequence 43751, A
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329	53.5	11.9	368	2	US-09-000-092-4	Sequence 4, Appli
330	53.5	11.9	368	2	US-09-000-092-8	Sequence 8, Appli
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333	53.5	11.9	368	2	US-08-874-102-11	Sequence 11, Appl
334	53.5	11.9	368	2	US-09-006-595A-11	Sequence 11, Appl
335	53.5	11.9	466	2	US-08-984-919A-33	Sequence 33, Appl
336	53.5	11.9	468	2	US-08-874-102-33	Sequence 33, Appl
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341	53.5	11.9	497	2	US-08-874-102-47	Sequence 47, Appl
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344	53.5	11.9	615	2	US-09-707-802-9	Sequence 9, Appli
345	53.5	11.9	615	2	US-09-991-326-9	Sequence 9, Appli
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350	53	11.8	43	1	US-08-332-562A-26	Sequence 26, Appl
351	53	11.8	73	2	US-09-621-976-6146	Sequence 6146, Ap
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353	53	11.8	88	2	US-08-311-731A-327	Sequence 327, App
354	53	11.8	119	1	US-08-602-010A-12	Sequence 12, Appl
355	53	11.8	119	1	US-08-680-726A-12	Sequence 12, Appl
356	53	11.8	119	2	US-09-092-409-12	Sequence 12, Appl
357	53	11.8	136	2	US-09-647-224A-22	Sequence 22, Appl
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362	53	11.8	170	2	US-09-245-764-12	Sequence 12, Appl
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364	53	11.8	171	2	US-09-245-764-14	Sequence 14, Appl
365	53	11.8	171	2	US-09-245-764-15	Sequence 15, Appl
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367	53	11.8	213	2	US-09-996-265-211	Sequence 211, App
368	53	11.8	214	1	US-08-458-516-12	Sequence 12, Appl
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377	53	11.8	315	2	US-09-949-016-11122	Sequence 11122, A
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379	53	11.8	317	2	US-10-027-736A-16	Sequence 16, Appl
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382	53	11.8	345	1	US-08-413-118-19	Sequence 19, Appl
383	53	11.8	345	1	US-08-413-118-20	Sequence 20, Appl
384	53	11.8	345	1	US-08-413-118-128	Sequence 128, App
385	53	11.8	345	1	US-08-680-726A-54	Sequence 54, Appl
386	53	11.8	345	1	US-08-332-562A-132	Sequence 132, App
387	53	11.8	345	2	US-08-473-446-19	Sequence 19, Appl
388	53	11.8	345	2	US-08-473-446-20	Sequence 20, Appl
389	53	11.8	345	2	US-08-473-446-128	Sequence 128, App
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399	53	11.8	808	2	US-10-104-047-3401	Sequence 3401, Ap
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401	53	11.8	858	2	US-09-206-551-18	Sequence 18, Appl
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403	53	11.8	1337	2	US-09-447-533-2	Sequence 2, Appli
404	53	11.8	1337	5	PCT-US95-05512-2	Sequence 2, Appli
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406	52.5	11.7	99	2	US-09-073-010-141	Sequence 141, App
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423	52.5	11.7	370	2	US-09-205-658-107	Sequence 107, App
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425	52.5	11.7	387	2	US-09-643-596B-136	Sequence 136, App
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430	52.5	11.7	460	2	US-09-143-707-6	Sequence 6, Appli
431	52.5	11.7	460	2	US-09-202-089-6	Sequence 6, Appli
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435	52.5	11.7	460	2	US-09-136-801-17	Sequence 17, Appl
436	52.5	11.7	460	2	US-09-332-929-17	Sequence 17, Appl
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440	52.5	11.7	460	2	US-09-690-189-6	Sequence 6, Appli
441	52.5	11.7	460	2	US-09-202-088A-17	Sequence 17, Appl
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444	52.5	11.7	613	2	US-09-949-016-7353	Sequence 7353, Ap
445	52.5	11.7	651	2	US-09-949-016-8426	Sequence 8426, Ap
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454	52.5	11.7	886	2	US-08-781-986A-5235	Sequence 5235, Ap
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458	52.5	11.7	1367	1	US-08-249-687C-2	Sequence 2, Appli
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466	52.5	11.7	3788	2	US-09-952-267B-76	Sequence 76, Appl
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477	52	11.6	221	2	US-09-911-154-4	Sequence 4, Appli
478	52	11.6	221	2	US-09-911-514-4	Sequence 4, Appli
479	52	11.6	221	2	US-09-911-513-4	Sequence 4, Appli
480	52	11.6	233	1	US-08-792-824-6	Sequence 6, Appli
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485	52	11.6	236	1	US-08-792-824-9	Sequence 9, Appli
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488	52	11.6	236	2	US-09-196-522-188	Sequence 188, App
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491	52	11.6	259	2	US-09-911-514-6	Sequence 6, Appli
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495	52	11.6	282	2	US-09-911-154-8	Sequence 8, Appli
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758	50	11.1	635	1	US-08-267-387-2	Sequence 2, Appli
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766	50	11.1	676	2	US-08-628-747-3	Sequence 3, Appli
767	50	11.1	676	2	US-08-402-253-3	Sequence 3, Appli
768	50	11.1	676	2	US-08-443-866B-3	Sequence 3, Appli
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779	50	11.1	856	2	US-08-475-668A-103	Sequence 103, App
780	50	11.1	856	2	US-08-485-551A-103	Sequence 103, App
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853	49.5	11.0	226	2	US-09-453-234-86	Sequence 86, Appl
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910	49	10.9	64	2	US-09-300-008B-44	Sequence 44, Appl
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935	49	10.9	386	2	US-09-769-402-2	Sequence 2, Appli
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937	49	10.9	386	2	US-10-280-047-2	Sequence 2, Appli
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955	49	10.9	713	2	US-08-487-072A-63	Sequence 63, Appl
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982	48.5	10.8	108	2	US-09-240-274-167	Sequence 167, App
983	48.5	10.8	108	2	US-09-848-798-32	Sequence 32, Appl
984	48.5	10.8	108	2	US-09-848-798-43	Sequence 43, Appl
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1006	48.5	10.8	248	2	US-09-252-991A-28060	Sequence 28060, A
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1012	48.5	10.8	264	2	US-08-370-476-120	Sequence 120, App
1013	48.5	10.8	264	2	US-08-468-544-16	Sequence 16, Appl
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1213	47.5	10.6	107	2	US-09-848-798-158	Sequence 158, App
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ALIGNMENTS

RESULT 1
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; Sequence 258, Application US/09991181
; Patent No. 6913919
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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Query Match 100.0%; Score 449; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-48;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 258, Application US/09990444
; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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Query Match 100.0%; Score 449; DB 2; Length 229;
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Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        171 RASSFHFDSEENKHRLIHFS 190
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RESULT 3
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
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; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
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Query Match 100.0%; Score 449; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-48;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 RASSFHFDSEENKHRLIHFS 80
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Db        171 RASSFHFDSEENKHRLIHFS 190


RESULT 4
US-09-992-598-258
; Sequence 258, Application US/09992598
; Patent No. 6956108
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C20
;  CURRENT APPLICATION NUMBER: US/09/992,598
;  CURRENT FILING DATE:  2001-11-14
;  PRIOR APPLICATION NUMBER: 60/049787
;  PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 449; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-48;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        111 KGPLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGW 170

Qy         61 RASSFHFDSEENKHRLIHFS 80
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Db        171 RASSFHFDSEENKHRLIHFS 190
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RESULT 5
US-09-989-735-258
; Sequence 258, Application US/09989735
; Patent No. 6972185
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
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; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C61
; CURRENT APPLICATION NUMBER: US/09/989,735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/088033
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; PRIOR APPLICATION NUMBER: 60/091978
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 449; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-48;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGPLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGW 60
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Qy 61 RASSFHFDSEENKHRLIHFS 80

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Db 171 RASSFHFDSEENKHRLIHFS 190

RESULT 6
US-09-989-726-258
; Sequence 258, Application US/09989726
; Patent No. 7018811
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
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; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
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; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C60
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, PRIOR APPLICATION NUMBER: 60/091982
, PRIOR FILING DATE: 1998-07-07
, PRIOR APPLICATION NUMBER: 60/092182
, PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 449; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-48;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 RASSFHFDSEENKHRLIHFS 80
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Db        171 RASSFHFDSEENKHRLIHFS 190
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RESULT 7
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; Sequence 258, Application US/09997514
; Patent No. 7019116
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C46
; CURRENT APPLICATION NUMBER: US/09/997,514
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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Query Match 100.0%; Score 449; DB 3; Length 229;
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Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        171 RASSFHFDSEENKHRLIHFS 190
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RESULT 8
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; Sequence 258, Application US/09989728
; Patent No. 7029873
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 449; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-48;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 RASSFHFDSEENKHRLIHFS 80
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Db        171 RASSFHFDSEENKHRLIHFS 190
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RESULT 9
US-09-997-349-258
; Sequence 258, Application US/09997349
; Patent No. 7034106
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
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; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
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; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C37
; CURRENT APPLICATION NUMBER: US/09/997,349
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David

; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
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; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
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; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Best Local Similarity 100.0%; Pred. No. 2.1e-48;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 12
US-08-793-273C-2
; Sequence 2, Application US/08793273C
; Patent No. 6482410
; GENERAL INFORMATION:
; APPLICANT: Crossin, Kathryn L.
; APPLICANT: Phillips, Greg
; APPLICANT: Prieto, Anne L.
; TITLE OF INVENTION: CYTOTACTIN DERIVATIVES THAT STIMULATE ATTACHMENT AND
; TITLE OF INVENTION: NEURITE OUTGROWTH, AND METHODS OF MAKING SAME
; FILE REFERENCE: BEC0022S
; CURRENT APPLICATION NUMBER: US/08/793,273C
; CURRENT FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: PCT/US95/11684

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,  PRIOR FILING DATE: 1995-09-14
,  PRIOR APPLICATION NUMBER: 08/308,359
,  PRIOR FILING DATE: 1994-09-16
;  NUMBER OF SEQ ID NOS: 30
,  SOFTWARE: PatentIn Ver. 2.1
, SEQ ID NO 2
,   LENGTH: 2199
,   TYPE: PRT
,   ORGANISM: Homo Sapiens
US-08-793-273C-2

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  Best Local Similarity   66.7%;  Pred. No. 39;
  Matches   12;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

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RESULT 13
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; Sequence 2, Application PC/TUS9511684
;  GENERAL INFORMATION:
;    APPLICANT:  THE SCRIPPS RESEARCH INSTITUTE
;    TITLE OF INVENTION:  CYTOTACTIN DERIVATIVES THAT STIMULATE
;    TITLE OF INVENTION:  ATTACHMENT AND NEURITE OUTGROWTH, AND METHODS OF MAKING
;    TITLE OF INVENTION:  AND USING SAME
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  The Scripps Research Institute, Office of
;      ADDRESSEE:  Patent Counsel
;      STREET:  10666 North Torrey Pines Road, TPC 8
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/11684
;      FILING DATE:  14-SEP-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/308,359
;      FILING DATE:  16-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Logan, April C.
;      REGISTRATION NUMBER:  33,950
;      REFERENCE/DOCKET NUMBER:  BEC0019P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-554-2937
;      TELEFAX:  619-554-6312
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2199 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-11684-2

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RESULT 14
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; Sequence 2, Application US/09796575
; Patent No. 6632671
; GENERAL INFORMATION:
;  APPLICANT: Genesegues, Inc.
;  TITLE OF INVENTION: NANOCAPSULE ENCAPSULATION SYSTEM AND METHOD
;  FILE REFERENCE: G332.12-0001
;  CURRENT APPLICATION NUMBER: US/09/796,575
;  CURRENT FILING DATE:  2001-02-28
;  PRIOR APPLICATION NUMBER: US 60/185,282
;  PRIOR FILING DATE: 2000-02-28
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 2200
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-796-575-2

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RESULT 15
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; Sequence 26951, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
;  APPLICANT: Keith Weinstock et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
;  TITLE OF INVENTION:  FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 107196.132
;  CURRENT APPLICATION NUMBER: US/09/248,796A
;  CURRENT FILING DATE:  1999-02-12
;  PRIOR APPLICATION NUMBER: US 60/074,725
;  PRIOR FILING DATE: 1998-02-13
;  PRIOR APPLICATION NUMBER: US 60/096,409
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 28208
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;   TYPE: PRT
;   ORGANISM: Candida albicans
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OM protein - protein search, using sw model

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Post-processing: Minimum Match 0%
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Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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564	449	100.0	229	4	US-10-174-587-198	Sequence 198, App
628	449	100.0	229	4	US-10-063-742-48	Sequence 48, Appl
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793	67	14.9	632	4	US-10-114-153-92	Sequence 92, Appl
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910	60.5	13.5	588	4	US-10-432-422-188	Sequence 188, App
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SUMMARIES

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6	67	14.9	631	7	US-11-447-460-12	Sequence 12, Appl
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12	63	14.0	213	7	US-11-254-182-64	Sequence 64, Appl
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14	63	14.0	213	7	US-11-106-762-24	Sequence 24, Appl
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180	55	12.2	198	7	US-11-388-642-76	Sequence 76, Appl
181	55	12.2	198	7	US-11-388-642-77	Sequence 77, Appl
182	55	12.2	198	7	US-11-388-642-78	Sequence 78, Appl
183	55	12.2	198	7	US-11-388-642-79	Sequence 79, Appl
184	55	12.2	198	7	US-11-388-642-81	Sequence 81, Appl
185	55	12.2	209	7	US-11-207-142-11	Sequence 11, Appl
186	55	12.2	213	7	US-11-263-230-209	Sequence 209, App
187	55	12.2	213	7	US-11-263-230-213	Sequence 213, App
188	55	12.2	213	7	US-11-263-230-215	Sequence 215, App
189	55	12.2	213	7	US-11-263-230-217	Sequence 217, App
190	55	12.2	213	7	US-11-263-230-219	Sequence 219, App
191	55	12.2	213	7	US-11-263-230-221	Sequence 221, App
192	55	12.2	213	7	US-11-263-230-223	Sequence 223, App
193	55	12.2	213	7	US-11-263-230-225	Sequence 225, App
194	55	12.2	213	7	US-11-263-230-227	Sequence 227, App
195	55	12.2	213	7	US-11-263-230-229	Sequence 229, App
196	55	12.2	213	7	US-11-263-230-231	Sequence 231, App
197	55	12.2	213	7	US-11-263-230-233	Sequence 233, App
198	55	12.2	213	7	US-11-263-230-235	Sequence 235, App
199	55	12.2	213	7	US-11-263-230-237	Sequence 237, App
200	55	12.2	213	7	US-11-263-230-239	Sequence 239, App
201	55	12.2	213	7	US-11-263-230-243	Sequence 243, App
202	55	12.2	213	7	US-11-263-230-245	Sequence 245, App
203	55	12.2	213	7	US-11-263-230-247	Sequence 247, App
204	55	12.2	213	7	US-11-263-230-249	Sequence 249, App
205	55	12.2	213	7	US-11-263-230-251	Sequence 251, App
206	55	12.2	213	7	US-11-263-230-253	Sequence 253, App
207	55	12.2	213	7	US-11-263-230-255	Sequence 255, App
208	55	12.2	213	7	US-11-263-230-257	Sequence 257, App
209	55	12.2	213	7	US-11-263-230-306	Sequence 306, App
210	55	12.2	213	7	US-11-263-230-312	Sequence 312, App
211	55	12.2	213	7	US-11-263-230-318	Sequence 318, App
212	55	12.2	213	7	US-11-263-230-324	Sequence 324, App
213	55	12.2	213	7	US-11-263-230-330	Sequence 330, App
214	55	12.2	213	7	US-11-263-230-333	Sequence 333, App
215	55	12.2	213	7	US-11-375-810-6	Sequence 6, Appli
216	55	12.2	213	7	US-11-375-810-16	Sequence 16, Appl
217	55	12.2	213	7	US-11-207-142-7	Sequence 7, Appli
218	55	12.2	230	7	US-11-284-236-52	Sequence 52, Appl
219	55	12.2	261	6	US-10-511-937-2998	Sequence 2998, Ap
220	55	12.2	261	7	US-11-363-149-21	Sequence 21, Appl
221	55	12.2	261	7	US-11-363-151-21	Sequence 21, Appl
222	55	12.2	275	7	US-11-293-697-4717	Sequence 4717, Ap
223	55	12.2	299	7	US-11-265-762-144	Sequence 144, App
224	55	12.2	333	6	US-10-953-349-19345	Sequence 19345, A
225	55	12.2	403	6	US-10-526-324-1302	Sequence 1302, Ap
226	55	12.2	526	6	US-10-547-528-6	Sequence 6, Appli
227	55	12.2	576	6	US-10-449-902-55245	Sequence 55245, A
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229	55	12.2	1213	7	US-11-056-355B-83584	Sequence 83584, A
230	55	12.2	1245	7	US-11-056-355B-83583	Sequence 83583, A
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232	54.5	12.1	113	7	US-11-290-687-75	Sequence 75, Appl
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234	54.5	12.1	113	7	US-11-290-687-77	Sequence 77, Appl
235	54.5	12.1	113	7	US-11-290-687-79	Sequence 79, Appl
236	54.5	12.1	113	7	US-11-290-687-80	Sequence 80, Appl
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238	54.5	12.1	113	7	US-11-290-687-85	Sequence 85, Appl
239	54.5	12.1	113	7	US-11-290-687-87	Sequence 87, Appl
240	54.5	12.1	113	7	US-11-290-687-88	Sequence 88, Appl
241	54.5	12.1	113	7	US-11-290-687-93	Sequence 93, Appl
242	54.5	12.1	113	7	US-11-290-687-95	Sequence 95, Appl
243	54.5	12.1	113	7	US-11-404-967-74	Sequence 74, Appl
244	54.5	12.1	113	7	US-11-404-967-75	Sequence 75, Appl
245	54.5	12.1	113	7	US-11-404-967-76	Sequence 76, Appl
246	54.5	12.1	113	7	US-11-404-967-77	Sequence 77, Appl
247	54.5	12.1	113	7	US-11-404-967-79	Sequence 79, Appl

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252	54.5	12.1	113	7	US-11-404-967-88	Sequence 88, Appl
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254	54.5	12.1	113	7	US-11-404-967-95	Sequence 95, Appl
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256	54.5	12.1	157	6	US-10-953-349-4044	Sequence 4044, Ap
257	54.5	12.1	175	6	US-10-953-349-4043	Sequence 4043, Ap
258	54.5	12.1	214	6	US-10-953-349-24686	Sequence 24686, A
259	54.5	12.1	214	7	US-11-056-355B-58097	Sequence 58097, A
260	54.5	12.1	261	6	US-10-953-349-22331	Sequence 22331, A
261	54.5	12.1	261	7	US-11-056-355B-55071	Sequence 55071, A
262	54.5	12.1	269	6	US-10-449-902-52682	Sequence 52682, A
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265	54.5	12.1	323	6	US-10-449-902-34872	Sequence 34872, A
266	54.5	12.1	325	6	US-10-953-349-24685	Sequence 24685, A
267	54.5	12.1	325	7	US-11-056-355B-58096	Sequence 58096, A
268	54.5	12.1	326	6	US-10-953-349-24684	Sequence 24684, A
269	54.5	12.1	326	7	US-11-056-355B-58095	Sequence 58095, A
270	54.5	12.1	368	7	US-11-056-355B-54215	Sequence 54215, A
271	54.5	12.1	381	7	US-11-174-307B-2946	Sequence 2946, Ap
272	54.5	12.1	381	7	US-11-056-355B-54214	Sequence 54214, A
273	54.5	12.1	384	7	US-11-056-355B-70547	Sequence 70547, A
274	54.5	12.1	384	7	US-11-056-355B-85617	Sequence 85617, A
275	54.5	12.1	399	6	US-10-374-780A-2612	Sequence 2612, Ap
276	54.5	12.1	399	7	US-11-056-355B-96313	Sequence 96313, A
277	54.5	12.1	415	7	US-11-056-355B-54213	Sequence 54213, A
278	54.5	12.1	441	6	US-10-511-937-2942	Sequence 2942, Ap
279	54.5	12.1	446	6	US-10-449-902-54555	Sequence 54555, A
280	54.5	12.1	470	7	US-11-056-355B-70546	Sequence 70546, A
281	54.5	12.1	482	7	US-11-056-355B-70545	Sequence 70545, A
282	54.5	12.1	489	7	US-11-174-307B-4450	Sequence 4450, Ap
283	54.5	12.1	681	6	US-10-449-902-55254	Sequence 55254, A
284	54.5	12.1	749	7	US-11-443-904-97	Sequence 97, Appl
285	54	12.0	198	7	US-11-388-570-84	Sequence 84, Appl
286	54	12.0	198	7	US-11-388-570-85	Sequence 85, Appl
287	54	12.0	198	7	US-11-388-642-84	Sequence 84, Appl
288	54	12.0	198	7	US-11-388-642-85	Sequence 85, Appl
289	54	12.0	219	7	US-11-256-332-163	Sequence 163, App
290	54	12.0	220	7	US-11-056-355B-6866	Sequence 6866, Ap
291	54	12.0	261	7	US-11-330-403-1789	Sequence 1789, Ap
292	54	12.0	328	7	US-11-330-403-15736	Sequence 15736, A
293	54	12.0	357	6	US-10-449-902-35968	Sequence 35968, A
294	54	12.0	358	7	US-11-090-997-1892	Sequence 1892, Ap
295	54	12.0	360	6	US-10-449-902-46751	Sequence 46751, A
296	54	12.0	373	6	US-10-449-902-28851	Sequence 28851, A
297	54	12.0	393	7	US-11-330-403-1326	Sequence 1326, Ap
298	54	12.0	406	6	US-10-449-902-37586	Sequence 37586, A
299	54	12.0	614	7	US-11-283-329-30	Sequence 30, Appl
300	54	12.0	614	7	US-11-363-149-18	Sequence 18, Appl
301	54	12.0	614	7	US-11-363-151-18	Sequence 18, Appl
302	54	12.0	710	7	US-11-330-403-11617	Sequence 11617, A
303	54	12.0	744	6	US-10-449-902-46615	Sequence 46615, A
304	54	12.0	1016	6	US-10-449-902-41144	Sequence 41144, A
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306	53.5	11.9	108	7	US-11-311-939-181	Sequence 181, App
307	53.5	11.9	113	7	US-11-290-687-86	Sequence 86, Appl
308	53.5	11.9	113	7	US-11-290-687-96	Sequence 96, Appl
309	53.5	11.9	113	7	US-11-404-967-86	Sequence 86, Appl
310	53.5	11.9	113	7	US-11-404-967-96	Sequence 96, Appl
311	53.5	11.9	115	7	US-11-256-332-96	Sequence 96, Appl
312	53.5	11.9	223	7	US-11-056-355B-38865	Sequence 38865, A
313	53.5	11.9	261	7	US-11-056-355B-38864	Sequence 38864, A
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315	53.5	11.9	282	7	US-11-056-355B-38863	Sequence 38863, A
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317	53.5	11.9	312	7	US-11-056-355B-97345	Sequence 97345, A
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319	53.5	11.9	380	6	US-10-449-902-48268	Sequence 48268, A
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323	53.5	11.9	740	7	US-11-330-403-14762	Sequence 14762, A
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325	53.5	11.9	1143	6	US-10-630-629-1	Sequence 1, Appli
326	53	11.8	105	7	US-11-333-197-40	Sequence 40, Appl
327	53	11.8	108	7	US-11-023-959A-108	Sequence 108, App
328	53	11.8	129	7	US-11-330-403-15760	Sequence 15760, A
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330	53	11.8	153	6	US-10-953-349-20446	Sequence 20446, A
331	53	11.8	153	7	US-11-056-355B-52730	Sequence 52730, A
332	53	11.8	168	6	US-10-449-902-33496	Sequence 33496, A
333	53	11.8	172	6	US-10-449-902-39562	Sequence 39562, A
334	53	11.8	194	7	US-11-330-403-574	Sequence 574, App
335	53	11.8	213	7	US-11-263-230-211	Sequence 211, App
336	53	11.8	214	7	US-11-183-218-55	Sequence 55, Appl
337	53	11.8	219	7	US-11-256-332-171	Sequence 171, App
338	53	11.8	232	7	US-11-330-403-14995	Sequence 14995, A
339	53	11.8	240	6	US-10-449-902-42947	Sequence 42947, A
340	53	11.8	243	6	US-10-574-398-24	Sequence 24, Appl
341	53	11.8	257	7	US-11-330-403-3787	Sequence 3787, Ap
342	53	11.8	269	6	US-10-449-902-47680	Sequence 47680, A
343	53	11.8	274	7	US-11-330-403-7757	Sequence 7757, Ap
344	53	11.8	276	6	US-10-953-349-12932	Sequence 12932, A
345	53	11.8	280	6	US-10-449-902-48801	Sequence 48801, A
346	53	11.8	310	7	US-11-486-345-42	Sequence 42, Appl
347	53	11.8	315	7	US-11-305-843-12	Sequence 12, Appl
348	53	11.8	315	7	US-11-486-345-41	Sequence 41, Appl
349	53	11.8	320	7	US-11-330-403-15713	Sequence 15713, A
350	53	11.8	320	7	US-11-330-403-15714	Sequence 15714, A
351	53	11.8	321	7	US-11-330-403-15688	Sequence 15688, A
352	53	11.8	323	7	US-11-486-345-43	Sequence 43, Appl
353	53	11.8	327	7	US-11-330-403-15705	Sequence 15705, A
354	53	11.8	327	7	US-11-330-403-15731	Sequence 15731, A
355	53	11.8	327	7	US-11-330-403-15738	Sequence 15738, A
356	53	11.8	328	7	US-11-330-403-15729	Sequence 15729, A
357	53	11.8	328	7	US-11-330-403-16287	Sequence 16287, A
358	53	11.8	354	7	US-11-330-403-12622	Sequence 12622, A
359	53	11.8	355	7	US-11-330-403-10809	Sequence 10809, A
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364	53	11.8	398	6	US-10-449-902-55839	Sequence 55839, A
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366	53	11.8	472	7	US-11-056-355B-4393	Sequence 4393, Ap
367	53	11.8	494	6	US-10-449-902-48860	Sequence 48860, A
368	53	11.8	512	7	US-11-330-403-15063	Sequence 15063, A
369	53	11.8	513	7	US-11-174-307B-274	Sequence 274, App
370	53	11.8	515	7	US-11-056-355B-4392	Sequence 4392, Ap
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372	53	11.8	524	7	US-11-330-403-10144	Sequence 10144, A
373	53	11.8	554	7	US-11-056-355B-44784	Sequence 44784, A
374	53	11.8	581	7	US-11-293-697-4401	Sequence 4401, Ap
375	53	11.8	600	7	US-11-293-697-2940	Sequence 2940, Ap
376	53	11.8	628	7	US-11-056-355B-86500	Sequence 86500, A
377	53	11.8	660	7	US-11-056-355B-71395	Sequence 71395, A
378	53	11.8	667	6	US-10-505-928-393	Sequence 393, App
379	53	11.8	679	7	US-11-056-355B-44783	Sequence 44783, A
380	53	11.8	744	7	US-11-330-403-2256	Sequence 2256, Ap
381	53	11.8	744	7	US-11-330-403-12223	Sequence 12223, A
382	53	11.8	747	7	US-11-330-403-10834	Sequence 10834, A
383	53	11.8	801	7	US-11-056-355B-90893	Sequence 90893, A
384	53	11.8	801	7	US-11-056-355B-94649	Sequence 94649, A
385	53	11.8	905	7	US-11-056-355B-90892	Sequence 90892, A
386	53	11.8	905	7	US-11-056-355B-94648	Sequence 94648, A
387	53	11.8	917	7	US-11-056-355B-90891	Sequence 90891, A
388	53	11.8	917	7	US-11-056-355B-94647	Sequence 94647, A
389	53	11.8	1337	7	US-11-416-492-4	Sequence 4, Appli
390	53	11.8	1464	6	US-10-537-642-27	Sequence 27, Appl
391	52.5	11.7	106	6	US-10-573-378-55	Sequence 55, Appl
392	52.5	11.7	114	7	US-11-256-332-99	Sequence 99, Appl
393	52.5	11.7	117	7	US-11-413-563-40	Sequence 40, Appl

394	52.5	11.7	164	7	US-11-330-403-15177	Sequence 15177, A
395	52.5	11.7	218	7	US-11-330-403-3124	Sequence 3124, Ap
396	52.5	11.7	283	6	US-10-415-326-19	Sequence 19, Appl
397	52.5	11.7	304	7	US-11-330-403-16483	Sequence 16483, A
398	52.5	11.7	307	6	US-10-953-349-24790	Sequence 24790, A
399	52.5	11.7	307	7	US-11-056-355B-59980	Sequence 59980, A
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403	52.5	11.7	398	7	US-11-330-403-16448	Sequence 16448, A
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405	52.5	11.7	453	6	US-10-449-902-45426	Sequence 45426, A
406	52.5	11.7	491	6	US-10-533-176-154	Sequence 154, App
407	52.5	11.7	491	6	US-10-533-232A-320	Sequence 320, App
408	52.5	11.7	491	7	US-11-330-403-11823	Sequence 11823, A
409	52.5	11.7	491	7	US-11-330-403-13681	Sequence 13681, A
410	52.5	11.7	491	7	US-11-330-403-15619	Sequence 15619, A
411	52.5	11.7	492	6	US-10-449-902-42958	Sequence 42958, A
412	52.5	11.7	492	6	US-10-449-902-52839	Sequence 52839, A
413	52.5	11.7	492	6	US-10-612-783-6675	Sequence 6675, Ap
414	52.5	11.7	492	7	US-11-330-403-2623	Sequence 2623, Ap
415	52.5	11.7	576	7	US-11-174-307B-4176	Sequence 4176, Ap
416	52.5	11.7	648	7	US-11-056-355B-75791	Sequence 75791, A
417	52.5	11.7	785	7	US-11-056-355B-75790	Sequence 75790, A
418	52.5	11.7	798	6	US-10-669-920-199	Sequence 199, App
419	52.5	11.7	844	6	US-10-374-780A-228	Sequence 228, App
420	52.5	11.7	858	7	US-11-056-355B-75789	Sequence 75789, A
421	52.5	11.7	867	7	US-11-343-271-6	Sequence 6, Appli
422	52.5	11.7	895	6	US-10-471-571A-922	Sequence 922, App
423	52.5	11.7	895	6	US-10-564-375-1	Sequence 1, Appli
424	52.5	11.7	1008	6	US-10-449-902-50652	Sequence 50652, A
425	52.5	11.7	1367	7	US-11-289-102-382	Sequence 382, App
426	52.5	11.7	1367	7	US-11-365-989-118	Sequence 118, App
427	52.5	11.7	2117	7	US-11-330-403-15081	Sequence 15081, A
428	52	11.6	214	7	US-11-274-452-9	Sequence 9, Appli
429	52	11.6	214	7	US-11-274-452-11	Sequence 11, Appl
430	52	11.6	215	7	US-11-396-495-13	Sequence 13, Appl
431	52	11.6	219	7	US-11-256-332-156	Sequence 156, App
432	52	11.6	231	7	US-11-274-452-13	Sequence 13, Appl
433	52	11.6	232	7	US-11-373-546-8	Sequence 8, Appli
434	52	11.6	232	7	US-11-373-546-12	Sequence 12, Appl
435	52	11.6	233	7	US-11-321-421-110	Sequence 110, App
436	52	11.6	241	7	US-11-056-355B-72251	Sequence 72251, A
437	52	11.6	241	7	US-11-056-355B-102405	Sequence 102405,
438	52	11.6	241	7	US-11-056-355B-113644	Sequence 113644,
439	52	11.6	242	7	US-11-056-355B-100348	Sequence 100348,
440	52	11.6	242	7	US-11-056-355B-111587	Sequence 111587,
441	52	11.6	243	7	US-11-256-332-256	Sequence 256, App
442	52	11.6	260	7	US-11-330-403-9231	Sequence 9231, Ap
443	52	11.6	278	6	US-10-953-349-25641	Sequence 25641, A
444	52	11.6	288	6	US-10-953-349-25640	Sequence 25640, A
445	52	11.6	291	7	US-11-056-355B-72250	Sequence 72250, A
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447	52	11.6	291	7	US-11-056-355B-113643	Sequence 113643,
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450	52	11.6	296	7	US-11-274-452-5	Sequence 5, Appli
451	52	11.6	298	7	US-11-056-355B-102403	Sequence 102403,
452	52	11.6	298	7	US-11-056-355B-113642	Sequence 113642,
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454	52	11.6	333	7	US-11-056-355B-64789	Sequence 64789, A
455	52	11.6	339	7	US-11-056-355B-64788	Sequence 64788, A
456	52	11.6	345	6	US-10-953-349-23136	Sequence 23136, A
457	52	11.6	345	7	US-11-056-355B-54649	Sequence 54649, A
458	52	11.6	355	7	US-11-056-355B-58718	Sequence 58718, A
459	52	11.6	361	7	US-11-056-355B-100347	Sequence 100347,
460	52	11.6	361	7	US-11-056-355B-111586	Sequence 111586,
461	52	11.6	363	6	US-10-953-349-25639	Sequence 25639, A
462	52	11.6	367	6	US-10-953-349-23135	Sequence 23135, A
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465	52	11.6	374	7	US-11-056-355B-54647	Sequence 54647, A
466	52	11.6	393	7	US-11-056-355B-58717	Sequence 58717, A
467	52	11.6	397	7	US-11-056-355B-38489	Sequence 38489, A
468	52	11.6	397	7	US-11-056-355B-102541	Sequence 102541,
469	52	11.6	397	7	US-11-056-355B-113780	Sequence 113780,
470	52	11.6	407	6	US-10-538-002-175	Sequence 175, App
471	52	11.6	408	7	US-11-056-355B-64787	Sequence 64787, A
472	52	11.6	418	6	US-10-449-902-34462	Sequence 34462, A
473	52	11.6	418	6	US-10-449-902-56242	Sequence 56242, A
474	52	11.6	441	7	US-11-056-355B-38488	Sequence 38488, A
475	52	11.6	441	7	US-11-056-355B-102540	Sequence 102540,
476	52	11.6	441	7	US-11-056-355B-113779	Sequence 113779,
477	52	11.6	452	7	US-11-056-355B-100346	Sequence 100346,
478	52	11.6	452	7	US-11-056-355B-111585	Sequence 111585,
479	52	11.6	470	6	US-10-449-902-31227	Sequence 31227, A
480	52	11.6	470	6	US-10-449-902-54114	Sequence 54114, A
481	52	11.6	472	7	US-11-056-355B-38487	Sequence 38487, A
482	52	11.6	472	7	US-11-056-355B-102539	Sequence 102539,
483	52	11.6	472	7	US-11-056-355B-113778	Sequence 113778,
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485	52	11.6	499	6	US-10-538-002-174	Sequence 174, App
486	52	11.6	508	6	US-10-449-902-47145	Sequence 47145, A
487	52	11.6	512	7	US-11-330-403-7812	Sequence 7812, Ap
488	52	11.6	515	7	US-11-330-403-6001	Sequence 6001, Ap
489	52	11.6	517	7	US-11-056-355B-42672	Sequence 42672, A
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496	52	11.6	518	7	US-11-056-355B-76764	Sequence 76764, A
497	52	11.6	532	6	US-10-374-780A-2290	Sequence 2290, Ap
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499	52	11.6	533	7	US-11-056-355B-42670	Sequence 42670, A
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506	52	11.6	716	7	US-11-056-355B-71220	Sequence 71220, A
507	52	11.6	749	6	US-10-559-952-6	Sequence 6, Appli
508	52	11.6	749	7	US-11-330-403-6670	Sequence 6670, Ap
509	52	11.6	799	7	US-11-361-415-83	Sequence 83, Appl
510	52	11.6	853	7	US-11-056-355B-71219	Sequence 71219, A
511	52	11.6	906	7	US-11-293-697-3128	Sequence 3128, Ap
512	52	11.6	926	7	US-11-056-355B-71218	Sequence 71218, A
513	52	11.6	3029	6	US-10-537-642-10	Sequence 10, Appl
514	52	11.6	3460	6	US-10-505-928-104	Sequence 104, App
515	52	11.6	3460	6	US-10-570-909-51	Sequence 51, Appl
516	51.5	11.5	109	7	US-11-249-296-40	Sequence 40, Appl
517	51.5	11.5	113	7	US-11-290-687-84	Sequence 84, Appl
518	51.5	11.5	113	7	US-11-290-687-92	Sequence 92, Appl
519	51.5	11.5	113	7	US-11-290-687-94	Sequence 94, Appl
520	51.5	11.5	113	7	US-11-404-967-84	Sequence 84, Appl
521	51.5	11.5	113	7	US-11-404-967-92	Sequence 92, Appl
522	51.5	11.5	113	7	US-11-404-967-94	Sequence 94, Appl
523	51.5	11.5	164	7	US-11-293-697-3415	Sequence 3415, Ap
524	51.5	11.5	186	6	US-10-449-902-33215	Sequence 33215, A
525	51.5	11.5	186	6	US-10-449-902-42659	Sequence 42659, A
526	51.5	11.5	186	6	US-10-449-902-49159	Sequence 49159, A
527	51.5	11.5	186	6	US-10-449-902-53612	Sequence 53612, A
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531	51.5	11.5	226	7	US-11-445-045-33	Sequence 33, Appl
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533	51.5	11.5	228	7	US-11-056-355B-55073	Sequence 55073, A
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537	51.5	11.5	246	7	US-11-056-355B-46584	Sequence 46584, A
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542	51.5	11.5	310	7	US-11-471-396-31	Sequence 31, Appl
543	51.5	11.5	317	7	US-11-330-403-3143	Sequence 3143, Ap
544	51.5	11.5	318	6	US-10-612-783-4339	Sequence 4339, Ap
545	51.5	11.5	322	7	US-11-056-355B-53979	Sequence 53979, A
546	51.5	11.5	342	6	US-10-612-783-4340	Sequence 4340, Ap
547	51.5	11.5	342	7	US-11-330-403-480	Sequence 480, App
548	51.5	11.5	342	7	US-11-330-403-4107	Sequence 4107, Ap
549	51.5	11.5	346	7	US-11-330-403-11612	Sequence 11612, A
550	51.5	11.5	376	7	US-11-056-355B-45013	Sequence 45013, A
551	51.5	11.5	376	7	US-11-056-355B-46583	Sequence 46583, A
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559	51.5	11.5	436	7	US-11-434-137-2082	Sequence 2082, Ap
560	51.5	11.5	436	7	US-11-434-184-2082	Sequence 2082, Ap
561	51.5	11.5	436	7	US-11-434-199-2082	Sequence 2082, Ap
562	51.5	11.5	436	7	US-11-434-203-2082	Sequence 2082, Ap
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565	51.5	11.5	492	7	US-11-330-403-8546	Sequence 8546, Ap
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567	51.5	11.5	626	7	US-11-056-355B-78556	Sequence 78556, A
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573	51.5	11.5	739	7	US-11-056-355B-84020	Sequence 84020, A
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581	51	11.4	97	7	US-11-434-137-7346	Sequence 7346, Ap
582	51	11.4	97	7	US-11-434-184-7346	Sequence 7346, Ap
583	51	11.4	97	7	US-11-434-199-7346	Sequence 7346, Ap
584	51	11.4	97	7	US-11-434-203-7346	Sequence 7346, Ap
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588	51	11.4	236	6	US-10-529-072-2	Sequence 2, Appli
589	51	11.4	236	7	US-11-290-687-27	Sequence 27, Appl
590	51	11.4	236	7	US-11-290-687-28	Sequence 28, Appl
591	51	11.4	236	7	US-11-404-967-27	Sequence 27, Appl
592	51	11.4	236	7	US-11-404-967-28	Sequence 28, Appl
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596	51	11.4	306	6	US-10-953-349-3608	Sequence 3608, Ap
597	51	11.4	310	7	US-11-174-307B-4602	Sequence 4602, Ap
598	51	11.4	321	7	US-11-330-403-16288	Sequence 16288, A
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601	51	11.4	331	6	US-10-953-349-3607	Sequence 3607, Ap
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606	51	11.4	363	7	US-11-056-355B-57910	Sequence 57910, A
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608	51	11.4	376	7	US-11-056-355B-83017	Sequence 83017, A
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611	51	11.4	402	7	US-11-056-355B-40984	Sequence 40984, A
612	51	11.4	406	7	US-11-056-355B-9749	Sequence 9749, Ap
613	51	11.4	424	7	US-11-366-965-421	Sequence 421, App
614	51	11.4	464	7	US-11-056-355B-88585	Sequence 88585, A
615	51	11.4	464	7	US-11-056-355B-92341	Sequence 92341, A
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619	51	11.4	516	7	US-11-330-403-6740	Sequence 6740, Ap
620	51	11.4	526	7	US-11-056-355B-91529	Sequence 91529, A
621	51	11.4	526	7	US-11-056-355B-95285	Sequence 95285, A
622	51	11.4	527	6	US-10-449-902-54307	Sequence 54307, A
623	51	11.4	528	7	US-11-330-403-2594	Sequence 2594, Ap
624	51	11.4	540	7	US-11-056-355B-88583	Sequence 88583, A
625	51	11.4	540	7	US-11-056-355B-92339	Sequence 92339, A
626	51	11.4	541	7	US-11-056-355B-91528	Sequence 91528, A
627	51	11.4	541	7	US-11-056-355B-95284	Sequence 95284, A
630	51	11.4	545	7	US-11-101-316-110	Sequence 110, App
631	51	11.4	545	7	US-11-293-697-3725	Sequence 3725, Ap
632	51	11.4	545	7	US-11-376-673-110	Sequence 110, App
633	51	11.4	555	7	US-11-056-355B-91527	Sequence 91527, A
634	51	11.4	555	7	US-11-056-355B-95283	Sequence 95283, A
635	51	11.4	684	7	US-11-174-307B-3706	Sequence 3706, Ap
636	51	11.4	685	7	US-11-293-697-3546	Sequence 3546, Ap
637	51	11.4	1035	6	US-10-700-439-160	Sequence 160, App
638	51	11.4	1123	7	US-11-330-403-6944	Sequence 6944, Ap
639	51	11.4	1214	7	US-11-056-355B-71658	Sequence 71658, A
640	51	11.4	1221	7	US-11-056-355B-71763	Sequence 71763, A
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644	51	11.4	1254	7	US-11-056-355B-71761	Sequence 71761, A
645	51	11.4	1373	6	US-10-669-920-412	Sequence 412, App
646	51	11.4	1420	7	US-11-283-329-156	Sequence 156, App
647	51	11.4	1424	7	US-11-283-329-154	Sequence 154, App
648	51	11.4	1605	7	US-11-056-355B-88407	Sequence 88407, A
649	51	11.4	1605	7	US-11-056-355B-92163	Sequence 92163, A
650	51	11.4	1646	7	US-11-056-355B-88406	Sequence 88406, A
651	51	11.4	1646	7	US-11-056-355B-92162	Sequence 92162, A
652	51	11.4	1773	7	US-11-056-355B-88405	Sequence 88405, A
653	51	11.4	1773	7	US-11-056-355B-92161	Sequence 92161, A
654	50.5	11.2	85	6	US-10-553-928-339	Sequence 339, App
655	50.5	11.2	106	6	US-10-553-938-59	Sequence 59, Appl
656	50.5	11.2	107	6	US-10-522-086-6	Sequence 6, Appli
657	50.5	11.2	108	7	US-11-290-249-8	Sequence 8, Appli
658	50.5	11.2	108	7	US-11-328-483-41	Sequence 41, Appl
659	50.5	11.2	170	7	US-11-313-356-76	Sequence 76, Appl
660	50.5	11.2	181	6	US-10-449-902-37798	Sequence 37798, A
661	50.5	11.2	185	6	US-10-953-349-33580	Sequence 33580, A
662	50.5	11.2	185	7	US-11-056-355B-7928	Sequence 7928, Ap
663	50.5	11.2	243	7	US-11-356-373-21	Sequence 21, Appl
664	50.5	11.2	244	7	US-11-056-355B-25750	Sequence 25750, A
665	50.5	11.2	258	6	US-10-953-349-25568	Sequence 25568, A
666	50.5	11.2	263	7	US-11-356-373-18	Sequence 18, Appl
667	50.5	11.2	278	6	US-10-449-902-34252	Sequence 34252, A
668	50.5	11.2	278	6	US-10-374-780A-865	Sequence 865, App
669	50.5	11.2	298	7	US-11-056-355B-44651	Sequence 44651, A
670	50.5	11.2	298	7	US-11-056-355B-47201	Sequence 47201, A
671	50.5	11.2	298	7	US-11-056-355B-50039	Sequence 50039, A
672	50.5	11.2	301	7	US-11-056-355B-25749	Sequence 25749, A
673	50.5	11.2	314	7	US-11-140-450-60	Sequence 60, Appl
674	50.5	11.2	332	6	US-10-511-455-33	Sequence 33, Appl
675	50.5	11.2	356	6	US-10-449-902-56255	Sequence 56255, A
676	50.5	11.2	367	7	US-11-056-355B-47761	Sequence 47761, A
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678	50.5	11.2	372	7	US-11-056-355B-108174	Sequence 108174,
679	50.5	11.2	372	7	US-11-056-355B-119413	Sequence 119413,
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682	50.5	11.2	394	7	US-11-330-403-7279	Sequence 7279, Ap
683	50.5	11.2	408	7	US-11-056-355B-13476	Sequence 13476, A
684	50.5	11.2	419	7	US-11-056-355B-108173	Sequence 108173,
685	50.5	11.2	419	7	US-11-056-355B-119412	Sequence 119412,
686	50.5	11.2	420	7	US-11-056-355B-47759	Sequence 47759, A
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695	50.5	11.2	496	7	US-11-330-403-12869	Sequence 12869, A
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710	50.5	11.2	775	7	US-11-056-355B-85284	Sequence 85284, A
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713	50.5	11.2	816	7	US-11-056-355B-85282	Sequence 85282, A
714	50.5	11.2	860	7	US-11-056-355B-73543	Sequence 73543, A
715	50.5	11.2	885	7	US-11-056-355B-73542	Sequence 73542, A
716	50.5	11.2	901	7	US-11-056-355B-73541	Sequence 73541, A
717	50.5	11.2	914	6	US-10-449-902-51797	Sequence 51797, A
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719	50.5	11.2	1822	6	US-10-505-928-700	Sequence 700, App
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721	50	11.1	140	7	US-11-324-769-18	Sequence 18, Appl
722	50	11.1	175	7	US-11-271-158-7	Sequence 7, Appli
723	50	11.1	175	7	US-11-271-158-19	Sequence 19, Appl
724	50	11.1	196	7	US-11-246-999-36	Sequence 36, Appl
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727	50	11.1	210	7	US-11-056-355B-118243	Sequence 118243,
728	50	11.1	219	7	US-11-342-353-13	Sequence 13, Appl
729	50	11.1	219	7	US-11-368-338-40	Sequence 40, Appl
730	50	11.1	219	7	US-11-256-332-161	Sequence 161, App
731	50	11.1	235	6	US-10-544-911A-70	Sequence 70, Appl
732	50	11.1	237	7	US-11-351-886-4	Sequence 4, Appli
733	50	11.1	245	7	US-11-056-355B-7167	Sequence 7167, Ap
734	50	11.1	261	6	US-10-953-349-7297	Sequence 7297, Ap
735	50	11.1	286	7	US-11-056-355B-23445	Sequence 23445, A
736	50	11.1	321	6	US-10-953-349-26953	Sequence 26953, A
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738	50	11.1	327	7	US-11-056-355B-23444	Sequence 23444, A
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741	50	11.1	341	6	US-10-449-902-48850	Sequence 48850, A
742	50	11.1	344	6	US-10-953-349-26952	Sequence 26952, A
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746	50	11.1	352	6	US-10-953-349-26951	Sequence 26951, A
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756	50	11.1	416	6	US-10-374-780A-250	Sequence 250, App
757	50	11.1	417	6	US-10-953-349-7295	Sequence 7295, Ap
758	50	11.1	428	7	US-11-330-403-3134	Sequence 3134, Ap
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760	50	11.1	445	6	US-10-449-902-37108	Sequence 37108, A
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768	50	11.1	512	7	US-11-330-403-1222	Sequence 1222, Ap
769	50	11.1	512	7	US-11-330-403-2550	Sequence 2550, Ap
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771	50	11.1	517	7	US-11-174-307B-3030	Sequence 3030, Ap
772	50	11.1	525	7	US-11-024-544A-18	Sequence 18, Appl
773	50	11.1	525	7	US-11-190-750-132	Sequence 132, App
774	50	11.1	525	7	US-11-264-784-84	Sequence 84, Appl
775	50	11.1	525	7	US-11-264-737-125	Sequence 125, App
776	50	11.1	525	7	US-11-265-761-97	Sequence 97, Appl
777	50	11.1	538	6	US-10-449-902-51323	Sequence 51323, A
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787	50	11.1	915	6	US-10-540-808-3	Sequence 3, Appli
788	50	11.1	929	7	US-11-293-697-3551	Sequence 3551, Ap
789	50	11.1	973	6	US-10-449-902-45586	Sequence 45586, A
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791	50	11.1	974	7	US-11-330-403-9008	Sequence 9008, Ap
792	50	11.1	989	7	US-11-366-965-490	Sequence 490, App
793	50	11.1	1159	6	US-10-449-902-41433	Sequence 41433, A
795	50	11.1	1523	6	US-10-533-365-236	Sequence 236, App
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798	49.5	11.0	108	7	US-11-311-939-127	Sequence 127, App
799	49.5	11.0	108	7	US-11-311-939-149	Sequence 149, App
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808	49.5	11.0	195	7	US-11-388-570-99	Sequence 99, Appl
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813	49.5	11.0	195	7	US-11-388-570-104	Sequence 104, App
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815	49.5	11.0	195	7	US-11-388-570-106	Sequence 106, App
816	49.5	11.0	195	7	US-11-388-570-107	Sequence 107, App
817	49.5	11.0	195	7	US-11-388-570-108	Sequence 108, App
818	49.5	11.0	195	7	US-11-388-570-109	Sequence 109, App
819	49.5	11.0	195	7	US-11-388-570-110	Sequence 110, App
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827	49.5	11.0	195	7	US-11-388-642-99	Sequence 99, Appl
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831	49.5	11.0	195	7	US-11-388-642-103	Sequence 103, App
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833	49.5	11.0	195	7	US-11-388-642-105	Sequence 105, App
834	49.5	11.0	195	7	US-11-388-642-106	Sequence 106, App
835	49.5	11.0	195	7	US-11-388-642-107	Sequence 107, App

836	49.5	11.0	195	7	US-11-388-642-108	Sequence 108, App
837	49.5	11.0	195	7	US-11-388-642-109	Sequence 109, App
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839	49.5	11.0	195	7	US-11-388-642-111	Sequence 111, App
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847	49.5	11.0	248	7	US-11-434-184-2414	Sequence 2414, Ap
848	49.5	11.0	248	7	US-11-434-199-2414	Sequence 2414, Ap
849	49.5	11.0	248	7	US-11-434-203-2414	Sequence 2414, Ap
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851	49.5	11.0	258	6	US-10-511-937-2999	Sequence 2999, Ap
852	49.5	11.0	269	7	US-11-389-432-176	Sequence 176, App
853	49.5	11.0	280	7	US-11-056-355B-17799	Sequence 17799, A
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865	49.5	11.0	447	6	US-10-505-928-329	Sequence 329, App
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878	49.5	11.0	796	7	US-11-361-415-81	Sequence 81, Appl
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881	49.5	11.0	1204	7	US-11-289-102-236	Sequence 236, App
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894	49	10.9	113	7	US-11-366-965-1075	Sequence 1075, Ap
895	49	10.9	136	7	US-11-290-687-19	Sequence 19, Appl
896	49	10.9	136	7	US-11-404-967-19	Sequence 19, Appl
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904	49	10.9	198	7	US-11-388-642-73	Sequence 73, Appl
905	49	10.9	212	7	US-11-330-403-7299	Sequence 7299, Ap
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910	49	10.9	214	7	US-11-317-786B-13	Sequence 13, Appl
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912	49	10.9	224	6	US-10-449-902-30304	Sequence 30304, A
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914	49	10.9	236	7	US-11-290-687-35	Sequence 35, Appl
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916	49	10.9	236	7	US-11-404-967-35	Sequence 35, Appl
917	49	10.9	246	6	US-10-449-902-32602	Sequence 32602, A
918	49	10.9	246	6	US-10-449-902-51800	Sequence 51800, A
919	49	10.9	253	6	US-10-953-349-26085	Sequence 26085, A
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922	49	10.9	254	7	US-11-056-355B-63691	Sequence 63691, A
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947	49	10.9	446	6	US-10-449-902-54347	Sequence 54347, A
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959	49	10.9	508	7	US-11-296-657-3	Sequence 3, Appli
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963	49	10.9	552	6	US-10-953-349-11688	Sequence 11688, A
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965	49	10.9	579	6	US-10-471-571A-736	Sequence 736, App
966	49	10.9	589	6	US-10-449-902-42573	Sequence 42573, A
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983	49	10.9	1456	6	US-10-505-928-69	Sequence 69, Appl
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985	49	10.9	1456	7	US-11-090-997-1258	Sequence 1258, Ap
986	49	10.9	1506	7	US-11-070-573-9	Sequence 9, Appli
987	49	10.9	1625	7	US-11-090-997-696	Sequence 696, App
988	49	10.9	1654	7	US-11-090-997-690	Sequence 690, App
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991	49	10.9	2301	7	US-11-335-891-30	Sequence 30, Appl
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1226	48	10.7	590	6	US-10-449-902-53617	Sequence 53617, A
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1228	48	10.7	592	6	US-10-539-228-813	Sequence 813, App
1229	48	10.7	592	6	US-10-669-920-838	Sequence 838, App
1230	48	10.7	602	7	US-11-330-403-3098	Sequence 3098, Ap
1231	48	10.7	618	6	US-10-449-902-48598	Sequence 48598, A
1232	48	10.7	663	6	US-10-612-783-6407	Sequence 6407, Ap
1233	48	10.7	708	7	US-11-056-355B-96430	Sequence 96430, A
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1235	48	10.7	753	7	US-11-056-355B-96429	Sequence 96429, A
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1239	48	10.7	844	6	US-10-539-228-464	Sequence 464, App
1240	48	10.7	844	6	US-10-669-920-970	Sequence 970, App
1241	48	10.7	845	6	US-10-669-920-968	Sequence 968, App
1242	48	10.7	915	6	US-10-449-902-46382	Sequence 46382, A
1243	48	10.7	1028	6	US-10-502-394-76	Sequence 76, Appl
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1245	48	10.7	1086	6	US-10-374-780A-2342	Sequence 2342, Ap
1246	48	10.7	1136	7	US-11-330-403-3321	Sequence 3321, Ap
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1248	48	10.7	2072	6	US-10-519-210-6	Sequence 6, Appli
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1251	48	10.7	2538	7	US-11-375-551-20	Sequence 20, Appl
1252	48	10.7	2538	7	US-11-070-573-23	Sequence 23, Appl
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1257	47.5	10.6	106	7	US-11-337-300-41	Sequence 41, Appl
1258	47.5	10.6	106	7	US-11-397-328-60	Sequence 60, Appl
1259	47.5	10.6	107	6	US-10-506-063A-16	Sequence 16, Appl
1260	47.5	10.6	107	6	US-10-516-260A-16	Sequence 16, Appl
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1263	47.5	10.6	107	7	US-11-328-483-158	Sequence 158, App
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1265	47.5	10.6	108	7	US-11-145-131A-8	Sequence 8, Appli
1266	47.5	10.6	108	7	US-11-328-483-177	Sequence 177, App
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1268	47.5	10.6	113	7	US-11-290-687-89	Sequence 89, Appl
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1278	47.5	10.6	234	7	US-11-211-917-72	Sequence 72, Appl
1279	47.5	10.6	235	7	US-11-224-577-12	Sequence 12, Appl
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1282	47.5	10.6	240	7	US-11-056-355B-4803	Sequence 4803, Ap
1283	47.5	10.6	240	7	US-11-317-786B-15	Sequence 15, Appl
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1285	47.5	10.6	244	7	US-11-317-786B-17	Sequence 17, Appl
1286	47.5	10.6	244	7	US-11-317-786B-19	Sequence 19, Appl
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1291	47.5	10.6	245	7	US-11-337-300-59	Sequence 59, Appl
1292	47.5	10.6	245	7	US-11-337-300-63	Sequence 63, Appl
1293	47.5	10.6	247	7	US-11-337-300-57	Sequence 57, Appl
1294	47.5	10.6	247	7	US-11-337-300-96	Sequence 96, Appl
1295	47.5	10.6	248	7	US-11-337-300-61	Sequence 61, Appl
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1297	47.5	10.6	249	7	US-11-337-300-67	Sequence 67, Appl
1298	47.5	10.6	249	7	US-11-337-300-69	Sequence 69, Appl
1299	47.5	10.6	249	7	US-11-337-300-90	Sequence 90, Appl
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1336	47.5	10.6	319	7	US-11-317-571-92	Sequence 92, Appl
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1339	47.5	10.6	319	7	US-11-317-571-119	Sequence 119, App
1340	47.5	10.6	319	7	US-11-317-571-128	Sequence 128, App
1341	47.5	10.6	319	7	US-11-317-571-137	Sequence 137, App
1342	47.5	10.6	319	7	US-11-317-571-146	Sequence 146, App
1343	47.5	10.6	319	7	US-11-317-571-155	Sequence 155, App
1344	47.5	10.6	319	7	US-11-317-571-164	Sequence 164, App
1345	47.5	10.6	319	7	US-11-317-571-173	Sequence 173, App
1346	47.5	10.6	319	7	US-11-317-571-182	Sequence 182, App
1347	47.5	10.6	319	7	US-11-317-571-191	Sequence 191, App
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1370	47.5	10.6	342	7	US-11-317-571-91	Sequence 91, Appl
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1374	47.5	10.6	342	7	US-11-317-571-127	Sequence 127, App
1375	47.5	10.6	342	7	US-11-317-571-136	Sequence 136, App
1376	47.5	10.6	342	7	US-11-317-571-145	Sequence 145, App
1377	47.5	10.6	342	7	US-11-317-571-154	Sequence 154, App
1378	47.5	10.6	342	7	US-11-317-571-163	Sequence 163, App
1379	47.5	10.6	342	7	US-11-317-571-172	Sequence 172, App
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1437	47.5	10.6	557	6	US-10-612-783-6715	Sequence 6715, Ap
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1474	47.5	10.6	917	7	US-11-056-355B-119946	Sequence 119946,
1475	47.5	10.6	920	7	US-11-056-355B-86405	Sequence 86405, A
1476	47.5	10.6	926	7	US-11-056-355B-86404	Sequence 86404, A
1477	47.5	10.6	945	7	US-11-056-355B-108706	Sequence 108706,
1478	47.5	10.6	945	7	US-11-056-355B-119945	Sequence 119945,
1479	47.5	10.6	947	7	US-11-056-355B-45584	Sequence 45584, A
1480	47.5	10.6	948	6	US-10-449-902-53220	Sequence 53220, A
1481	47.5	10.6	949	7	US-11-056-355B-45154	Sequence 45154, A
1482	47.5	10.6	949	7	US-11-056-355B-48388	Sequence 48388, A
1483	47.5	10.6	973	6	US-10-537-648-12	Sequence 12, Appl
1484	47.5	10.6	1049	7	US-11-368-333-24	Sequence 24, Appl
1485	47.5	10.6	1049	7	US-11-368-334-18	Sequence 18, Appl
1486	47.5	10.6	1178	7	US-11-020-808-23	Sequence 23, Appl
1487	47.5	10.6	2529	6	US-10-553-928-262	Sequence 262, App
1488	47.5	10.6	2893	6	US-10-553-928-209	Sequence 209, App
1489	47.5	10.6	3176	7	US-11-105-233-155	Sequence 155, App
1490	47	10.5	45	6	US-10-953-349-13432	Sequence 13432, A
1491	47	10.5	61	6	US-10-449-902-47463	Sequence 47463, A
1492	47	10.5	72	7	US-11-248-008-61	Sequence 61, Appl
1493	47	10.5	72	7	US-11-248-008-62	Sequence 62, Appl
1494	47	10.5	72	7	US-11-248-008-63	Sequence 63, Appl
1495	47	10.5	108	6	US-10-526-072-4	Sequence 4, Appli
1496	47	10.5	108	7	US-11-150-871A-190	Sequence 190, App
1497	47	10.5	112	6	US-10-953-349-588	Sequence 588, App
1498	47	10.5	112	7	US-11-056-355B-21690	Sequence 21690, A
1499	47	10.5	112	7	US-11-056-355B-101486	Sequence 101486,
1500	47	10.5	112	7	US-11-056-355B-112725	Sequence 112725,

Search completed: November 21, 2006, 20:48:27
Job time : 23.6361 secs

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OM protein - protein search, using sw model

Run on: November 21, 2006, 19:59:58 ; Search time 14.9235 Seconds
(without alignments)
515.785 Million cell updates/sec

Title: US-10-063-553-48_COPY_111_190
Perfect score: 449
Sequence: 1 KGPLMCNSPSNSNANCEFSL.....RASSFHFDSEENKHRLIHFS 80

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	78.5	17.5	281	2	T51961	ATAF1-like protein
2	73	16.3	413	2	S01076	aspartate transami
3	70	15.6	490	2	S52830	HMS1 protein - yea
4	70	15.6	1011	2	T13669	neuromusculin - fr
5	68	15.1	2201	2	A32160	tenascin-C - human
6	67	14.9	296	2	AH1173	conserved hypothet
7	66	14.7	575	2	A54861	tenascin - rat (fr
8	66	14.7	1217	2	T00270	hypothetical prote
9	65.5	14.6	620	2	T49067	transcription fact
10	65.5	14.6	656	2	B49423	semaphorin I - fru
11	65	14.5	652	2	H96924	probable phosphohy
12	64.5	14.4	330	2	T43061	hypothetical prote
13	64.5	14.4	461	2	T25671	hypothetical prote
14	64.5	14.4	475	2	T39486	hypothetical prote
15	64.5	14.4	503	2	T38303	SWI/SNF complex tr
16	64	14.3	228	2	T16678	hypothetical prote
17	64	14.3	992	2	A42318	glycogen phosphory
18	64	14.3	1500	2	T03824	probable immediate
19	63	14.0	418	2	E86395	hypothetical prote
20	63	14.0	1165	1	S45879	chitin synthase (E
21	63	14.0	2051	2	T13164	plexin B - fruit f
22	62.5	13.9	296	2	AI1530	conserved hypothet
23	62.5	13.9	413	2	S29027	aspartate transami
24	62.5	13.9	646	2	JQ2150	B west mating prot
25	62.5	13.9	1748	1	JN0786	integrin beta-4 ch
26	62.5	13.9	1811	2	T00035	nonstructural poly
27	62	13.8	971	2	S50912	probable membrane
28	61.5	13.7	417	2	AG1934	folylpolyglutamate
29	61.5	13.7	487	2	T49424	hypothetical prote
30	61.5	13.7	647	2	JQ2149	B west mating prot
31	61.5	13.7	1034	2	S49947	SMT4 protein - yea
32	61	13.6	326	2	G84748	hypothetical prote
33	61	13.6	412	2	S13035	aspartate transami
34	61	13.6	413	2	S29028	aspartate transami
35	61	13.6	413	2	JT0439	aspartate transami
36	61	13.6	1810	1	A32230	tenascin precursor
37	61	13.6	2019	1	JQ1322	tenascin precursor
38	60.5	13.5	444	2	D97142	surface-layer rela
39	60.5	13.5	661	2	S37592	beta-fructofuranos
40	60.5	13.5	661	2	S37591	beta-fructofuranos
41	60.5	13.5	661	2	S37590	beta-fructofuranos
42	60.5	13.5	937	2	A56517	nucleoporin Nup98
43	60.5	13.5	992	2	S49835	hypothetical prote
44	60	13.4	292	2	T19669	hypothetical prote
45	60	13.4	292	2	G88783	protein C33A12.16
46	60	13.4	577	2	T32336	hypothetical prote
47	59.5	13.3	557	2	JC5487	cellulase (EC 3.2.
48	59.5	13.3	821	2	T41364	hypothetical prote
49	59	13.1	284	2	T06129	zinc finger protei
50	59	13.1	412	2	A26341	aspartate transami
51	59	13.1	433	2	S31436	Ig upsilon chain -
52	59	13.1	493	2	I39541	cytolytic enteroto
53	59	13.1	554	2	G96598	protein F20N2.6 [i
54	59	13.1	677	1	A45264	system b(0,+) amin
55	59	13.1	741	2	JS0606	homeobox protein A
56	59	13.1	763	2	S17998	gene COX1 intron 4
57	59	13.1	838	2	E89473	protein F52D2.6 [i
58	59	13.1	1006	2	T41104	probable transcrip
59	59	13.1	2352	2	T43431	alpha-glucan synth
60	58.5	13.0	508	2	T19350	hypothetical prote
61	58.5	13.0	640	2	S23008	insulin-like growt
62	58.5	13.0	1615	2	JE0372	low density lipopr
63	58.5	13.0	1748	1	JQ1555	genome polyprotein
64	58	12.9	261	2	I68718	MHC class II histo
65	58	12.9	375	2	A64300	aspartate transami
66	58	12.9	405	2	A83038	hypothetical prote
67	58	12.9	465	2	S03325	transforming prote
68	58	12.9	486	2	S07633	hematopoietic line
69	58	12.9	486	2	I49760	LckBP1 protein - m
70	58	12.9	528	2	S63009	hypothetical prote
71	58	12.9	795	2	T31180	hypothetical prote
72	58	12.9	1666	2	T43169	hypothetical prote
73	57.5	12.8	176	2	I53630	cell surface glyco
74	57.5	12.8	269	2	I54432	MHC class II histo
75	57.5	12.8	275	1	F65090	3',5'-cyclic-nucle
76	57.5	12.8	275	1	G85963	3',5'-cyclic-nucle
77	57.5	12.8	275	1	H91118	3',5'-cyclic-nucle
78	57.5	12.8	413	2	S51667	serine/threonine k
79	57.5	12.8	546	2	T32382	hypothetical prote
80	57.5	12.8	574	2	AC1414	ABC transporter re
81	57.5	12.8	640	2	B84887	probable SCARECROW
82	57.5	12.8	959	2	T25704	hypothetical prote
83	57.5	12.8	1291	1	A28334	protein-tyrosine-p
84	57.5	12.8	1807	2	JC6319	integrin beta-4 ch
85	57.5	12.8	3005	2	S33642	homeotic protein z
86	57	12.7	219	2	S52028	Ig kappa chain - m
87	57	12.7	307	2	A45600	asparagine-rich bl
88	57	12.7	446	2	F84506	En/Spm-like transp
89	57	12.7	471	2	AH1810	isochorismate synt
90	57	12.7	619	1	KSNCLO	laccase (EC 1.10.3
91	57	12.7	619	1	KSNCLT	laccase (EC 1.10.3
92	57	12.7	813	2	T04220	H+-transporting AT
93	57	12.7	1042	2	T29307	hypothetical prote
94	57	12.7	1411	2	S55123	hypothetical prote
95	57	12.7	2761	2	T21064	hypothetical prote
96	56.5	12.6	169	2	T31484	hypothetical prote
97	56.5	12.6	180	1	HLHUC3	MHC class II histo
98	56.5	12.6	251	2	S40995	hypothetical prote
99	56.5	12.6	263	2	T46093	hypothetical prote
100	56.5	12.6	457	2	S18239	glycerol-3-phospha
101	56.5	12.6	569	2	E84904	probable laccase (
102	56.5	12.6	740	2	H82807	beta-glucosidase X

103	56.5	12.6	768	2	JC6564	cellobiose oxidase
104	56.5	12.6	874	2	AC2287	hypothetical prote
105	56.5	12.6	891	1	RDBHNP	nitrate reductase
106	56.5	12.6	1018	2	T30986	period protein - C
107	56.5	12.6	1125	2	T39052	hypothetical serin
108	56.5	12.6	1447	1	VGIHE3	E2 glycoprotein pr
109	56.5	12.6	1447	1	VGIHE2	E2 glycoprotein pr
110	56.5	12.6	4351	2	T00252	MEGF1 protein - ra
111	56.5	12.6	5138	2	B96695	hypothetical prote
112	56	12.5	238	2	A45544	BoLA-DQ beta-1 - b
113	56	12.5	247	2	I45942	MHC class II - bov
114	56	12.5	259	2	S64423	probable membrane
115	56	12.5	261	1	HLHU2C	MHC class II histo
116	56	12.5	261	2	I45928	MHC class II - bov
117	56	12.5	447	2	A84718	hypothetical prote
118	56	12.5	468	2	T22397	hypothetical prote
119	56	12.5	492	2	I39591	hemolysin - Aeromo
120	56	12.5	518	2	T23745	hypothetical prote
121	56	12.5	555	2	C83444	probable AMP-bindi
122	56	12.5	703	2	A97312	membrane associate
123	56	12.5	711	2	D83897	catalase katB [imp
124	56	12.5	714	2	S56208	hypothetical prote
125	56	12.5	729	2	T46328	probable adenosine
126	56	12.5	731	2	S56028	protein YKR018c ho
127	56	12.5	953	2	T01093	luminidependens pr
128	56	12.5	1161	2	B70172	DNA polymerase III
129	56	12.5	1308	2	B32494	transposable eleme
130	55.5	12.4	218	2	B49346	butyrate-acetoacet
131	55.5	12.4	276	2	A69437	dehydrase homolog
132	55.5	12.4	288	2	A90135	SAM-dependent meth
133	55.5	12.4	417	2	B97249	fusion HD-GYP doma
134	55.5	12.4	441	2	S29921	hypothetical prote
135	55.5	12.4	501	2	S51160	nitrate reductase
136	55.5	12.4	544	2	C96943	uncharacterized me
137	55.5	12.4	646	2	JN0473	P-selectin precurs
138	55.5	12.4	683	2	T03146	probable glycoprot
139	55.5	12.4	699	2	I37369	epican - human
140	55.5	12.4	704	1	S39004	finger protein MSN
141	55.5	12.4	858	1	A42239	adenylate cyclase
142	55.5	12.4	884	2	S66308	nitrate reductase
143	55.5	12.4	886	2	A59223	nitrate reductase
144	55.5	12.4	912	1	RDBHNS	nitrate reductase
145	55.5	12.4	915	1	RDBHNH	nitrate reductase
146	55.5	12.4	1016	2	T30990	period protein - C
147	55.5	12.4	1056	2	A53767	mucin MUC5B, trach
148	55.5	12.4	1874	1	JQ0533	genome polyprotein
149	55	12.2	183	2	A32339	MHC class II histo
150	55	12.2	183	2	I54288	MHC class II DQ3.1
151	55	12.2	183	2	I79496	MHC HLA-DQ-beta ch
152	55	12.2	218	2	G71260	probable ribulose-
153	55	12.2	224	2	A31459	MHC class II histo
154	55	12.2	233	2	E83580	conserved hypothet
155	55	12.2	261	1	HLHU1C	MHC class II histo
156	55	12.2	261	1	HLHUDB	MHC class II histo
157	55	12.2	261	2	I55996	MHC HLA-DQ-beta ce
158	55	12.2	261	2	B37044	MHC class II histo
159	55	12.2	261	2	I54480	HLA DQ-beta - huma
160	55	12.2	261	2	B32527	class II histocomp
161	55	12.2	268	2	D29312	MHC class II histo
162	55	12.2	287	2	T26411	hypothetical prote
163	55	12.2	358	2	I38429	connexin40 - human
164	55	12.2	359	2	E86706	hypothetical prote
165	55	12.2	363	2	JC7750	CVC domain-contain
166	55	12.2	406	2	S60962	hypothetical prote
167	55	12.2	413	2	S21560	aspartate transami
168	55	12.2	443	2	F87488	prolyl-tRNA synthe
169	55	12.2	458	2	S50919	hypothetical prote
170	55	12.2	486	2	A25976	aerolysin precurso
171	55	12.2	571	1	HNNZP2	hemagglutinin-neur
172	55	12.2	571	1	HNNZT2	hemagglutinin-neur
173	55	12.2	582	2	T38743	hypothetical zinc
174	55	12.2	586	2	JC7277	Sarcophaga-derived
175	55	12.2	593	2	T38547	probable cell divi
176	55	12.2	601	2	T00119	probable transcrip
177	55	12.2	650	2	S23217	beta-fructofuranos
178	55	12.2	708	2	S52317	quinohemoprotein e
179	55	12.2	956	1	QQBEK2	UL105 protein - hu
180	55	12.2	1052	1	A44937	kinetoplast-associ
181	55	12.2	1191	2	T13850	gene u-shaped prot
182	55	12.2	1194	2	E96624	hypothetical prote
183	55	12.2	1245	2	G86404	probable P-glycopr
184	55	12.2	1280	2	A39117	170K lectin precur
185	55	12.2	1450	2	C86880	hypothetical prote
186	55	12.2	2843	1	RBHUAP	adenomatous polypo
187	54.5	12.1	155	2	T49557	hypothetical prote
188	54.5	12.1	219	2	I45937	MHC cell surface g
189	54.5	12.1	232	2	I47094	MHC class II OLA-D
190	54.5	12.1	237	2	S68702	tryptase (EC 3.4.2
191	54.5	12.1	261	2	I45943	MHC class II - bov
192	54.5	12.1	323	2	T06506	glutenin low molec
193	54.5	12.1	348	2	S57601	ribonuclease H (EC
194	54.5	12.1	361	2	A91037	probable peptidase
195	54.5	12.1	361	2	C85881	probable peptidase
196	54.5	12.1	373	2	D71636	hypothetical prote
197	54.5	12.1	396	2	S01660	glycerol-3-phospha
198	54.5	12.1	448	2	S40439	tubulin alpha-2 ch
199	54.5	12.1	449	2	S55911	tubulin alpha-1 ch
200	54.5	12.1	449	2	T21415	hypothetical prote
201	54.5	12.1	477	2	S53362	mucin 5AC (clone J
202	54.5	12.1	482	2	T02538	hypothetical prote
203	54.5	12.1	506	2	D84609	hypothetical prote
204	54.5	12.1	528	1	A31854	lanosterol 14alpha
205	54.5	12.1	681	1	A36500	transferrin precur
206	54.5	12.1	760	2	S70294	FUN21 protein - ye
207	54.5	12.1	774	2	A86454	hypothetical prote
208	54.5	12.1	811	1	FOLJSP	gag polyprotein -
209	54.5	12.1	859	1	VCLJCT	env polyprotein pr
210	54.5	12.1	859	2	S24571	env protein - huma
211	54.5	12.1	916	2	S07554	nitrate reductase
212	54.5	12.1	1034	2	AB2013	hypothetical prote
213	54.5	12.1	1036	2	A29832	HPI layer surface
214	54.5	12.1	1106	2	T25065	hypothetical prote
215	54.5	12.1	1133	2	T01757	hypothetical prote
216	54.5	12.1	1241	2	JU0466	potassium transpor
217	54.5	12.1	1599	2	T16210	hypothetical prote
218	54.5	12.1	1776	1	RRWPYM	genome polyprotein
219	54.5	12.1	2524	2	A35844	Xotch protein - Af
220	54.5	12.1	6658	2	T13931	projectin - fruit
221	54	12.0	115	2	AB2223	hypothetical prote
222	54	12.0	140	2	S20914	lysozyme (EC 3.2.1
223	54	12.0	140	2	S41577	lysozyme (EC 3.2.1
224	54	12.0	140	2	S41574	lysozyme (EC 3.2.1
225	54	12.0	140	2	S41573	lysozyme (EC 3.2.1
226	54	12.0	214	2	S45465	heat shock protein
227	54	12.0	221	2	S25168	CHT28 protein - ch
228	54	12.0	223	1	CSNCM	peptidylprolyl iso
229	54	12.0	237	2	C86309	Similar to Ubiquit
230	54	12.0	260	2	I45938	MHC cell surface g
231	54	12.0	261	2	I68732	MHC class II histo
232	54	12.0	276	2	H96985	probable hydrolase
233	54	12.0	360	2	S48365	hypothetical prote
234	54	12.0	422	2	I50516	retinoid X recepto
235	54	12.0	425	2	T50184	mammalian swi/snf
236	54	12.0	447	2	T13204	hypothetical prote
237	54	12.0	485	2	S26575	hemolysin - Aeromo
238	54	12.0	504	2	S54744	cellulase (EC 3.2.
239	54	12.0	513	2	T41011	hypothetical prote
240	54	12.0	614	2	A32608	thyroid hormone re
241	54	12.0	636	2	T41673	hypothetical zinc
242	54	12.0	713	2	B75489	hypothetical prote
243	54	12.0	771	2	T38616	hypothetical prote
244	54	12.0	802	2	T21315	hypothetical prote
245	54	12.0	849	2	T01286	probable RNA-bindi
246	54	12.0	851	2	S12159	env protein - huma
247	54	12.0	890	2	T11805	nitrate reductase
248	54	12.0	920	2	S52301	nitrate reductase

249	54	12.0	938	2	T39006	related to yeast z
250	54	12.0	964	2	T41547	hypothetical prote
251	54	12.0	978	2	T16948	hypothetical prote
252	54	12.0	989	2	A54505	serine-repeat anti
253	54	12.0	997	2	B71617	SERA antigen/papai
254	54	12.0	1224	2	T07446	DNA-directed RNA p
255	54	12.0	1446	2	T30916	carboxypeptidase D
256	54	12.0	1742	2	S24600	projectin - fruit
257	54	12.0	1746	1	S19694	tenascin precursor
258	54	12.0	1945	2	T13937	plexin A - fruit f
259	54	12.0	2718	2	A23475	G surface protein
260	53.5	11.9	114	2	A34353	anti-peptide Fab'
261	53.5	11.9	122	2	AI1116	hypothetical prote
262	53.5	11.9	125	2	S40315	Ig kappa chain - h
263	53.5	11.9	175	2	T23437	hypothetical prote
264	53.5	11.9	261	2	F96722	hypothetical prote
265	53.5	11.9	264	2	S65070	chitinase (EC 3.2.
266	53.5	11.9	289	2	A48913	KRAB zinc finger p
267	53.5	11.9	308	2	E71697	probable proteinas
268	53.5	11.9	357	2	S09269	Ig alpha chain C r
269	53.5	11.9	403	2	E42521	A39R protein - vac
270	53.5	11.9	427	2	G82827	6-phosphofructokin
271	53.5	11.9	448	2	T22194	hypothetical prote
272	53.5	11.9	451	2	S13337	tubulin alpha-2 ch
273	53.5	11.9	455	2	T32189	zinc finger protei
274	53.5	11.9	474	2	A90520	ABC transporter pe
275	53.5	11.9	482	2	B83113	catalase PA4236 [i
276	53.5	11.9	517	2	S77255	hypothetical prote
277	53.5	11.9	617	2	S19254	nitrate reductase
278	53.5	11.9	642	2	S55521	beta-fructofuranos
279	53.5	11.9	661	2	T16597	hypothetical prote
280	53.5	11.9	678	2	H88187	protein C18H9.8 [i
281	53.5	11.9	751	2	T15230	hypothetical prote
282	53.5	11.9	823	2	H83724	hypothetical prote
283	53.5	11.9	825	2	T47164	hypothetical prote
284	53.5	11.9	900	2	S47029	nitrate reductase
285	53.5	11.9	909	2	JN0665	nitrate reductase
286	53.5	11.9	936	2	T26521	hypothetical prote
287	53.5	11.9	1131	2	T38744	hypothetical prote
288	53.5	11.9	1239	1	A32579	neuroglian - fruit
289	53.5	11.9	1513	2	T44045	hypothetical prote
290	53.5	11.9	1520	2	T44231	hypothetical prote
291	53.5	11.9	1712	2	C71618	hypothetical prote
292	53.5	11.9	2399	2	H71879	toxin-like outer m
293	53	11.8	140	2	A83285	hypothetical prote
294	53	11.8	144	2	T41370	hypothetical prote
295	53	11.8	203	2	T23943	hypothetical prote
296	53	11.8	207	2	T34054	hypothetical prote
297	53	11.8	232	2	B90129	26S proteasome SU
298	53	11.8	263	2	D83085	conserved hypothet
299	53	11.8	302	2	E64800	probable glutamate
300	53	11.8	302	2	A85566	probable periplasm
301	53	11.8	302	2	F90715	probable periplasm
302	53	11.8	310	2	JL0119	Fc gamma (IgG) rec
303	53	11.8	317	2	JL0118	Fc gamma (IgG) rec
304	53	11.8	323	2	S06946	Fc gamma (IgG) rec
305	53	11.8	339	2	A42259	endo-beta-N-acetyl
306	53	11.8	341	2	S31236	hypothetical prote
307	53	11.8	350	2	B82281	ferric vibriobacti
308	53	11.8	352	2	T23464	hypothetical prote
309	53	11.8	355	1	A55473	early switch prote
310	53	11.8	355	2	T07160	glutamate-ammonia
311	53	11.8	360	2	T06786	6a-hydroxymaackiai
312	53	11.8	367	2	T00815	probable Ta11-like
313	53	11.8	413	1	XNPGDC	aspartate transami
314	53	11.8	417	2	B55473	early switch prote
315	53	11.8	426	2	C55473	early switch prote
316	53	11.8	428	2	A53689	transcription fact
317	53	11.8	436	2	B86469	protein F12K21.16
318	53	11.8	443	2	T14916	mitosis-specific c
319	53	11.8	445	2	D84385	oligopeptide ABC t
320	53	11.8	461	2	T11819	glycerol-3-phospha
321	53	11.8	484	2	T16695	hypothetical prote
322	53	11.8	504	2	S00390	Ig gamma chain (cl
323	53	11.8	530	2	F89581	protein xol-1 [imp
324	53	11.8	533	1	TVFVFP	protein-tyrosine k
325	53	11.8	536	2	S66716	glutamate-tRNA lig
326	53	11.8	634	2	S31925	beta-fructofuranos
327	53	11.8	642	1	S34416	transcription fact
328	53	11.8	649	2	AH3546	outer membrane pro
329	53	11.8	660	2	T00902	hypothetical prote
330	53	11.8	666	2	I52648	class A helix-loop
331	53	11.8	667	2	A41311	transcription fact
332	53	11.8	687	2	S69723	hypothetical prote
333	53	11.8	744	2	S68115	catalase (EC 1.11.
334	53	11.8	782	1	G64157	probable organic s
335	53	11.8	838	2	T04449	hypothetical prote
336	53	11.8	852	2	S41886	DNA repair protein
337	53	11.8	858	1	VCLJG2	env polyprotein pr
338	53	11.8	911	2	T08108	nitrate reductase
339	53	11.8	917	2	E96807	nitrate reductase
340	53	11.8	917	2	S35228	nitrate reductase
341	53	11.8	969	2	T23256	hypothetical prote
342	53	11.8	1121	2	T52631	1-phosphatidylinos
343	53	11.8	1159	2	S62562	probable nuclear p
344	53	11.8	1337	1	I38670	protein-tyrosine-p
345	53	11.8	1344	2	H84557	hypothetical prote
346	53	11.8	1365	2	T00833	RNA-directed DNA p
347	53	11.8	1806	2	T23298	hypothetical prote
348	53	11.8	4688	2	F82885	hypothetical prote
349	52.5	11.7	99	2	D70582	probable PE protei
350	52.5	11.7	210	2	T49785	hypothetical prote
351	52.5	11.7	222	2	S22517	S-allele-associate
352	52.5	11.7	257	1	S50294	hypothetical prote
353	52.5	11.7	261	2	G90612	cytochrome c oxida
354	52.5	11.7	272	2	T09132	26S proteasome bet
355	52.5	11.7	304	2	A97768	probable protease
356	52.5	11.7	327	1	JQ0965	chitinase (EC 3.2.
357	52.5	11.7	357	2	C69223	anion permease - M
358	52.5	11.7	361	2	A41535	glutaminyl-peptide
359	52.5	11.7	414	2	A70214	hypothetical prote
360	52.5	11.7	419	2	T18420	hypothetical prote
361	52.5	11.7	449	2	A48466	tubulin alpha chai
362	52.5	11.7	457	2	T15271	hypothetical prote
363	52.5	11.7	462	2	S44490	RXR type hormone r
364	52.5	11.7	470	2	T10193	glycerol-3-phospha
365	52.5	11.7	472	2	S51768	glycerol-3-phospha
366	52.5	11.7	491	1	CSRZ	catalase (EC 1.11.
367	52.5	11.7	499	1	S30007	probable UTP-gluco
368	52.5	11.7	536	2	T04222	hypothetical prote
369	52.5	11.7	556	2	S51858	probable membrane
370	52.5	11.7	795	2	T21487	hypothetical prote
371	52.5	11.7	798	2	B27079	fibronectin recept
372	52.5	11.7	803	2	S45916	hypothetical prote
373	52.5	11.7	837	2	S54624	ROD1 protein - yea
374	52.5	11.7	844	2	T00529	hypothetical prote
375	52.5	11.7	852	1	VCLJGG	env polyprotein pr
376	52.5	11.7	891	2	G89957	hypothetical prote
377	52.5	11.7	985	2	I51549	receptor tyrosine
378	52.5	11.7	1015	2	A42915	type II cAMP-depen
379	52.5	11.7	1017	2	T42384	inositol-1,4,5-tri
380	52.5	11.7	1036	1	A34755	nitrogen regulator
381	52.5	11.7	1106	2	T19948	hypothetical prote
382	52.5	11.7	1146	2	S64402	probable transcrip
383	52.5	11.7	1211	2	S54500	alpha,alpha-trehal
384	52.5	11.7	1367	1	IGHUR1	insulin-like growt
385	52.5	11.7	1445	2	A59437	KIAA1204 protein [
386	52.5	11.7	1449	1	A43573	E2 glycoprotein pr
387	52.5	11.7	1449	1	VGIHFS	E2 glycoprotein pr
388	52.5	11.7	1449	2	S47423	E2 glycoprotein pr
389	52.5	11.7	1806	2	AF1717	probable peptidogl
390	52.5	11.7	3014	1	JC5620	genome polyprotein
391	52	11.6	133	2	S57885	T-cell receptor al
392	52	11.6	167	2	I58352	p16INK4a - mouse
393	52	11.6	194	1	YQEC7P	fimbrial protein 9
394	52	11.6	215	2	JE0243	Ig kappa chain NIG

395	52	11.6	239	2	T34305	hypothetical prote
396	52	11.6	287	2	A45854	leucocyte common a
397	52	11.6	289	2	T25277	hypothetical prote
398	52	11.6	291	2	T01241	probable MYB famil
399	52	11.6	301	2	C69143	hypothetical prote
400	52	11.6	305	2	AD3378	hypothetical prote
401	52	11.6	373	2	T10341	late expression fa
402	52	11.6	426	2	T20253	hypothetical prote
403	52	11.6	437	2	S55392	msh potein - fruit
404	52	11.6	471	2	D90094	hypothetical prote
405	52	11.6	505	2	F71218	hypothetical prote
406	52	11.6	514	2	T11249	cytochrome-c oxida
407	52	11.6	516	2	F82070	2-isopropylmalate
408	52	11.6	533	2	H86282	protein F10B6.34 [
409	52	11.6	572	2	S77249	hypothetical prote
410	52	11.6	597	2	T23961	hypothetical prote
411	52	11.6	611	2	T21747	hypothetical prote
412	52	11.6	638	2	B83890	hypothetical prote
413	52	11.6	681	2	S33316	structural protein
414	52	11.6	681	2	A45705	type I transmembra
415	52	11.6	729	2	T52187	probable transposa
416	52	11.6	799	1	TVRTTB	nerve growth facto
417	52	11.6	855	2	A45713	Env transmembrane
418	52	11.6	865	2	E84718	hypothetical prote
419	52	11.6	903	2	E88221	protein T01H3.2 [i
420	52	11.6	926	2	T48391	protein kinase-lik
421	52	11.6	1273	1	TDRTLT	leukocyte common a
422	52	11.6	1398	2	S56814	microtubule-intera
423	52	11.6	1444	1	A30588	140K adhesin precu
424	52	11.6	2958	2	S64921	probable membrane
425	52	11.6	4981	2	T18489	hypothetical prote
426	51.5	11.5	98	2	PH1069	Ig light chain V r
427	51.5	11.5	102	2	S35882	AL0 protein - Indi
428	51.5	11.5	113	2	G71071	hypothetical prote
429	51.5	11.5	124	2	S40336	Ig kappa chain V-J
430	51.5	11.5	143	2	A95253	PTS system, IIA co
431	51.5	11.5	145	2	T16598	hypothetical prote
432	51.5	11.5	146	2	D42402	cell surface glyco
433	51.5	11.5	148	2	G98117	hypothetical prote
434	51.5	11.5	194	2	H22845	hypothetical prote
435	51.5	11.5	207	2	G69381	flagellin (flaB1-2
436	51.5	11.5	210	2	A85018	probable copper-co
437	51.5	11.5	211	2	E71334	hypothetical prote
438	51.5	11.5	257	2	I54285	MHC class II histo
439	51.5	11.5	261	2	A26344	carbonate dehydrat
440	51.5	11.5	262	2	G81954	cytochrome C1 prec
441	51.5	11.5	262	2	T34547	hypothetical prote
442	51.5	11.5	266	2	D81011	ubiquinol-cytochro
443	51.5	11.5	278	2	D36791	hypothetical prote
444	51.5	11.5	280	2	AF3144	non-heme chloroper
445	51.5	11.5	312	2	C84511	hypothetical prote
446	51.5	11.5	312	2	C75124	hypothetical prote
447	51.5	11.5	313	2	T49129	hypothetical prote
448	51.5	11.5	320	2	A40216	flavonol 4'-sulfot
449	51.5	11.5	324	2	E85513	probable integrase
450	51.5	11.5	324	2	G90662	probable integrase
451	51.5	11.5	326	2	F98143	non-heme chloroper
452	51.5	11.5	332	2	AH2533	hypothetical prote
453	51.5	11.5	344	2	T29264	hypothetical prote
454	51.5	11.5	376	2	T05420	cyclin delta-3 - A
455	51.5	11.5	377	2	T31604	hypothetical prote
456	51.5	11.5	387	2	D88968	protein T27B7.3 [i
457	51.5	11.5	395	2	S51449	probable membrane
458	51.5	11.5	446	2	S46786	serine-tRNA ligase
459	51.5	11.5	447	2	T06004	1-aminocyclopropan
460	51.5	11.5	465	2	B71716	transhydrogenase c
461	51.5	11.5	484	2	D64214	hypothetical prote
462	51.5	11.5	492	2	T09756	catalase (EC 1.11.
463	51.5	11.5	511	1	VGVN	spike glycoprotein
464	51.5	11.5	513	2	S58200	probable membrane
465	51.5	11.5	527	2	JE0373	low density lipopr
466	51.5	11.5	537	2	S26857	isocitrate lyase (
467	51.5	11.5	538	2	S62566	PHD finger protein
468	51.5	11.5	551	2	S05667	glucan 1,4-alpha-m
469	51.5	11.5	570	2	S56132	cellulase (EC 3.2.
470	51.5	11.5	576	2	S75958	hypothetical prote
471	51.5	11.5	576	2	T38293	hypothetical serin
472	51.5	11.5	578	1	BVBYD1	GCD1 protein - yea
473	51.5	11.5	578	2	S66353	L-ascorbate oxidas
474	51.5	11.5	610	2	S50539	hypothetical prote
475	51.5	11.5	618	2	T49177	hypothetical prote
476	51.5	11.5	620	2	JC4925	XmnI methyltransfe
477	51.5	11.5	648	2	B81686	conserved hypothet
478	51.5	11.5	717	1	S29923	transforming prote
479	51.5	11.5	766	2	B85440	receptor kinase-li
480	51.5	11.5	792	2	T26050	hypothetical prote
481	51.5	11.5	854	2	AC2309	hypothetical prote
482	51.5	11.5	862	2	I49583	differentiation an
483	51.5	11.5	868	2	A46512	CD22 homolog/B lym
484	51.5	11.5	911	2	T08105	nitrate reductase
485	51.5	11.5	959	2	B44402	nuclear pore compl
486	51.5	11.5	965	2	T12545	hypothetical prote
487	51.5	11.5	1007	2	G96606	disease resistance
488	51.5	11.5	1107	2	S61667	probable membrane
489	51.5	11.5	1142	2	S59359	GIN4 protein - yea
490	51.5	11.5	1335	2	H86489	protein T32E20.13
491	51.5	11.5	1338	2	T18416	hypothetical prote
492	51.5	11.5	1518	2	A44811	glucosyltransferas
493	51.5	11.5	1528	2	S13743	DNA strand transfe
494	51.5	11.5	3635	2	T10053	laminin alpha 5 ch
495	51.5	11.5	4753	1	A47437	LDL-receptor-relat
496	51.5	11.5	5005	2	F82884	hypothetical prote
497	51.5	11.5	26926	1	I38344	titin, cardiac mus
498	51	11.4	160	2	C64171	hypothetical prote
499	51	11.4	174	2	T48419	hypothetical prote
500	51	11.4	191	2	E75132	molybdopterin-guan
501	51	11.4	205	2	B31906	hypothetical prote
502	51	11.4	221	2	T03954	hypothetical prote
503	51	11.4	253	2	T40687	hypothetical prote
504	51	11.4	287	2	C82158	ROK family protein
505	51	11.4	290	2	G72858	AcOrf-70 protein -
506	51	11.4	319	2	AD1108	other proteins hom
507	51	11.4	322	2	T25416	hypothetical prote
508	51	11.4	329	2	H83907	cytochrome aa3 qui
509	51	11.4	331	2	F86142	F633.5 protein - A
510	51	11.4	333	2	AF0407	lipoprotein [impor
511	51	11.4	352	2	G85606	hypothetical prote
512	51	11.4	352	2	F90797	hypothetical prote
513	51	11.4	388	2	S59860	hypothetical prote
514	51	11.4	397	2	I39184	bomapin - human
515	51	11.4	402	2	A84581	probable disease r
516	51	11.4	407	2	C45600	asparagine-rich bl
517	51	11.4	417	2	A45794	tubulin alpha chai
518	51	11.4	430	2	T23899	hypothetical prote
519	51	11.4	430	2	I39727	mannopine biosynth
520	51	11.4	470	2	T25578	hypothetical prote
521	51	11.4	481	2	F97472	hypothetical prote
522	51	11.4	488	2	E70234	conserved hypothet
523	51	11.4	512	2	H86216	protein T23G18.16
524	51	11.4	555	2	H96762	hypothetical prote
525	51	11.4	578	2	S55102	PSP2 protein - yea
526	51	11.4	580	2	T46024	hypothetical prote
527	51	11.4	642	2	S53434	plasma protein S p
528	51	11.4	684	2	S45758	proliferating-cell
529	51	11.4	710	2	T41352	probable transcrip
530	51	11.4	714	2	C90100	hypothetical prote
531	51	11.4	732	2	F84394	helicase [imported
532	51	11.4	753	2	A27041	tyrosine kinase-re
533	51	11.4	758	2	S47866	SPT21 protein - ye
534	51	11.4	773	2	D89010	protein R08F11.7 [
535	51	11.4	795	2	T20939	hypothetical prote
536	51	11.4	798	2	S01659	integrin beta-1 ch
537	51	11.4	799	1	IJMSFB	fibronectin recept
538	51	11.4	799	2	JC4126	integrin beta olig
539	51	11.4	805	2	T21957	hypothetical prote
540	51	11.4	807	2	T02916	hypothetical prote

541	51	11.4	839	1	TQZMCA	probable transposa
542	51	11.4	874	2	S62486	probable leucyl tr
543	51	11.4	879	2	S64755	hypothetical prote
544	51	11.4	882	2	C83234	hypothetical prote
545	51	11.4	890	2	A98017	probable 2-compone
546	51	11.4	890	2	C85861	probable 2-compone
547	51	11.4	890	2	F64991	yojN protein - Esc
548	51	11.4	900	2	T19689	hypothetical prote
549	51	11.4	995	2	S67564	hypothetical prote
550	51	11.4	1021	2	S64506	protein kinase BUB
551	51	11.4	1034	2	A36108	integrin alpha-V c
552	51	11.4	1041	2	D82792	conserved hypothet
553	51	11.4	1079	2	PC7034	Na+ bicarbonate co
554	51	11.4	1092	2	JX0312	differentiation-st
555	51	11.4	1097	2	S17308	leukemia inhibitor
556	51	11.4	1112	2	S28289	hypothetical prote
557	51	11.4	1187	1	TVHUY2	protein-tyrosine k
558	51	11.4	1205	2	T41987	hypothetical prote
559	51	11.4	1209	2	T46027	hypothetical prote
560	51	11.4	1247	2	F86405	probable P-glycopr
561	51	11.4	1265	2	T51498	hypothetical prote
562	51	11.4	1379	1	S01254	hepatocyte growth
563	51	11.4	1385	2	A88554	protein C38C10.5a
564	51	11.4	1391	2	B88554	protein C38C10.5b
565	51	11.4	1424	2	T03851	thyroid hormone re
566	51	11.4	1604	2	B86287	F9L1.23 protein -
567	51	11.4	1839	2	S77626	mannuronan C-5-epi
568	51	11.4	2197	2	B71600	variant-specific s
569	51	11.4	3124	2	A40020	collagen alpha 1(X
570	50.5	11.2	125	2	A53627	fibroblast growth
571	50.5	11.2	233	2	T00202	occlusion-derived
572	50.5	11.2	254	2	S20741	chitinase (EC 3.2.
573	50.5	11.2	264	2	H90102	translational init
574	50.5	11.2	280	2	F81984	hypothetical prote
575	50.5	11.2	281	2	A97604	probable oxidoredu
576	50.5	11.2	281	2	AB2826	aldo/keto reductas
577	50.5	11.2	283	2	S73523	probable lipoprote
578	50.5	11.2	324	1	UBCHA8	tubulin alpha-8 ch
579	50.5	11.2	325	2	G70334	hypothetical prote
580	50.5	11.2	332	2	S49758	probable membrane
581	50.5	11.2	338	2	S73441	MG032 homolog B01_
582	50.5	11.2	340	2	T48288	hypothetical prote
583	50.5	11.2	342	2	S57814	oxidase like prote
584	50.5	11.2	361	1	F65012	hypothetical prote
585	50.5	11.2	361	2	S67590	mannose-1-phosphat
586	50.5	11.2	361	2	AH1469	internalin protein
587	50.5	11.2	376	2	B96714	hypothetical prote
588	50.5	11.2	420	2	T47998	pectinacetylestera
589	50.5	11.2	427	2	AH2141	type I restriction
590	50.5	11.2	446	2	H90094	hypothetical prote
591	50.5	11.2	454	2	S65970	replicative DNA he
592	50.5	11.2	455	2	T49176	hypothetical prote
593	50.5	11.2	459	2	T11489	NADH2 dehydrogenas
594	50.5	11.2	492	2	T09754	catalase (EC 1.11.
595	50.5	11.2	494	2	S62697	catalase (EC 1.11.
596	50.5	11.2	541	2	T33312	hypothetical prote
597	50.5	11.2	550	2	G86225	hypothetical prote
598	50.5	11.2	561	2	T23564	hypothetical prote
599	50.5	11.2	567	2	B84650	probable selenium-
600	50.5	11.2	568	2	T28041	hypothetical prote
601	50.5	11.2	592	2	S25705	Ig mu chain - shee
602	50.5	11.2	610	2	S05807	SAN1 protein - yea
603	50.5	11.2	624	2	A84150	hypothetical prote
604	50.5	11.2	660	2	S71276	beta-fructofuranos
605	50.5	11.2	664	2	E86257	beta-fructosidase
606	50.5	11.2	683	1	A41785	system b(0,+) amin
607	50.5	11.2	687	2	S56939	probable membrane
608	50.5	11.2	688	2	T32750	hypothetical prote
609	50.5	11.2	720	2	E72074	1,4-alpha-glucan b
610	50.5	11.2	720	2	G86549	glucan branching e
611	50.5	11.2	743	2	C56695	transducin-like en
612	50.5	11.2	769	2	T08431	gene bobby sox pro
613	50.5	11.2	795	2	E86247	receptor-like prot
614	50.5	11.2	827	2	T04789	hypothetical prote
615	50.5	11.2	869	2	S53098	envelope polyprote
616	50.5	11.2	904	1	RDNTNS	nitrate reductase
617	50.5	11.2	904	1	RDNTNT	nitrate reductase
618	50.5	11.2	911	1	RDTONH	nitrate reductase
619	50.5	11.2	926	1	RDSPNH	nitrate reductase
620	50.5	11.2	960	2	T50383	homolog to yeast c
621	50.5	11.2	964	2	JC5545	integrin beta-4 pr
622	50.5	11.2	974	1	A40213	optic lobe develop
623	50.5	11.2	1050	2	T27753	hypothetical prote
624	50.5	11.2	1070	2	T34385	hypothetical prote
625	50.5	11.2	1087	2	S58147	protein kinase - f
626	50.5	11.2	1148	2	T09073	splicing factor Si
627	50.5	11.2	1195	2	S61886	chitin synthase (E
628	50.5	11.2	1228	2	G90581	hypothetical prote
629	50.5	11.2	1292	2	T09229	galactose binding
630	50.5	11.2	1325	2	S62497	probable nucleopor
631	50.5	11.2	1466	2	A36426	SPA2 protein - yea
632	50.5	11.2	1607	2	T04583	TMV resistance pro
633	50.5	11.2	1692	2	A33988	adenylate cyclase
634	50.5	11.2	1708	2	F69189	protoporphyrin IX
635	50.5	11.2	1875	2	A36429	integrin beta-4 ch
636	50.5	11.2	2167	2	S50658	bud emergence prot
637	50.5	11.2	3623	2	T08618	intrinsic factor-B
638	50	11.1	115	2	T51208	hypothetical prote
639	50	11.1	118	2	F58932	ribosomal protein
640	50	11.1	165	2	A82246	probable phosphata
641	50	11.1	175	1	CYBOAB	alpha-crystallin c
642	50	11.1	175	1	CYHUAB	alpha-crystallin c
643	50	11.1	175	2	A53871	alpha-crystallin c
644	50	11.1	191	2	T19668	hypothetical prote
645	50	11.1	202	1	DHRT	Ig delta chain C r
646	50	11.1	215	2	JE0242	Ig kappa chain NIG
647	50	11.1	217	2	T50521	hypothetical prote
648	50	11.1	243	2	T24981	hypothetical prote
649	50	11.1	245	2	T41291	conserved hypothet
650	50	11.1	261	2	A60404	MHC class II histo
651	50	11.1	261	2	B60404	MHC class II histo
652	50	11.1	270	2	T43491	hypothetical prote
653	50	11.1	271	2	C82841	cysteine proteinas
654	50	11.1	311	2	A69095	cobalt transport A
655	50	11.1	321	2	AG2936	transglycosylase A
656	50	11.1	321	2	H98345	hypothetical prote
657	50	11.1	327	1	HLHUCD	T-cell surface gly
658	50	11.1	345	2	AI2217	low specificity L-
659	50	11.1	354	2	JT0594	site-specific DNA-
660	50	11.1	368	2	S46601	hypothetical prote
661	50	11.1	370	2	A96547	hypothetical prote
662	50	11.1	374	2	T24162	hypothetical prote
663	50	11.1	379	2	T04762	chitinase homolog
664	50	11.1	397	1	Z6BPT9	ribonucleoside-tri
665	50	11.1	410	2	G90362	hypothetical prote
666	50	11.1	416	2	E86384	probable zinc fing
667	50	11.1	418	2	A37344	acrosin (EC 3.4.21
668	50	11.1	431	2	F90316	dsrP protein, prob
669	50	11.1	436	1	A70409	hypothetical prote
670	50	11.1	438	1	HVRKC2	Ig mu chain C regi
671	50	11.1	456	2	T33822	hypothetical prote
672	50	11.1	459	2	A25928	cellulase (EC 3.2.
673	50	11.1	473	2	B85187	glycoprotein homol
674	50	11.1	494	2	A48657	monophenol monooxy
675	50	11.1	497	2	S74404	o-succinylbenzoate
676	50	11.1	497	2	T15812	hypothetical prote
677	50	11.1	505	2	S39962	endoglucanase - Er
678	50	11.1	512	2	AF3628	nitrate reductase
679	50	11.1	513	2	T37806	probable flavoprot
680	50	11.1	520	2	C64213	ribose transport s
681	50	11.1	522	2	S77073	hypothetical prote
682	50	11.1	524	2	G64243	hypothetical prote
683	50	11.1	524	2	S46007	hypothetical prote
684	50	11.1	568	2	B86400	T17H3.1 protein -
685	50	11.1	584	1	ALBY	alpha-glucosidase
686	50	11.1	584	2	S64627	alpha-glucosidase

687	50	11.1	584	2	S46183	alpha-glucosidase
688	50	11.1	592	1	S13391	endo-1,4-beta-xyla
689	50	11.1	603	2	S61504	glycogen(starch) s
690	50	11.1	605	2	T07123	nine-cis-epoxycaro
691	50	11.1	621	2	T20307	hypothetical prote
692	50	11.1	631	2	S67268	hypothetical prote
693	50	11.1	672	2	T20310	hypothetical prote
694	50	11.1	676	1	KXHUS	plasma protein S p
695	50	11.1	682	2	T18847	hypothetical prote
696	50	11.1	710	2	S30154	low-temperature-in
697	50	11.1	747	1	QRECFE	ferrichrome-iron r
698	50	11.1	747	2	B85499	outer membrane rec
699	50	11.1	747	2	B90648	outer membrane rec
700	50	11.1	750	2	S67100	protein-tyrosine-p
701	50	11.1	758	1	S45477	SEC18 protein - ye
702	50	11.1	758	2	S65169	hypothetical prote
703	50	11.1	771	1	WMVZ9J	ribonucleoside-dip
704	50	11.1	771	1	WZVZH4	ribonucleoside-dip
705	50	11.1	771	2	T28496	ribonucleoside-dip
706	50	11.1	771	2	B36843	ribonucleoside-dip
707	50	11.1	771	2	H72157	L4L protein - vari
708	50	11.1	798	2	F96714	probable protease
709	50	11.1	813	2	A40601	ferripyoverdine re
710	50	11.1	815	2	H83345	ferripyoverdine re
711	50	11.1	857	1	QQBE1L	glycoprotein B - h
712	50	11.1	879	2	B84765	hypothetical prote
713	50	11.1	961	2	A55380	faciogenital dyspl
714	50	11.1	974	2	S15038	cell division cont
715	50	11.1	1009	2	S61174	hypothetical prote
716	50	11.1	1046	2	T30199	chitinase (EC 3.2.
717	50	11.1	1048	2	S64758	SCD25 protein (ver
718	50	11.1	1139	1	E64234	cytadherence-acces
719	50	11.1	1145	2	T33606	hypothetical prote
720	50	11.1	1206	2	T30555	nitric-oxide synth
721	50	11.1	1323	2	S27224	N-methyl-D-asparta
722	50	11.1	1323	2	I78557	N-methyl-D-asparta
723	50	11.1	1356	1	C45219	N-methyl-D-asparta
724	50	11.1	1827	1	UUHU	sucrose alpha-gluc
725	50	11.1	2279	2	T42531	acetyl-CoA carboxy
726	50	11.1	2280	2	T38906	acetyl-CoA carboxy
727	50	11.1	2327	2	T31733	hypothetical prote
728	50	11.1	2655	2	D96595	probable acetyl-Co
729	50	11.1	3328	2	T30835	breast cancer tumo
730	50	11.1	3329	2	T42205	breast cancer susc
731	50	11.1	3343	2	S44887	ZK112.7 protein -
732	50	11.1	4131	2	T21085	hypothetical prote
733	50	11.1	4725	1	A44357	dynein heavy chain
734	49.5	11.0	92	2	S37512	Ig kappa chain V r
735	49.5	11.0	102	2	B83934	hypothetical prote
736	49.5	11.0	119	2	D84845	hypothetical prote
737	49.5	11.0	165	2	S68776	myogenin - rainbow
738	49.5	11.0	187	2	I84461	MHC HLA-SB beta ch
739	49.5	11.0	187	2	T51876	hypothetical prote
740	49.5	11.0	207	2	AG2553	hypothetical prote
741	49.5	11.0	222	2	F96918	beta-phosphoglucom
742	49.5	11.0	224	1	HLHUS1	MHC class II histo
743	49.5	11.0	224	2	I68751	MHC class II lymph
744	49.5	11.0	229	2	A28909	MHC class II histo
745	49.5	11.0	232	1	HLMSE2	H-2 class II histo
746	49.5	11.0	233	2	I55654	MHC class II prote
747	49.5	11.0	237	2	A21200	H-2 class II histo
748	49.5	11.0	241	2	I48657	I-E(b-beta) protei
749	49.5	11.0	243	2	A53506	folate receptor ty
750	49.5	11.0	244	2	C90580	DNA processing pro
751	49.5	11.0	258	1	HLHUPB	MHC class II histo
752	49.5	11.0	258	1	HLHUS2	MHC class II histo
753	49.5	11.0	258	2	I54458	MHC class II histo
754	49.5	11.0	258	2	I59621	HLA-DPB1 - human
755	49.5	11.0	261	2	AH2960	ABC transporter, m
756	49.5	11.0	261	2	F98322	nitrate transport
757	49.5	11.0	261	2	T11525	cytochrome-c oxida
758	49.5	11.0	264	1	HLMSE1	H-2 class II histo
759	49.5	11.0	264	1	HLMSEB	H-2 class II histo
760	49.5	11.0	264	2	S11650	class II histocomp
761	49.5	11.0	264	2	A30529	H-2 class II histo
762	49.5	11.0	264	2	I48422	MHC class II histo
763	49.5	11.0	267	2	AC3232	conjugal transfer
764	49.5	11.0	269	2	S61633	YNT20 protein - ye
765	49.5	11.0	278	2	B65006	hypothetical prote
766	49.5	11.0	293	2	G86901	hypothetical prote
767	49.5	11.0	317	2	F70185	phosphomevalonate
768	49.5	11.0	319	2	F75420	hypothetical prote
769	49.5	11.0	324	2	S56694	chitinase (EC 3.2.
770	49.5	11.0	325	2	A69930	conserved hypothet
771	49.5	11.0	326	2	A28129	sporulation-specif
772	49.5	11.0	328	2	E82324	immunogenic protei
773	49.5	11.0	335	2	G82708	malate dehydrogena
774	49.5	11.0	342	2	S63654	hypothetical COI i
775	49.5	11.0	361	2	T14800	hypothetical prote
776	49.5	11.0	371	2	A61275	tubulin alpha-2 ch
777	49.5	11.0	376	2	S45763	hypothetical prote
778	49.5	11.0	387	2	AG3218	acetylornithine de
779	49.5	11.0	411	1	UBCHA	tubulin alpha chai
780	49.5	11.0	418	2	JC7872	stearoyl-CoA 9-des
781	49.5	11.0	426	2	H97765	proline-tRNA ligas
782	49.5	11.0	432	2	G71695	proline-tRNA ligas
783	49.5	11.0	434	2	AE0226	conserved hypothet
784	49.5	11.0	444	2	A56635	tubulin alpha chai
785	49.5	11.0	444	2	S25004	tubulin alpha chai
786	49.5	11.0	448	1	UBCHA5	tubulin alpha-5 ch
787	49.5	11.0	448	2	A25873	tubulin alpha chai
788	49.5	11.0	448	2	I77427	tubulin alpha chai
789	49.5	11.0	449	2	S00253	tubulin alpha chai
790	49.5	11.0	449	2	I77428	tubulin alpha chai
791	49.5	11.0	450	2	S43138	tubulin alpha chai
792	49.5	11.0	451	1	UBPGA	tubulin alpha chai
793	49.5	11.0	451	1	UBRTA	tubulin alpha chai
794	49.5	11.0	451	2	A23035	tubulin alpha chai
795	49.5	11.0	451	2	C24903	tubulin alpha-3 ch
796	49.5	11.0	451	2	JC4133	tubulin alpha chai
797	49.5	11.0	451	2	I77403	tubulin alpha-1 ch
798	49.5	11.0	451	2	A24903	tubulin alpha-1 ch
799	49.5	11.0	451	2	B24903	tubulin alpha-2 ch
800	49.5	11.0	451	2	I77424	tubulin alpha chai
801	49.5	11.0	451	2	I77425	tubulin alpha chai
802	49.5	11.0	452	2	A60671	tubulin alpha chai
803	49.5	11.0	452	2	S11207	tubulin alpha chai
804	49.5	11.0	477	2	JS0597	t-plasminogen acti
805	49.5	11.0	477	2	F64805	RhsA protein [impo
806	49.5	11.0	479	2	F82328	aspartokinase III,
807	49.5	11.0	480	2	S38134	GLG1 protein - yea
808	49.5	11.0	493	2	F95940	probable xanthine
809	49.5	11.0	495	2	T33065	hypothetical prote
810	49.5	11.0	522	2	T19762	hypothetical prote
811	49.5	11.0	529	2	T00677	hypothetical prote
812	49.5	11.0	542	2	AH2191	hypothetical prote
813	49.5	11.0	543	2	S56830	probable purine nu
814	49.5	11.0	562	2	S57951	beta-fructofuranos
815	49.5	11.0	608	2	T18437	hypothetical prote
816	49.5	11.0	620	1	UYPVAP	noncapsid protein
817	49.5	11.0	632	2	D84921	probable serine pr
818	49.5	11.0	638	2	E84799	similar to axi 1 p
819	49.5	11.0	639	2	S71268	beta-fructofuranos
820	49.5	11.0	645	2	A49013	tumor cell suppres
821	49.5	11.0	658	2	T08153	cysteine proteinas
822	49.5	11.0	669	2	A46511	envelope protein -
823	49.5	11.0	686	2	D69647	catalase (EC 1.11.
824	49.5	11.0	728	2	A96652	protein F23N19.3 [
825	49.5	11.0	760	2	S19374	probable membrane
826	49.5	11.0	762	2	A54411	amine oxidase (cop
827	49.5	11.0	763	2	A47563	glucose-6-phosphat
828	49.5	11.0	770	2	S60676	cellobiose oxidase
829	49.5	11.0	773	2	I46059	beta-1 integrin su
830	49.5	11.0	790	1	TVHUTT	nerve growth facto
831	49.5	11.0	850	2	S56015	gastric mucin MUC5
832	49.5	11.0	859	2	S70584	nitrate reductase

833	49.5	11.0	859	2	AE2217	hypothetical prote
834	49.5	11.0	868	1	JC4283	nitrate reductase
835	49.5	11.0	877	2	C46356	env polyprotein -
836	49.5	11.0	942	2	T37539	probable guanine n
837	49.5	11.0	985	2	B86084	hypothetical prote
838	49.5	11.0	997	2	S44457	period clock prote
839	49.5	11.0	1028	2	G96769	unknown protein F9
840	49.5	11.0	1030	2	T16114	hypothetical prote
841	49.5	11.0	1043	2	F97302	hypothetical prote
842	49.5	11.0	1082	2	T31112	ATPase 2 (EC 3.6.1
843	49.5	11.0	1131	2	S22266	FUN30 protein - ye
844	49.5	11.0	1181	2	C86349	F8K7.4 protein - A
845	49.5	11.0	1237	2	A54080	protein-tyrosine-p
846	49.5	11.0	1377	2	E86034	rhsA protein in rh
847	49.5	11.0	1377	2	C65159	rhsA protein precu
848	49.5	11.0	1394	2	H91236	RhsH core protein
849	49.5	11.0	1397	2	A85570	rhsC protein in rh
850	49.5	11.0	1397	2	C64805	rhsC protein precu
851	49.5	11.0	1399	2	A99720	RhsC core protein
852	49.5	11.0	1402	2	F84480	probable retroelem
853	49.5	11.0	1409	2	F91187	rhsA core protein
854	49.5	11.0	1411	2	E65145	rhsB protein precu
855	49.5	11.0	1590	2	B86398	protein T7N9.24 [i
856	49.5	11.0	1661	2	T31330	head-activator bin
857	49.5	11.0	1677	2	T46095	hypothetical prote
858	49.5	11.0	1677	2	T14267	Xin protein, stage
859	49.5	11.0	1711	2	T21432	hypothetical prote
860	49.5	11.0	1908	2	T42707	hypothetical prote
861	49.5	11.0	2123	2	F86348	hypothetical prote
862	49.5	11.0	2330	1	RRIWMV	genome polyprotein
863	49.5	11.0	2331	2	S44054	genome polyprotein
864	49.5	11.0	2559	2	T09144	probable guanine n
865	49.5	11.0	2957	2	T33152	hypothetical prote
866	49.5	11.0	4307	2	T20721	hypothetical prote
867	49	10.9	55	2	AD1852	hypothetical prote
868	49	10.9	77	2	G28840	Ig kappa chain V r
869	49	10.9	89	2	F69268	hypothetical prote
870	49	10.9	101	1	ARRA3	allergen Ra3 - com
871	49	10.9	107	2	S57444	Ig kappa chain V-J
872	49	10.9	111	1	CCTO	cytochrome c [vali
873	49	10.9	128	2	T40464	probable RNA bindi
874	49	10.9	130	2	A82853	hypothetical prote
875	49	10.9	135	1	CBRT5M	cytochrome b5, out
876	49	10.9	157	2	S73704	hypothetical prote
877	49	10.9	158	2	B86169	hypothetical prote
878	49	10.9	175	2	JC5971	alpha-b crystallin
879	49	10.9	213	2	G86195	hypothetical prote
880	49	10.9	226	2	AH1138	conserved hypothet
881	49	10.9	228	2	B90369	hypothetical prote
882	49	10.9	234	2	D84768	hypothetical prote
883	49	10.9	239	2	S14470	asparagine-rich pr
884	49	10.9	247	1	QQBEF1	HXLF3 protein prec
885	49	10.9	259	2	F42528	B25R protein - vac
886	49	10.9	263	2	G82259	probable rare lipo
887	49	10.9	274	2	I50682	tenascin - chicken
888	49	10.9	285	1	YXECIC	isochorismatase (E
889	49	10.9	285	2	F85558	isochorismatase (E
890	49	10.9	285	2	B90708	isochorismatase (E
891	49	10.9	289	2	T12682	hypothetical prote
892	49	10.9	294	2	S39606	class I histocompa
893	49	10.9	294	2	G84504	probable VSF-1-lik
894	49	10.9	295	2	T22039	hypothetical prote
895	49	10.9	301	2	S51439	hypothetical prote
896	49	10.9	311	2	F83695	hypothetical prote
897	49	10.9	319	2	A72284	oligopeptide ABC t
898	49	10.9	328	2	I51215	inhibin alpha-subu
899	49	10.9	328	2	T25231	hypothetical prote
900	49	10.9	337	2	T15071	hypothetical prote
901	49	10.9	343	2	S44834	F54H12.3 protein -
902	49	10.9	343	2	T27230	hypothetical prote
903	49	10.9	354	1	S00574	alkanal monooxygen
904	49	10.9	356	2	E84495	En/Spm-like transp
905	49	10.9	358	2	F84053	transcription regu
906	49	10.9	362	2	T52038	probable phytochel
907	49	10.9	363	2	S56273	probable membrane
908	49	10.9	377	2	S67448	hypothetical prote
909	49	10.9	385	2	A86165	protein F15K9.6 [i
910	49	10.9	389	2	S08031	nucleocapsid prote
911	49	10.9	393	1	HVRKC1	Ig mu chain C regi
912	49	10.9	410	2	I50494	serine proteinase
913	49	10.9	426	2	I36948	Ig epsilon-chain -
914	49	10.9	427	1	T49031	acid phosphatase (
915	49	10.9	428	2	S22377	aspartate transami
916	49	10.9	438	1	HVRKCS	Ig mu chain C regi
917	49	10.9	444	2	C84789	hypothetical prote
918	49	10.9	444	2	JC1141	metacyclic-form-sp
919	49	10.9	461	1	HVRKC0	Ig mu chain C regi
920	49	10.9	461	2	A31820	thyroid hormone re
921	49	10.9	462	2	H64145	hypothetical prote
922	49	10.9	472	2	E81784	glutamate-ammonia
923	49	10.9	472	2	F81208	glutamate-ammonia
924	49	10.9	474	2	A40721	neuroblast prolife
925	49	10.9	492	2	A34272	testosterone 7alph
926	49	10.9	510	2	T44810	conserved hypothet
927	49	10.9	510	2	H69893	conserved hypothet
928	49	10.9	513	2	F83162	nitrate reductase
929	49	10.9	513	2	E71683	NADH2 dehydrogenas
930	49	10.9	523	1	S61713	carboxypeptidase C
931	49	10.9	526	1	A34164	cholesterol monoox
932	49	10.9	536	2	G64752	xylan 1,4-beta-xyl
933	49	10.9	552	2	T04653	receiver-like prot
934	49	10.9	558	2	T02704	hypothetical prote
935	49	10.9	562	2	S16594	regulatory protein
936	49	10.9	605	2	T27397	hypothetical prote
937	49	10.9	611	2	T03890	hypothetical prote
938	49	10.9	613	2	T15489	hypothetical prote
939	49	10.9	623	2	T39001	probable exonuclea
940	49	10.9	626	2	H96810	probable RNA-bindi
941	49	10.9	649	2	S67787	hypothetical prote
942	49	10.9	651	2	T12083	beta-fructofuranos
943	49	10.9	667	2	AD0295	probable formyl tr
944	49	10.9	675	1	KXMSS	plasma protein S p
945	49	10.9	700	1	HYHUMB	meprin A (EC 3.4.2
946	49	10.9	712	1	VCLJS4	env polyprotein pr
947	49	10.9	713	2	JN0133	WD-40 repeat regul
948	49	10.9	779	2	C96805	hypothetical prote
949	49	10.9	802	2	T21464	hypothetical prote
950	49	10.9	843	2	S44868	kinesin heavy chai
951	49	10.9	848	2	S48273	probable transcrip
952	49	10.9	849	2	I50617	protein-tyrosine k
953	49	10.9	859	1	VCLJST	env polyprotein pr
954	49	10.9	860	1	C35905	endopeptidase Clp
955	49	10.9	874	2	JC4930	S-layer protein pr
956	49	10.9	876	2	G90592	hypothetical prote
957	49	10.9	886	2	A57172	probable hormone r
958	49	10.9	887	2	T11566	envelope glycoprot
959	49	10.9	905	2	G83314	NADH dehydrogenase
960	49	10.9	927	2	F82818	conserved hypothet
961	49	10.9	944	2	T41711	probable alpha-tre
962	49	10.9	953	2	A86351	hypothetical prote
963	49	10.9	1031	1	A38713	kinesin heavy chai
964	49	10.9	1089	2	T21582	hypothetical prote
965	49	10.9	1143	2	T10636	hypothetical prote
966	49	10.9	1191	1	A44051	DNA-binding protei
967	49	10.9	1193	2	G71605	hypothetical prote
968	49	10.9	1217	2	F97177	alpha-glucosidase
969	49	10.9	1250	2	S14177	SCD25 protein (ver
970	49	10.9	1391	2	T20406	hypothetical prote
971	49	10.9	1441	2	A86685	prophage pi1 prote
972	49	10.9	1456	1	A36563	mannose receptor p
973	49	10.9	1463	2	C86482	protein F5J5.1 [im
974	49	10.9	1524	2	S68553	surface layer prot
975	49	10.9	1844	2	D71612	hypothetical prote
976	49	10.9	2274	2	T30258	adenomatous polypo
977	49	10.9	2301	1	GNNYTN	genome polyprotein
978	49	10.9	2670	2	T37919	GCN1 homolog - fis

979	49	10.9	2704	2	S09118	G surface protein
980	49	10.9	3848	2	T17414	TipC protein - sli
981	49	10.9	4572	2	S57908	hypothetical 527K
982	49	10.9	6642	2	T29757	protein UNC-89 - C
983	48.5	10.8	108	2	S30521	Ig kappa chain V r
984	48.5	10.8	110	2	S22890	T-cell receptor al
985	48.5	10.8	111	2	S57889	T cell receptor Er
986	48.5	10.8	114	2	S46375	Ig kappa chain V-J
987	48.5	10.8	122	2	AE1477	hypothetical prote
988	48.5	10.8	128	2	S40345	Ig kappa chain V-J
989	48.5	10.8	132	2	S23374	T-cell receptor al
990	48.5	10.8	153	2	JC5854	polyketide synthas
991	48.5	10.8	159	2	B84669	hypothetical prote
992	48.5	10.8	210	2	T27168	hypothetical prote
993	48.5	10.8	217	2	C86350	protein F8K7.12 [i
994	48.5	10.8	218	2	AB1764	late competence pr
995	48.5	10.8	230	2	S09778	hypothetical prote
996	48.5	10.8	236	2	B88923	protein W03F9.2 [i
997	48.5	10.8	243	2	E37386	hypothetical prote
998	48.5	10.8	243	2	S01923	hypothetical prote
999	48.5	10.8	263	2	F84849	hypothetical prote
1000	48.5	10.8	264	2	I56056	MHC E-beta-f - mou
1001	48.5	10.8	274	2	T16003	hypothetical prote
1002	48.5	10.8	276	2	JC4161	probable chloride
1003	48.5	10.8	300	2	JC4367	NAD(P)-arginine AD
1004	48.5	10.8	302	1	ORBP15	replication protei
1005	48.5	10.8	319	2	AH2062	aldo/keto reductas
1006	48.5	10.8	320	2	S59947	chitinase (EC 3.2.
1007	48.5	10.8	320	2	C72421	oligopeptide ABC t
1008	48.5	10.8	331	2	G96785	protein F10A5.24 [
1009	48.5	10.8	333	2	G95380	probable periplasm
1010	48.5	10.8	337	2	S24222	CD44 protein - hum
1011	48.5	10.8	341	2	S51766	dioxygenase - eggp
1012	48.5	10.8	343	2	T45987	hypothetical prote
1013	48.5	10.8	358	2	AH1376	hypothetical prote
1014	48.5	10.8	360	2	T18529	protein phosphatas
1015	48.5	10.8	372	2	I52196	homeobox transcrip
1016	48.5	10.8	380	2	T09661	ascorbate oxidase
1017	48.5	10.8	383	2	T23041	hypothetical prote
1018	48.5	10.8	421	2	A56550	Krox-20 - African
1019	48.5	10.8	428	2	S22379	aspartate transami
1020	48.5	10.8	433	2	S77340	hypothetical prote
1021	48.5	10.8	446	2	T03021	mitosis-specific c
1022	48.5	10.8	446	2	A26724	tubulin alpha-2 ch
1023	48.5	10.8	453	2	T48240	hypothetical prote
1024	48.5	10.8	458	2	AC1632	chromosome replica
1025	48.5	10.8	459	2	E86446	glycerol-3-phospha
1026	48.5	10.8	462	2	B86262	F13K23.11 protein
1027	48.5	10.8	473	2	AI0587	deoxyribodipyrimid
1028	48.5	10.8	473	2	S22321	deoxyribodipyrimid
1029	48.5	10.8	482	2	S60757	catalase (EC 1.11.
1030	48.5	10.8	487	2	S42442	nuclear protein EB
1031	48.5	10.8	489	2	A49388	catalase (EC 1.11.
1032	48.5	10.8	502	2	A48679	differentiated ker
1033	48.5	10.8	514	2	T11859	cytochrome-c oxida
1034	48.5	10.8	518	2	T05196	hypothetical prote
1035	48.5	10.8	524	2	T27177	catalase (EC 1.11.
1036	48.5	10.8	535	2	D96586	hypothetical prote
1037	48.5	10.8	547	2	T39250	hypothetical prote
1038	48.5	10.8	586	2	T20816	hypothetical prote
1039	48.5	10.8	590	2	I39685	polyhydroxyalkanoi
1040	48.5	10.8	596	2	T26950	hypothetical prote
1041	48.5	10.8	601	2	T47249	nuclear envelope p
1042	48.5	10.8	608	2	T14731	glycogen(starch) s
1043	48.5	10.8	624	2	T48587	peptide transporte
1044	48.5	10.8	641	2	S41439	gene NS-1 protein
1045	48.5	10.8	650	2	S75072	probable phytoene
1046	48.5	10.8	653	2	E82872	transketolase I UU
1047	48.5	10.8	665	2	T46570	dosage-dependent c
1048	48.5	10.8	679	2	E90560	hypothetical prote
1049	48.5	10.8	690	2	F97164	flagellar biosynth
1050	48.5	10.8	695	2	B72129	probable outer mem
1051	48.5	10.8	695	2	F86493	probable outer mem
1052	48.5	10.8	704	2	C81542	conserved hypothet
1053	48.5	10.8	704	2	G81051	hypothetical prote
1054	48.5	10.8	709	2	B83376	catalase HPII PA21
1055	48.5	10.8	726	2	AI0147	probable ATP-depen
1056	48.5	10.8	740	2	E81823	hypothetical prote
1057	48.5	10.8	745	2	T12518	hypothetical prote
1058	48.5	10.8	750	2	S55180	phospholipase D ho
1059	48.5	10.8	787	2	S54535	hypothetical prote
1060	48.5	10.8	798	2	A28193	integrin beta-1 ch
1061	48.5	10.8	803	1	IJCH3	integrin, band 3 p
1062	48.5	10.8	807	2	B71605	hypothetical prote
1063	48.5	10.8	811	2	T17863	vitellogenin II ho
1064	48.5	10.8	814	2	B71675	valine-tRNA ligase
1065	48.5	10.8	823	2	B81282	probable integral
1066	48.5	10.8	830	2	A30359	P-selectin precurs
1067	48.5	10.8	833	1	A31593	heat shock transcr
1068	48.5	10.8	835	2	T30030	hypothetical prote
1069	48.5	10.8	862	2	T49593	hypothetical prote
1070	48.5	10.8	863	2	F85343	hypothetical prote
1071	48.5	10.8	914	2	S46593	finger protein AZF
1072	48.5	10.8	949	2	T29334	hypothetical prote
1073	48.5	10.8	955	2	T21612	hypothetical prote
1074	48.5	10.8	958	2	S64249	hypothetical prote
1075	48.5	10.8	989	2	C83035	hypothetical prote
1076	48.5	10.8	1068	2	G86452	hypothetical prote
1077	48.5	10.8	1121	2	S54504	hypothetical prote
1078	48.5	10.8	1167	2	T42704	hypothetical prote
1079	48.5	10.8	1199	2	A40670	nuclear envelope p
1080	48.5	10.8	1364	2	T00250	MEGF2 protein - hu
1081	48.5	10.8	1400	2	T31555	hypothetical prote
1082	48.5	10.8	1403	2	T11583	probable translati
1083	48.5	10.8	1487	1	CGHU6C	collagen alpha 1(I
1084	48.5	10.8	1560	2	T00080	hypothetical prote
1085	48.5	10.8	1589	2	T13826	translation initia
1086	48.5	10.8	1630	2	A53577	ascites sialoglyco
1087	48.5	10.8	1770	2	S56221	hypothetical prote
1088	48.5	10.8	1804	2	H96597	hypothetical prote
1089	48.5	10.8	2254	2	D86215	protein T6D22.14 [
1090	48.5	10.8	2386	1	FNHU	fibronectin precur
1091	48.5	10.8	3511	2	A59295	unconventional myo
1092	48	10.7	99	2	B53116	Ig epsilon chain C
1093	48	10.7	103	2	T50954	hypothetical prote
1094	48	10.7	108	1	K1HUHU	Ig kappa chain V-I
1095	48	10.7	111	1	CCMB	cytochrome c - mun
1096	48	10.7	112	1	CCRZ	cytochrome c [vali
1097	48	10.7	112	2	S22891	T-cell receptor al
1098	48	10.7	112	2	S64448	hypothetical prote
1099	48	10.7	115	2	E53116	Ig epsilon chain C
1100	48	10.7	118	2	S61051	hypothetical prote
1101	48	10.7	126	2	C53116	Ig epsilon chain C
1102	48	10.7	134	2	S53074	hypothetical prote
1103	48	10.7	138	2	T34049	hypothetical prote
1104	48	10.7	145	2	T48552	glutaredoxin-like
1105	48	10.7	151	2	S21987	probable heme-bind
1106	48	10.7	151	2	S17326	probable heme-bind
1107	48	10.7	151	2	S17322	probable heme-bind
1108	48	10.7	160	2	T29392	hypothetical prote
1109	48	10.7	165	2	H90355	hypothetical prote
1110	48	10.7	189	2	AI2534	transposase all756
1111	48	10.7	198	1	A60620	prolactin - green
1112	48	10.7	213	1	JX0295	ribonuclease (EC 3
1113	48	10.7	217	2	F82612	hypothetical prote
1114	48	10.7	219	2	PC4203	Ig kappa chain (mo
1115	48	10.7	226	2	AG1496	conserved hypothet
1116	48	10.7	227	2	PH1215	Ig epsilon chain C
1117	48	10.7	228	2	S03050	Ig gamma chain (cl
1118	48	10.7	236	2	T45067	hypothetical prote
1119	48	10.7	242	2	S60143	cellulase (EC 3.2.
1120	48	10.7	243	2	PH1216	Ig epsilon chain C
1121	48	10.7	246	2	T32510	hypothetical prote
1122	48	10.7	258	1	DHMS	Ig delta chain C r
1123	48	10.7	262	1	JQ1738	coat protein - sha
1124	48	10.7	263	2	T43629	hypothetical prote

1125	48	10.7	278	2	S29615	whiG protein - Str
1126	48	10.7	280	2	E96589	hypothetical prote
1127	48	10.7	285	2	I51412	hypothetical trans
1128	48	10.7	289	2	S48664	distal-less 3 prot
1129	48	10.7	289	2	I53082	homeoprotein - rat
1130	48	10.7	291	1	DHMSM	Ig delta chain C r
1131	48	10.7	294	2	G85474	homeodomain-like p
1132	48	10.7	301	2	T06112	homeotic protein T
1133	48	10.7	307	2	AF3239	conserved hypothet
1134	48	10.7	309	2	B84550	hypothetical prote
1135	48	10.7	316	2	A71129	hypothetical prote
1136	48	10.7	317	2	T24468	hypothetical prote
1137	48	10.7	318	1	S75765	stearoyl-CoA 9-des
1138	48	10.7	319	2	AE1469	other protein homo
1139	48	10.7	321	2	S75026	hypothetical prote
1140	48	10.7	334	2	T47693	hypothetical prote
1141	48	10.7	342	2	T29557	hypothetical prote
1142	48	10.7	348	2	E83920	hypothetical prote
1143	48	10.7	351	2	T32093	hypothetical prote
1144	48	10.7	355	2	C39725	hypothetical prote
1145	48	10.7	363	2	A56940	integral membrane
1146	48	10.7	367	2	AF1188	hypothetical prote
1147	48	10.7	369	1	S57525	alcohol dehydrogen
1148	48	10.7	369	2	B71624	hypothetical prote
1149	48	10.7	375	2	T39329	hypothetical prote
1150	48	10.7	377	2	F72165	A17L protein - var
1151	48	10.7	377	2	T28558	hypothetical prote
1152	48	10.7	377	2	H36849	A16L protein - var
1153	48	10.7	379	2	H82284	queuine tRNA-ribos
1154	48	10.7	380	1	S73751	high affinity tran
1155	48	10.7	392	2	T19869	hypothetical prote
1156	48	10.7	394	2	AH1858	3-dehydroquinate s
1157	48	10.7	408	2	T38386	hypothetical wd-40
1158	48	10.7	408	2	T34467	hypothetical prote
1159	48	10.7	409	2	S40740	cyclin A homolog -
1160	48	10.7	412	2	G82406	long-chain fatty a
1161	48	10.7	417	2	S44062	phosphoglycerate k
1162	48	10.7	417	2	H96733	hypothetical prote
1163	48	10.7	417	2	T33376	hypothetical prote
1164	48	10.7	418	2	T25092	hypothetical prote
1165	48	10.7	420	2	C86197	hypothetical prote
1166	48	10.7	421	2	T33523	hypothetical prote
1167	48	10.7	426	2	H71636	3-oxoacyl-[acyl-ca
1168	48	10.7	428	1	EHHU	Ig epsilon chain C
1169	48	10.7	430	2	JC5125	aspartate transami
1170	48	10.7	430	2	D70193	hypothetical prote
1171	48	10.7	430	2	A65215	hypothetical 49.4
1172	48	10.7	435	2	E86266	protein F3F19.23 [
1173	48	10.7	435	2	S52203	vsf-1 protein - to
1174	48	10.7	436	2	T07816	S-locus-specific g
1175	48	10.7	437	2	S11925	S-locus-specific g
1176	48	10.7	438	1	S11225	transcription fact
1177	48	10.7	440	2	C71863	probable aminotran
1178	48	10.7	440	2	E64570	nifS-like protein
1179	48	10.7	440	2	T26471	hypothetical prote
1180	48	10.7	458	2	A56055	CAP59 protein - Cr
1181	48	10.7	459	1	S31083	glycerol-3-phospha
1182	48	10.7	462	2	T17480	endo-xylanase homo
1183	48	10.7	479	1	S15031	paired box transcr
1184	48	10.7	482	2	S55950	hypothetical prote
1185	48	10.7	484	2	G82825	leucine aminopepti
1186	48	10.7	485	2	D88548	protein ZK507.6 [i
1187	48	10.7	501	2	T39801	hypothetical sh3-c
1188	48	10.7	503	2	A84434	Mutator-like trans
1189	48	10.7	505	2	T15159	hypothetical prote
1190	48	10.7	506	2	A99252	hypothetical prote
1191	48	10.7	506	2	AC3034	hypothetical prote
1192	48	10.7	515	2	AF2321	hypothetical prote
1193	48	10.7	517	2	I40798	cellulase (EC 3.2.
1194	48	10.7	525	2	T47409	hypothetical prote
1195	48	10.7	525	2	T23304	hypothetical prote
1196	48	10.7	532	2	C97228	probable peptide A
1197	48	10.7	532	2	T49467	related to COP1-in
1198	48	10.7	534	2	T23305	hypothetical prote
1199	48	10.7	543	2	T48239	hypothetical prote
1200	48	10.7	546	2	AF2268	type II site-speci
1201	48	10.7	553	2	A47504	epoxide hydrolase
1202	48	10.7	554	2	A47503	epoxide hydrolase
1203	48	10.7	566	2	S50979	RHC21 protein - ye
1204	48	10.7	573	2	B86247	hypothetical prote
1205	48	10.7	578	2	T41715	hypothetical prote
1206	48	10.7	582	2	S37047	beta-fructofuranos
1207	48	10.7	587	2	D84426	hypothetical prote
1208	48	10.7	591	2	T48395	GT2-like protein -
1209	48	10.7	595	2	B86798	prophage pi3 prote
1210	48	10.7	601	2	S27777	80K protein (allel
1211	48	10.7	604	2	T08302	hypothetical prote
1212	48	10.7	605	2	H88640	protein F52C12.2 [
1213	48	10.7	607	2	T24172	hypothetical prote
1214	48	10.7	614	2	T29937	hypothetical prote
1215	48	10.7	621	2	S35092	plakoglobin - mous
1216	48	10.7	625	2	T06184	sucrose-fructan 6-
1217	48	10.7	642	2	T15708	hypothetical prote
1218	48	10.7	644	2	JQ0160	3-isopropylmalate
1219	48	10.7	656	2	T38741	major facilitator
1220	48	10.7	670	2	T28391	ORF MSV230 hypothe
1221	48	10.7	703	2	T12696	NADH2 dehydrogenas
1222	48	10.7	717	2	T06041	hypothetical prote
1223	48	10.7	717	2	E86812	sugar hydrolase [i
1224	48	10.7	719	2	T00266	hypothetical prote
1225	48	10.7	724	2	D96949	secreted protein c
1226	48	10.7	731	2	B86132	hypothetical prote
1227	48	10.7	732	1	EKHUX	protein-glutamine
1228	48	10.7	735	2	G91290	hypothetical prote
1229	48	10.7	745	2	D86461	F14M2.9 protein -
1230	48	10.7	758	2	S54522	hypothetical prote
1231	48	10.7	792	1	A39914	dipeptidyl-peptida
1232	48	10.7	872	2	S73785	DNA polymerase III
1233	48	10.7	914	1	S07047	iodide peroxidase
1234	48	10.7	915	2	T03589	probable aspartate
1235	48	10.7	919	2	T16459	hypothetical prote
1236	48	10.7	940	2	D89723	protein F39D8.1b [
1237	48	10.7	945	2	T21998	hypothetical prote
1238	48	10.7	961	2	S67568	probable membrane
1239	48	10.7	962	2	JC5808	G protein-coupled
1240	48	10.7	992	2	T38817	hypothetical prote
1241	48	10.7	1035	2	T13962	sodium bicarbonate
1242	48	10.7	1062	2	G86325	hypothetical prote
1243	48	10.7	1070	2	F90106	IAP100 protein [im
1244	48	10.7	1079	2	T14031	sodium bicarbonate
1245	48	10.7	1093	1	S50614	regulatory protein
1246	48	10.7	1096	2	A96607	protein disease re
1247	48	10.7	1172	2	AD2310	hypothetical prote
1248	48	10.7	1215	2	C84848	hypothetical prote
1249	48	10.7	1261	2	E59430	PTPL1-associated R
1250	48	10.7	1341	2	S66835	probable membrane
1251	48	10.7	1480	2	T05566	hypothetical prote
1252	48	10.7	1583	2	F86366	protein F26F24.8 [
1253	48	10.7	1606	2	T34073	paranemin - chicke
1254	48	10.7	1635	2	AI0452	hemolysin [importe
1255	48	10.7	1795	2	T30332	avirulence protein
1256	48	10.7	1840	2	T29091	transitin - chicke
1257	48	10.7	2004	2	T30185	hypothetical prote
1258	48	10.7	2109	1	ZLVNNJ	genome polyprotein
1259	48	10.7	2303	1	GNNYTM	genome polyprotein
1260	48	10.7	2485	1	H71621	serine/threonine-s
1261	48	10.7	2630	2	T08868	polyprotein P1 - A
1262	48	10.7	2902	2	C71953	toxin-like outer m
1263	48	10.7	4563	1	LPHUB	apolipoprotein B-1
1264	48	10.7	4639	1	A54794	dynein heavy chain
1265	48	10.7	6831	2	A88852	protein unc-22 [im
1266	48	10.7	6839	2	S57242	twitchin [similari
1267	48	10.7	7160	2	T27935	hypothetical prote
1268	47.5	10.6	76	2	B88318	protein age-1 [imp
1269	47.5	10.6	85	2	A42056	ribosomal protein
1270	47.5	10.6	92	2	S37516	Ig kappa chain V r

1271	47.5	10.6	108	2	S34007	Ig kappa chain V r
1272	47.5	10.6	114	2	S54905	Ig kappa chain V r
1273	47.5	10.6	118	2	S21918	T-cell receptor al
1274	47.5	10.6	129	2	JC2144	lysozyme (EC 3.2.1
1275	47.5	10.6	156	1	WZBE25	gene 25 protein -
1276	47.5	10.6	161	1	UBURAL	tubulin alpha chai
1277	47.5	10.6	172	2	AG3532	D-lactate dehydrog
1278	47.5	10.6	177	2	C42463	hypothetical prote
1279	47.5	10.6	197	2	T19892	hypothetical prote
1280	47.5	10.6	222	2	F64757	membrane protein y
1281	47.5	10.6	227	2	B37206	class II histocomp
1282	47.5	10.6	231	2	S62530	hypothetical prote
1283	47.5	10.6	239	2	H81674	ubiquinone/menaqui
1284	47.5	10.6	240	2	A61544	tubulin alpha chai
1285	47.5	10.6	244	2	B64220	tRNA-pseudouridine
1286	47.5	10.6	252	2	A86449	hypothetical prote
1287	47.5	10.6	256	2	S02855	class II histocomp
1288	47.5	10.6	267	2	B64644	hypothetical prote
1289	47.5	10.6	274	1	E64065	3',5'-cyclic-nucle
1290	47.5	10.6	275	1	AG0889	3',5'-cyclic-nucle
1291	47.5	10.6	278	2	H71119	hypothetical prote
1292	47.5	10.6	280	2	H81038	conserved hypothet
1293	47.5	10.6	291	2	A81696	stationary-phase s
1294	47.5	10.6	291	2	B70562	hypothetical prote
1295	47.5	10.6	294	2	S68784	cathepsin L - Para
1296	47.5	10.6	294	2	S36932	chitinase (EC 3.2.
1297	47.5	10.6	309	2	T52453	ATP-dependent Clp
1298	47.5	10.6	310	2	T52041	probable ATP-depen
1299	47.5	10.6	312	2	AG1789	secreted protein w
1300	47.5	10.6	314	2	E70116	hypothetical prote
1301	47.5	10.6	318	2	S23155	envelope glycoprot
1302	47.5	10.6	319	1	S61150	thioredoxin-disulf
1303	47.5	10.6	321	2	S57482	chitinase class 1
1304	47.5	10.6	321	2	A85829	fucose synthetase
1305	47.5	10.6	321	2	F90983	fucose synthetase
1306	47.5	10.6	322	2	T28190	hypothetical prote
1307	47.5	10.6	325	2	AC1047	lysine-tRNA ligase
1308	47.5	10.6	326	2	A45452	transcription fact
1309	47.5	10.6	326	2	T33343	hypothetical prote
1310	47.5	10.6	330	2	G91204	hypothetical prote
1311	47.5	10.6	330	2	H95166	transcription regu
1312	47.5	10.6	334	2	T03157	probable capsid as
1313	47.5	10.6	334	2	S25785	hypothetical prote
1314	47.5	10.6	334	2	T17213	hypothetical prote
1315	47.5	10.6	339	2	S39979	chitinase (EC 3.2.
1316	47.5	10.6	340	2	S40414	chitinase (EC 3.2.
1317	47.5	10.6	342	1	S48948	thioredoxin-disulf
1318	47.5	10.6	346	2	T27812	hypothetical prote
1319	47.5	10.6	355	2	D71429	hypothetical prote
1320	47.5	10.6	367	2	A86051	hypothetical prote
1321	47.5	10.6	371	2	B83900	gentisate 1,2-diox
1322	47.5	10.6	379	2	T51784	AtPP-like protein
1323	47.5	10.6	387	2	S46123	hypothetical prote
1324	47.5	10.6	390	2	H86388	probable bHLH tran
1325	47.5	10.6	396	2	T51387	UVB-resistance pro
1326	47.5	10.6	396	2	A57090	CSA protein - huma
1327	47.5	10.6	398	2	B30565	phospholipase C (E
1328	47.5	10.6	400	1	JQ1575	major surface anti
1329	47.5	10.6	409	2	T11743	pP47 protein - pig
1330	47.5	10.6	413	1	S03631	homeotic protein S
1331	47.5	10.6	415	2	PC4407	envelope protein -
1332	47.5	10.6	417	2	B59392	Wnt10a protein pro
1333	47.5	10.6	418	1	A53888	thermolabile hemol
1334	47.5	10.6	419	2	A90888	hypothetical prote
1335	47.5	10.6	419	2	H85729	hypothetical prote
1336	47.5	10.6	421	2	AF3316	aspartate transami
1337	47.5	10.6	430	2	I48142	B-lymphocyte antig
1338	47.5	10.6	435	2	E96784	hypothetical prote
1339	47.5	10.6	439	2	S58327	cobalt accumulatio
1340	47.5	10.6	446	1	D69340	cobalamin biosynth
1341	47.5	10.6	448	2	F71862	glutamate dehydrog
1342	47.5	10.6	449	2	B26488	tubulin alpha-2 ch
1343	47.5	10.6	450	2	A26488	tubulin alpha-1 ch
1344	47.5	10.6	450	2	A56622	tubulin alpha chai
1345	47.5	10.6	450	2	I77426	tubulin alpha chai
1346	47.5	10.6	450	2	S52152	tubulin alpha chai
1347	47.5	10.6	451	2	A48433	tubulin alpha chai
1348	47.5	10.6	451	2	S43425	tubulin alpha chai
1349	47.5	10.6	451	2	F97337	uncharacterized se
1350	47.5	10.6	452	2	S42033	tubulin alpha chai
1351	47.5	10.6	473	1	RGBYM3	regulatory protein
1352	47.5	10.6	488	1	WMBE42	DNA-binding protei
1353	47.5	10.6	489	2	S23410	FUN19 protein - ye
1354	47.5	10.6	493	2	H69634	glutamate synthase
1355	47.5	10.6	500	2	JC7668	dipeptidyl-peptida
1356	47.5	10.6	513	2	T20068	hypothetical prote
1357	47.5	10.6	513	2	A44150	structural protein
1358	47.5	10.6	514	2	T10974	cytochrome-c oxida
1359	47.5	10.6	518	2	S50465	PAC2 protein - yea
1360	47.5	10.6	527	2	S64060	probable membrane
1361	47.5	10.6	534	2	T41081	hypothetical prote
1362	47.5	10.6	537	2	A23770	asparagine-rich pr
1363	47.5	10.6	550	2	B84900	hypothetical prote
1364	47.5	10.6	551	2	T02752	probable laccase (
1365	47.5	10.6	562	2	H82077	type IV pilus asse
1366	47.5	10.6	568	2	S70873	tapB protein - Aer
1367	47.5	10.6	571	2	S24789	jararhagin C precu
1368	47.5	10.6	579	2	A57057	orphan nuclear hor
1369	47.5	10.6	582	1	BNRT3S	myelin-associated
1370	47.5	10.6	591	2	T30895	sugar transport pr
1371	47.5	10.6	605	1	S07314	glycogen(starch) s
1372	47.5	10.6	614	1	S36173	fragile X mental r
1373	47.5	10.6	618	2	T20450	hypothetical prote
1374	47.5	10.6	626	1	BNRT3	myelin-associated
1375	47.5	10.6	629	2	T48940	hypothetical prote
1376	47.5	10.6	632	1	A40724	fragile X mental r
1377	47.5	10.6	636	1	S31157	beta-fructofuranos
1378	47.5	10.6	636	1	S31155	beta-fructofuranos
1379	47.5	10.6	637	2	B33785	myelin-associated
1380	47.5	10.6	641	2	S41434	gene NS-1 protein
1381	47.5	10.6	644	2	T15652	hypothetical prote
1382	47.5	10.6	648	2	E88960	protein T08B1.1 [i
1383	47.5	10.6	680	2	H84774	probable homeodoma
1384	47.5	10.6	680	2	T25832	hypothetical prote
1385	47.5	10.6	688	2	A43491	env polyprotein -
1386	47.5	10.6	688	2	AI2516	hypothetical prote
1387	47.5	10.6	704	2	T31227	traN protein homol
1388	47.5	10.6	746	2	G02838	enhancer-of-zeste
1389	47.5	10.6	752	2	S23818	hypothetical prote
1390	47.5	10.6	758	2	D71072	hypothetical prote
1391	47.5	10.6	769	2	C83710	transcription regu
1392	47.5	10.6	795	1	A70322	endopeptidase La (
1393	47.5	10.6	802	2	C95136	conserved domain p
1394	47.5	10.6	804	1	YUMU	sucrose synthase (
1395	47.5	10.6	806	2	A41341	microbial serine p
1396	47.5	10.6	808	2	T51232	scarecrow-like pro
1397	47.5	10.6	809	2	F97183	membrane carboxype
1398	47.5	10.6	812	2	E97831	valine-tRNA ligase
1399	47.5	10.6	817	2	S53919	hypothetical prote
1400	47.5	10.6	828	2	E98004	hypothetical prote
1401	47.5	10.6	841	1	S39365	outer membrane ush
1402	47.5	10.6	861	2	A48825	Notch homolog Motc
1403	47.5	10.6	869	2	A47665	env protein gp120(
1404	47.5	10.6	872	1	S53319	acetaldehyde dehyd
1405	47.5	10.6	873	2	T50171	hypothetical prote
1406	47.5	10.6	881	2	S25445	nitrate reductase
1407	47.5	10.6	906	2	E84948	NADH2 dehydrogenas
1408	47.5	10.6	911	1	B3HU	band 3 anion trans
1409	47.5	10.6	917	1	RDMUNH	nitrate reductase
1410	47.5	10.6	918	2	A41667	nitrate reductase
1411	47.5	10.6	918	2	D88544	protein R08D7.6 [i
1412	47.5	10.6	918	2	G88545	protein F59B2.12 [
1413	47.5	10.6	943	2	S31132	hypothetical prote
1414	47.5	10.6	948	2	T41496	conserved hypothet
1415	47.5	10.6	974	2	T04910	hypothetical prote
1416	47.5	10.6	980	2	S54986	regulatory protein

1417	47.5	10.6	991	2	A46421	kainate-selective
1418	47.5	10.6	1015	2	T13062	CLOCK protein - fr
1419	47.5	10.6	1023	2	T13068	CLOCK protein - fr
1420	47.5	10.6	1027	2	T13071	CLOCK protein - fr
1421	47.5	10.6	1164	2	S71792	phosphatidylinosit
1422	47.5	10.6	1164	2	G71827	hypothetical prote
1423	47.5	10.6	1166	2	S70413	DNA-directed RNA p
1424	47.5	10.6	1178	2	S78475	mannosylphosphoryl
1425	47.5	10.6	1284	2	T40879	probable hélicase
1426	47.5	10.6	1308	2	A90428	serine proteinase,
1427	47.5	10.6	1388	2	T00063	hypothetical prote
1428	47.5	10.6	1433	2	S54587	CAT8 protein - yea
1429	47.5	10.6	1457	2	T14577	protein kinase Yak
1430	47.5	10.6	1459	2	T30196	kinesin motor prot
1431	47.5	10.6	1460	2	D81675	polymorphic membra
1432	47.5	10.6	1639	2	S05603	major merozoite su
1433	47.5	10.6	1663	1	C3RT	complement C3 prec
1434	47.5	10.6	1664	2	T18216	integrin-like prot
1435	47.5	10.6	1687	2	T30244	phosphodiesterase
1436	47.5	10.6	1719	2	T30174	exoribonuclease, v
1437	47.5	10.6	1856	2	C95008	immunoglobulin A1
1438	47.5	10.6	2055	2	T00093	hypothetical prote
1439	47.5	10.6	2131	2	S01446	hypothetical prote
1440	47.5	10.6	2163	2	S50675	pre-mRNA splicing
1441	47.5	10.6	2194	1	GNNYE7	genome polyprotein
1442	47.5	10.6	2229	2	T16199	hypothetical prote
1443	47.5	10.6	2338	2	I73957	kinase-related pro
1444	47.5	10.6	2391	2	T18410	carbamoyl-phosphat
1445	47.5	10.6	2477	1	SJCHA	spectrin alpha cha
1446	47.5	10.6	2477	2	S14428	fibronectin precur
1447	47.5	10.6	2529	2	B64635	toxin-like outer m
1448	47.5	10.6	2869	2	T18518	apolipoprotein(a)
1449	47.5	10.6	2893	2	A64556	toxin-like outer m
1450	47.5	10.6	3176	2	CGHU3A	collagen alpha 3(V
1451	47	10.5	78	2	C84636	hypothetical prote
1452	47	10.5	80	2	T10087	metallothionein -
1453	47	10.5	82	2	I57802	Ig lambda2-like ch
1454	47	10.5	98	1	KRSHH4	keratin high-sulfu
1455	47	10.5	98	2	I47086	BIIIB4 high-sulfur
1456	47	10.5	108	1	K1HUWS	Ig kappa chain V-I
1457	47	10.5	110	2	B30583	T-cell receptor de
1458	47	10.5	111	1	CCED	cytochrome c - Eur
1459	47	10.5	111	1	CCPO	cytochrome c - pot
1460	47	10.5	111	1	CCRM	cytochrome c - cuc
1461	47	10.5	112	2	T04008	cytochrome c - Ara
1462	47	10.5	113	2	A29281	T-cell receptor al
1463	47	10.5	117	2	S46376	Ig kappa chain V-J
1464	47	10.5	131	2	S45059	AC1 protein (clone
1465	47	10.5	138	2	S24087	envelope protein -
1466	47	10.5	139	2	T25747	hypothetical prote
1467	47	10.5	146	2	I37296	dopamine transport
1468	47	10.5	152	2	S14236	Ig gamma-1 chain C
1469	47	10.5	157	2	H69849	hypothetical prote
1470	47	10.5	165	2	B72727	hypothetical prote
1471	47	10.5	178	2	F82808	toluene tolerance
1472	47	10.5	183	2	A37410	H-2 class II histo
1473	47	10.5	190	2	AI3086	transcription regu
1474	47	10.5	199	2	A33653	tubulin alpha chai
1475	47	10.5	201	2	H98199	probable transcrip
1476	47	10.5	221	2	T43159	ubiquitin-protein
1477	47	10.5	222	2	T37522	conserved hypothet
1478	47	10.5	227	2	T37499	probable ubiquitin
1479	47	10.5	228	2	I58170	LERK-7 precursor -
1480	47	10.5	234	2	AH2634	hypothetical prote
1481	47	10.5	237	2	F97416	hypothetical prote
1482	47	10.5	239	2	A97358	glucose-inhibited
1483	47	10.5	245	2	I55951	MHC class II E-bet
1484	47	10.5	258	2	B90121	proliferating cell
1485	47	10.5	259	2	E84427	hypothetical prote
1486	47	10.5	263	2	B84778	hypothetical prote
1487	47	10.5	264	2	A60497	H-2 class II histo
1488	47	10.5	266	2	C95288	probable ABC trans
1489	47	10.5	275	2	T32010	hypothetical prote
1490	47	10.5	279	2	T26555	hypothetical prote
1491	47	10.5	282	2	H65116	hypothetical prote
1492	47	10.5	283	2	A59238	dUTP diphosphatase
1493	47	10.5	286	2	T18957	hypothetical prote
1494	47	10.5	286	2	T49876	hypothetical prote
1495	47	10.5	292	2	F70594	hypothetical prote
1496	47	10.5	293	2	JQ1675	frxC protein - Chl
1497	47	10.5	293	2	T06100	adenylyl-sulfate k
1498	47	10.5	298	2	I51410	transcription fact
1499	47	10.5	299	2	T25610	hypothetical prote
1500	47	10.5	300	2	S65554	protochlorophyllid

ALIGNMENTS

RESULT 1
T51961
ATAF1-like protein [imported] - Picea mariana (fragment)
C;Species: Picea mariana
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C;Accession: T51961
R;Perry, D.J.; Bousquet, J.
Genetics 149, 1089-1098, 1998
A;Title: Sequence-tagged-site (STS) markers of arbitrary genes. Development, characteriz
A;Reference number: Z25268; MUID:98278823; PMID:9611216
A;Accession: T51961
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-281 <PER>
A;Cross-references: UNIPROT:O65061; UNIPARC:UPI00000AA7FF; EMBL:AF051222; PIDN:AAC32123.1
C;Genetics:
A;Note: Sb29

Query Match 17.5%; Score 78.5; DB 2; Length 281;
Best Local Similarity 29.0%; Pred. No. 0.53;
Matches 31; Conservative 14; Mismatches 27; Indels 35; Gaps 8;

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Qy          5 MCNSPSNSN---ANCEF---SLKNISD-----------IHP--ESFNLQW---------- 35
              :| || |||    | :|    |     ||           :|   | | ||
Db        146 LCVSPMNSNICLQNLDFFQNSTTPFSDSTLKAPVQNTTFNPISSSINHQWTNCNSTDLMS 205

Qy         36 -FFND-SCAPPTGFNKPTS-NDTMASGWRASSFHFDSEENKHRLIHF 79
                || ||: |: |::| |  : : | :|  :|   |:| :  | :|
Db        206 GLHNDSSCSKPSSFSEPISEKEEVQSSFRLENF---SQEQQQSLFNF 249
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RESULT 2
S01076
aspartate transaminase (EC 2.6.1.1), cytosolic - mouse
N;Alternate names: aspartate aminotransferase, cytosolic
C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: S01076; B25349
R;Obaru, K.; Tsuzuki, T.; Setoyama, C.; Shimada, K.
J. Mol. Biol. 200, 13-22, 1988
A;Title: Structural organization of the mouse aspartate aminotransferase isoenzyme genes.
A;Reference number: S01076; MUID:88245178; PMID:3379636
A;Accession: S01076
A;Molecule type: DNA
A;Residues: 1-413 <OBA>
A;Cross-references: UNIPROT:P05201; UNIPARC:UPI000016CC1D; EMBL:X07302; NID:g50032; PIDN:
A;Note: the authors translated the codon AAT for residue 291 as Ile
R;Obaru, K.; Nomiyama, H.; Shimada, K.; Nagashima, F.; Morino, Y.
J. Biol. Chem. 261, 16976-16983, 1986
A;Title: Cloning and sequence analysis of mRNA for mouse aspartate aminotransferase isoer
A;Reference number: A92571; MUID:87057413; PMID:3782150
A;Accession: B25349
A;Molecule type: mRNA
A;Residues: 1-290,'I',292-413 <OB2>
A;Cross-references: UNIPARC:UPI0000001834; GB:J02623; NID:g466500; PIDN:AAA37263.1; PID:g
C;Genetics:
A;Introns: 40/1; 100/3; 142/1; 179/3; 214/3; 265/1; 320/2; 368/1

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C;Superfamily: aspartate aminotransferase
C;Keywords: aminotransferase; cytosol; phosphoprotein; pyridoxal phosphate
F;259/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

  Query Match            16.3%;  Score 73;  DB 2;  Length 413;
  Best Local Similarity   26.2%;  Pred. No. 3.2;
  Matches   21;  Conservative    7;  Mismatches   26;  Indels   26;  Gaps    3;

Qy          3 PLMCNSPSNSNANCEFSLKNISDIHP--------ESFNLQWFFND-------------SC 41
              |:  :||:  | |  ||     || |          :|| | ||             :|
Db        133 PIYVSSPTWENHNAVFSAAGFKDIRPYCYWDAEKRGLDLQGFLNDLENAPEFSIFVLHAC 192

Qy         42 APPTGFNKPTSNDTMASGWR 61
              |     : ||  |     |:
Db        193 A-----HNPTGTDPTPEQWK 207


RESULT 3
S52830
HMS1 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YM9916.09; protein YMR070w
C;Species: Saccharomyces cerevisiae
C;Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S52830; S59820
R;Pearson, D.; Bowman, S.
submitted to the EMBL Data Library, April 1995
A;Reference number: S52814
A;Accession: S52830
A;Molecule type: DNA
A;Residues: 1-490 <PEA>
A;Cross-references: UNIPROT:P54785; UNIPARC:UPI000012F3CA; EMBL:Z48952; NID:g763008; PID
A;Experimental source: strain AB972
R;Madison, J.; Winston, F.
submitted to the EMBL Data Library, April 1995
A;Reference number: S59820
A;Accession: S59820
A;Molecule type: DNA
A;Residues: 1-490 <MAD>
A;Cross-references: UNIPARC:UPI000012F3CA; EMBL:U25279; NID:g805129; PIDN:AAC49982.1; PI
C;Genetics:
A;Gene: SGD:MOT3; HMS1
A;Cross-references: MIPS:YMR070w; SGD:S0004674
A;Map position: 13R

  Query Match            15.6%;  Score 70;  DB 2;  Length 490;
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  Matches   16;  Conservative    8;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          7 NSPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSN 53
              || ||:| |   :  | ::|||  |      | : |    :: ||:|
Db        139 NSTSNNNNNNNNNNNNNNIHPNQFTAAANMNSNAAAAAYYSFPTAN 185


RESULT 4
T13669
neuromusculin - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13669
R;Kania, A.; Han, P.L.; Kim, Y.T.; Bellen, H.
Neuron 11, 673-687, 1993
A;Title: Neuromusculin, a Drosophila gene expressed in peripheral neuronal precursors an
A;Reference number: Z17697; MUID:94000831; PMID:8398154
A;Accession: T13669
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1011 <KAN>
A;Cross-references: UNIPROT:Q24273; UNIPARC:UPI0000043BE8; EMBL:L23146; NID:g385073; PID
C;Genetics:
A;Gene: nrm
A;Cross-references: FlyBase:FBgn0005629

 Query Match            15.6%;  Score 70;  DB 2;  Length 1011;
  Best Local Similarity   28.3%;  Pred. No. 17;
  Matches   28;  Conservative   12;  Mismatches   19;  Indels   40;  Gaps    7;

Qy          4 LMCN----SPS---------NSN-----ANCEFSLKNISDIHP-----ESFNLQWFFNDS 40
              | ||    :||         ||        :|| : :::  | |     ||    :|:| |
Db        494 LFCNVLDANPSVLTKVRWYANSTLLKELPDCEETREDLCHIDPSKLLLESIGRGFFYNYS 553

Qy         41 CAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRLIHF 79
              |    |||         |:||   |      |:|  |:|:
Db        554 C---EGFN--------AAGWGPRS------EDKELLVHY 575


RESULT 5
A32160
tenascin-C - human
N;Alternate names: hexabrachion
C;Species: Homo sapiens (man)
C;Date: 31-Jul-1989 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: I38337; A32160; S14015; S16166; S50208; S49354
R;Gherzi, R.; Carnemolla, B.; Siri, A.; Ponassi, M.; Balza, E.; Zardi, L.
J. Biol. Chem. 270, 3429-3434, 1995
A;Title: Human tenascin gene. Structure of the 5'-region, identification, and characteri
A;Reference number: A55974; MUID:95155442; PMID:7531707
A;Accession: I38337
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2201 <RES>
A;Cross-references: UNIPROT:P24821; UNIPARC:UPI0000034A0E; EMBL:X78565; NID:g556844; PIDN
R;Gulcher, J.R.; Nies, D.E.; Marton, L.S.; Stefansson, K.
Proc. Natl. Acad. Sci. U.S.A. 86, 1588-1592, 1989
A;Title: An alternatively spliced region of the human hexabrachion contains a repeat of p
A;Reference number: A32160; MUID:89160821; PMID:2466295
A;Accession: A32160
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 431-538,'R',540-1065,'H',1067-1599,'LWLHPRASN',1609-2054,'L' <GUL>
A;Cross-references: UNIPARC:UPI000016AAC6; GB:M24630; NID:g514363; PIDN:AAA52703.1; PID:g
R;Siri, A.; Carnemolla, B.; Saginati, M.; Leprini, A.; Casari, G.; Baralle, F.; Zardi, L.
Nucleic Acids Res. 19, 525-531, 1991
A;Title: Human tenascin: primary structure, pre-mRNA splicing patterns and localization o
A;Reference number: S14015; MUID:91187670; PMID:1707164
A;Accession: S14015
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-243,245-369,'V',371-679,'R',681-1676,'I',1678-2139,'TR',2142,2144-2201 <SIF
A;Cross-references: UNIPARC:UPI0000155D15; EMBL:X56160; NID:g37226; PIDN:CAA39628.1; PID:
R;Nies, D.E.; Hemesath, T.J.; Kim, J.H.; Gulcher, J.R.; Stefansson, K.
J. Biol. Chem. 266, 2818-2823, 1991
A;Title: The complete cDNA sequence of human hexabrachion (tenascin). A multidomain prote
A;Reference number: S16166; MUID:91131572; PMID:1704365
A;Accession: S16166
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-538,'R',540-1065,'H',1067-1599,'LWLHPRASN',1609-2054,'LH',2055-2201 <NIE>
A;Cross-references: UNIPARC:UPI000016AAC5; EMBL:M55618; NID:g184483; PIDN:AAA88083.1; PII
R;Glumoff, V.; Savontaus, M.; Vehanen, J.; Vuorio, E.
Biochim. Biophys. Acta 1219, 613-622, 1994
A;Title: Analysis of aggrecan and tenascin gene expression in mouse skeletal tissues by N
A;Reference number: S50206; MUID:95035091; PMID:7524681
A;Accession: S50208
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 46-125 <GLU>
A;Cross-references: UNIPARC:UPI0000177AF4; EMBL:X80280
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C;Genetics:
A;Gene: GDB:HXB
A;Cross-references: GDB:120073; OMIM:187380
A;Map position: 9q33-9q33
C;Superfamily: tenascin; EGF homology; fibrinogen beta/gamma homology; fibronectin type I
C;Keywords: alternative splicing; extracellular matrix
F;408-434/Domain: EGF homology <EGF>
F;622-703/Domain: fibronectin type III repeat homology <FN3A>
```

```
F;711-794/Domain: fibronectin type III repeat homology <FN3B>
F;892-976/Domain: fibronectin type III repeat homology <FN3C>
F;1437-1519/Domain: fibronectin type III repeat homology <FN3D>
F;1619-1701/Domain: fibronectin type III repeat homology <FN3E>
F;1709-1790/Domain: fibronectin type III repeat homology <FN3F>
F;1798-1878/Domain: fibronectin type III repeat homology <FN3G>
F;1886-1966/Domain: fibronectin type III repeat homology <FN3H>
F;1981-2189/Domain: fibrinogen beta/gamma homology <FBG>

  Query Match             15.1%;  Score 68;  DB 2;  Length 2201;
  Best Local Similarity   66.7%;  Pred. No. 66;
  Matches   12;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         22 NISDIHPESFNLQWFFND 39
              |:||| |||||| |   |
Db       1445 NVSDITPESFNLSWMATD 1462


RESULT 6
AH1173
conserved hypothetical protein homolog lmo0792 [imported] - Listeria monocytogenes (stra
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004
C;Accession: AH1173
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1173
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-296 <GLA>
A;Cross-references: UNIPROT:Q8Y8V0; UNIPARC:UPI00000554C1; GB:NC_003210; PIDN:CAC98870.1
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo0792
C;Superfamily: nitrilase (carbon-nitrogen hydrolase)

  Query Match             14.9%;  Score 67;  DB 2;  Length 296;
  Best Local Similarity   28.4%;  Pred. No. 9.7;
  Matches   19;  Conservative   15;  Mismatches   23;  Indels   10;  Gaps    3;

Qy          9 PSNSNANCEFSLKNISDIHPESFNLQWF---FNDSCAPP--TGFNKPTSNDTMASGWRAS 63
              |:|  || : ::: | : | :  :|  |   :::  |||    || |     :|:|: |
Db         15 PNNKEANLKLAIQYIKEAHEKGADLVLFPEMWSNGYAPPFEDAFNHP-----LATGFGAE 69

Qy         64 SFHFDSE 70
              | :  |
Db         70 RFKWLDE 76


RESULT 7
A54861
tenascin - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 09-Jul-2004
C;Accession: A54861
R;LaFleur, D.W.; Fagin, J.A.; Forrester, J.S.; Rubin, S.A.; Sharifi, B.G.
J. Biol. Chem. 269, 20757-20763, 1994
A;Title: Cloning and characterization of alternatively spliced isoforms of rat tenascin.
ial smooth muscle cells.
A;Reference number: A54861; MUID:94327661; PMID:7519614
A;Accession: A54861
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-575 <LAF>
A;Cross-references: UNIPROT:Q62657; UNIPARC:UPI00000E6D79; GB:U09361; NID:g487638; PIDN:
C;Superfamily: tenascin; EGF homology; fibrinogen beta/gamma homology; fibronectin type
F;17-99/Domain: fibronectin type III repeat homology <FN3A>
F;199-281/Domain: fibronectin type III repeat homology <FN3B>
F;290-372/Domain: fibronectin type III repeat homology <FN3C>
F;381-463/Domain: fibronectin type III repeat homology <FN3D>
F;471-552/Domain: fibronectin type III repeat homology <FN3E>

  Query Match             14.7%;  Score 66;  DB 2;  Length 575;
  Best Local Similarity   66.7%;  Pred. No. 25;
  Matches   12;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         22 NISDIHPESFNLQWFFND 39
              |||| |||||| |   |
Db        298 NISDVTPESFNLSWTATD 315


RESULT 8
T00270
hypothetical protein KIAA0596 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C;Accession: T00270
R;Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.
DNA Res. 5, 31-39, 1998
A;Title: Prediction of the coding sequences of unidentified human genes. IX. The complete
A;Reference number: Z14086; MUID:98290545; PMID:9628581
A;Accession: T00270
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1217 <NAG>
A;Cross-references: UNIPROT:O60336; UNIPARC:UPI000017C1B9; EMBL:AB011168; NID:g3043715; I
A;Experimental source: brain
C;Genetics:
A;Note: KIAA0596

  Query Match             14.7%;  Score 66;  DB 2;  Length 1217;
  Best Local Similarity   27.5%;  Pred. No. 57;
  Matches   19;  Conservative   15;  Mismatches   19;  Indels   16;  Gaps    3;

Qy         10 SNSNANCEFSLKNISD------IHPESFNLQWFFNDSCAPPTGFNKPTSNDTM------A 57
              ::|   |||| : : |      ::||  :     | :| ||: |   :|::|:      :
Db         80 TSSGLLCEFSDRRLLDKWVELRVYPEVKD----SNQACLPPSSFITCSSDNTIRLWNTES 135

Qy         58 SGWRASSFH 66
              ||   |: |
Db        136 SGVHGSTLH 144


RESULT 9
T49067
transcription factor-like protein - Arabidopsis thaliana
N;Alternate names: protein T5P19.310
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 31-Dec-2004
C;Accession: T49067
R;Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Rudd, S.; Lemcke, K.; M
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z25014
A;Accession: T49067
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-620 <BEN>
A;Cross-references: UNIPROT:Q9LXX4; UNIPARC:UPI00000A4F6F; EMBL:AL163972; GSPDB:GN00061;
A;Experimental source: cultivar Columbia; BAC clone T5P19
C;Genetics:
A;Gene: ATSP:T5P19.310
A;Map position: 3
A;Introns: 480/1
C;Superfamily: bZIP transcription factor; fos/jun DNA-binding domain homology

  Query Match             14.6%;  Score 65.5;  DB 2;  Length 620;
  Best Local Similarity   28.9%;  Pred. No. 31;
  Matches   22;  Conservative   16;  Mismatches   33;  Indels    5;  Gaps    3;

Qy          6 CNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDS---CAPPTGFNKPTSND-TMASGWR 61
```

```
              |||  |:   |    |: : |   :||:  :| :::   | ||    :  | | | |||
Db         31 CNSNSDQVRNSISDLRFLID-DDDSFDDLYFPSENESFCIPPDATKREMSGDFTPASGIS 89

Qy         62 ASSFHFDSEENKHRLI 77
                : |:|:| : ::
Db         90 GDCVNEDTEKNTNGVL 105


RESULT 10
B49423
semaphorin I - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 07-May-1999
C;Accession: B49423
R;Kolodkin, A.L.; Matthes, D.J.; Goodman, C.S.
Cell 75, 1389-1399, 1993
A;Title: The Semaphorin genes encode a family of transmembrane and secreted growth cone
A;Reference number: A49423; MUID:94094332; PMID:8269517
A;Accession: B49423
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-656 <KOL>
A;Cross-references: UNIPARC:UPI000017BED0; GB:L26082
C;Genetics:
A;Gene: semaI
A;Cross-references: FlyBase:FBgn0011259

  Query Match            14.6%;  Score 65.5;  DB 2;  Length 656;
  Best Local Similarity  31.8%;  Pred. No. 33;
  Matches   21;  Conservative    7;  Mismatches   27;  Indels   11;  Gaps    2;

Qy          7 NSPSNS---NANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRAS 63
              |:||||   :| | |:|::|:|     | |   | :  |     |          |
Db        202 NTPSNSIPGSAVCAFALQDIADTFEGQFKEQTGINSNWLPVNNAKVPDP--------RPG 253

Qy         64 SFHFDS 69
              | | ||
Db        254 SCHNDS 259


RESULT 11
H96924
probable phosphohydrolases, Icc family [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: H96924
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: H96924
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-652 <KUR>
A;Cross-references: UNIPROT:Q97MJ1; UNIPARC:UPI00000C9DB9; GB:AE001437; PIDN:AAK78187.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0205

  Query Match            14.5%;  Score 65;  DB 2;  Length 652;
  Best Local Similarity  26.3%;  Pred. No. 37;
  Matches   25;  Conservative    5;  Mismatches   25;  Indels   40;  Gaps    3;

Qy         10 SNSNANCEFSLK------NISDI------HPESFNLQWFFNDSCAPPT------------ 45
              :||| |   ||       : |||       |   |  |: |:| | ||
Db         33 ANSNNNAAISLAGSSGSGDFSDIVLSPGSDPSELNFNWYSNNSNATPTVEVALKSDANDS 92

Qy         46 ----------------GFNKPTSNDTMASGWRASS 64
                           |    |||    || : ||
Db         93 DFPANKCSTFTGKTSQGNLNFTSNKVSVSGLKPSS 127


RESULT 12
T43061
hypothetical protein - fission yeast (Schizosaccharomyces pombe) (fragment)
C;Species: Schizosaccharomyces pombe
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43061
R;Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A;Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A;Reference number: Z17323; MUID:98162722; PMID:9501991
A;Accession: T43061
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-330 <YOS>
A;Cross-references: UNIPROT:O14470; UNIPARC:UPI0000169115; EMBL:D89227; NID:g1749661; PII
A;Experimental source: strain PR745

  Query Match            14.4%;  Score 64.5;  DB 2;  Length 330;
  Best Local Similarity  30.0%;  Pred. No. 20;
  Matches   27;  Conservative    5;  Mismatches   33;  Indels   25;  Gaps    6;

Qy         15 NCE----FSLKNIS-DIHPESFNLQWF---FNDS---CAPPTGFN----KPTSN------ 53
              ||      :|||   || |  :    |   || |   |     ||    || ||
Db         26 NCSQTWYHNLKNKKYDICPNCYKQGRFSSSFNSSDFLCMDAIDFNHDEEKPWSNQETLLL 85

Qy         54 ----DTMASGWRASSFHFDSEENKHRLIHF 79
                  :|   |   : |  |   :  ||||
Db         86 LEAIETYGDDWNQIALHVGSRTKEQCLIHF 115


RESULT 13
T25671
hypothetical protein D2092.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25671
R;Gattung, S.; Maggi, L.
submitted to the EMBL Data Library, February 1997
A;Description: The sequence of C. elegans cosmid D2092.
A;Reference number: Z20067
A;Accession: T25671
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-461 <GAT>
A;Cross-references: UNIPROT:P91197; UNIPARC:UPI00000611E5; EMBL:U88167; PIDN:AAB42223.1;
A;Experimental source: strain Bristol N2; clone D2092
C;Genetics:
A;Gene: CESP:D2092.3
A;Map position: 1
A;Introns: 36/1; 80/3; 119/2; 191/1; 243/1; 274/1; 303/1; 382/2
C;Superfamily: acetylcholine receptor

  Query Match            14.4%;  Score 64.5;  DB 2;  Length 461;
  Best Local Similarity  26.5%;  Pred. No. 29;
  Matches   18;  Conservative   12;  Mismatches   27;  Indels   11;  Gaps    2;

Qy          1 KGPLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGW 60
              | || || ||| :|  |  :  :  :| |   :  |           :||   :: : : |
Db        378 KNPLDCNLPSN-HAGYEAQILLLHSVHTELRRVVAF----------YNKEEHDERIQTDW 426

Qy         61 RASSFHFD 68
              | ::   |
Db        427 RFAAMVVD 434


RESULT 14
T39486
hypothetical protein SPBC15D4.10c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39486
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lucas, M.; Gaillardin, C.
submitted to the EMBL Data Library, August 1997
```

A;Reference number: Z21858
A;Accession: T39486
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-475 <LYN>
A;Cross-references: UNIPROT:O74315; UNIPARC:UPI000006A222; EMBL:AL031349; PIDN:CAA20485.
A;Experimental source: strain 972h-; cosmid c15D4
C;Genetics:
A;Gene: SPDB:SPBC15D4.10c
A;Map position: 2
A;Introns: 419/1

Query Match 14.4%; Score 64.5; DB 2; Length 475;
Best Local Similarity 30.3%; Pred. No. 30;
Matches 27; Conservative 7; Mismatches 32; Indels 23; Gaps 5;

```
Qy          7 NSPSNS---NANCEFSLKNISD-----------IHPESFNLQ---WFFNDS----CAPPT 45
              | |   |    | | :||| | |            ::|   | :|    |          | |
Db        318 NQPQQSAFQNLNTQFSLPNNSQPVFGHTSLTQPVNPNGFTVQPPATFMQQPQGPFVPPNT 377

Qy         46 GFNKPTSNDTMASGWRASSFHFDSEENKH 74
                | | :| |  |   || |  |:  ||:
Db        378 TFESPFANVT--SKISASGFSNDNPANKN 404
```

RESULT 15
T38303
SWI/SNF complex transcription regulator - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38303
R;Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.; Wood, V.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z21785
A;Accession: T38303
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-503 <SKE>
A;Cross-references: UNIPROT:O14470; UNIPARC:UPI000006C8C4; EMBL:Z99163; PIDN:CAB16236.1;
A;Experimental source: strain 972h-; cosmid c23H3
C;Genetics:
A;Gene: SPDB:SPAC23H3.10
A;Map position: 1

Query Match 14.4%; Score 64.5; DB 2; Length 503;
Best Local Similarity 30.0%; Pred. No. 32;
Matches 27; Conservative 5; Mismatches 33; Indels 25; Gaps 6;

```
Qy         15 NCE----FSLKNIS-DIHPESFNLQWF---FNDS---CAPPTGFN----KPTSN------ 53
              ||       :|||   || |  :    |   || |   |     ||    || ||
Db        199 NCSQTWYHNLKNKKYDICPNCYKQGRFSSSFNSSDFLCMDAIDFNHDEEKPWSNQETLLL 258

Qy         54 ----DTMASGWRASSFHFDSEENKHRLIHF 79
                 :|    |   : |  |   :  ||||
Db        259 LEAIETYGDDWNQIALHVGSRTKEQCLIHF 288
```

Search completed: November 21, 2006, 20:09:36
Job time : 28.9235 secs

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OM protein - protein search, using sw model

Run on: November 21, 2006, 19:59:24 ; Search time 117.187 Seconds
(without alignments)
631.482 Million cell updates/sec

Title: US-10-063-553-48_COPY_111_190
Perfect score: 449
Sequence: 1 KGPLMCNSPSNSNANCEFSL.....RASSFHFDSEENKHRLIHFS 80

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	449	100.0	229	2	Q53R12_HUMAN	Q53r12 homo sapien
2	449	100.0	229	2	Q5U609_HUMAN	Q5u609 homo sapien
3	449	100.0	229	2	Q6UWS1_HUMAN	Q6uws1 homo sapien
4	449	100.0	229	2	Q9H5X9_HUMAN	Q9h5x9 homo sapien
5	264	58.8	230	2	Q3T0Z4_BOVIN	Q3t0z4 bos taurus
6	237.5	52.9	226	2	Q9CQY8_MOUSE	Q9cqy8 m 11 days p
7	237.5	52.9	226	2	Q9D3R0_MOUSE	Q9d3r0 mus musculu
8	231.5	51.6	226	2	Q9D3Q0_MOUSE	Q9d3q0 mus musculu
9	93	20.7	242	2	Q4KL96_XENLA	Q4kl96 xenopus lae
10	83.5	18.6	277	2	Q66S52_9UROC	Q66s52 oikopleura
11	83	18.5	342	2	Q9PT67_XENLA	Q9pt67 xenopus lae
12	82	18.3	142	2	Q695C3_PICMA	Q695c3 picea maria
13	82	18.3	148	2	O65095_PICMA	O65095 picea maria
14	80	17.8	352	2	Q9PRJ8_XENLA	Q9prj8 xenopus lae
15	79	17.6	808	2	Q70W02_CIOIN	Q70w02 ciona intes
16	78.5	17.5	149	2	Q695B5_PICGL	Q695b5 picea glauc
17	78.5	17.5	149	2	Q695B6_PICMA	Q695b6 picea maria
18	78.5	17.5	149	2	Q695B7_PICMA	Q695b7 picea maria
19	78.5	17.5	149	2	Q695B8_PICAB	Q695b8 picea abies
20	78.5	17.5	154	2	Q9SPX7_PICAB	Q9spx7 picea abies
21	78.5	17.5	156	2	O65096_PICMA	O65096 picea maria
22	78.5	17.5	281	2	O65061_PICMA	O65061 picea maria
23	78	17.4	832	2	Q8IBT8_PLAF7	Q8ibt8 plasmodium
24	77.5	17.3	151	2	Q695B3_PICMA	Q695b3 picea maria
25	77.5	17.3	156	2	O65097_PICMA	O65097 picea maria
26	76.5	17.0	149	2	Q695B0_TSUCA	Q695b0 tsuga canad
27	76.5	17.0	149	2	Q695B1_PSEMZ	Q695b1 pseudotsuga
28	76.5	17.0	149	2	Q695B2_PINCE	Q695b2 pinus cembr
29	76.5	17.0	149	2	Q695B4_PICGL	Q695b4 picea glauc
30	76.5	17.0	154	2	Q9SPW4_PICGL	Q9spw4 picea glauc
31	75	16.7	853	2	O93245_ONCMY	O93245 oncorhynchu
32	75	16.7	989	2	Q6FP46_CANGA	Q6fp46 candida gla
33	74.5	16.6	296	2	Q4EFP8_LISMO	Q4efp8 listeria mo
34	74.5	16.6	296	2	Q722C5_LISMF	Q722c5 listeria mo
35	73.5	16.4	353	2	Q9PT68_XENLA	Q9pt68 xenopus lae
36	73	16.3	145	2	Q695C2_PICAB	Q695c2 picea abies
37	73	16.3	150	2	Q9SPX8_PICAB	Q9spx8 picea abies
38	73	16.3	412	1	AATC_MOUSE	P05201 mus musculu
39	73	16.3	413	2	Q3UJH8_MOUSE	Q3ujh8 mus musculu
40	72	16.0	854	2	O93244_ONCMY	O93244 oncorhynchu
41	72	16.0	1443	2	Q5A450_CANAL	Q5a450 candida alb
42	71	15.8	352	2	Q5WM45_XENTR	Q5wm45 xenopus tro
43	71	15.8	852	2	Q6CLB3_KLULA	Q6clb3 kluyveromyc
44	70.5	15.7	146	2	Q695B9_PICGL	Q695b9 picea glauc
45	70.5	15.7	146	2	Q695C0_PICGL	Q695c0 picea glauc
46	70.5	15.7	146	2	Q695C1_PICAB	Q695c1 picea abies
47	70.5	15.7	151	2	Q9SPW5_PICGL	Q9spw5 picea glauc
48	70.5	15.7	151	2	Q9SPX9_PICAB	Q9spx9 picea abies
49	70.5	15.7	527	2	Q8BYW9_MOUSE	Q8byw9 m 16 days n
50	70	15.6	490	1	MOT3_YEAST	P54785 saccharomyc
51	70	15.6	1011	2	Q24273_DROME	Q24273 drosophila
52	70	15.6	1087	2	Q9VNP2_DROME	Q9vnp2 drosophila
53	68.5	15.3	710	2	Q5CN99_CRYHO	Q5cn99 cryptospori
54	68.5	15.3	710	2	Q5CRR2_CRYPV	Q5crr2 cryptospori
55	68.5	15.3	890	2	Q54YH9_DICDI	Q54yh9 dictyosteli
56	68	15.1	293	2	Q692Q7_9CLOS	Q692q7 citrus tris
57	68	15.1	415	2	Q3ST19_NITWN	Q3st19 nitrobacter
58	68	15.1	459	2	Q7PXC3_ANOGA	Q7pxc3 anopheles g
59	68	15.1	2201	1	TENA_HUMAN	P24821 homo sapien
60	68	15.1	2201	2	Q5T7S3_HUMAN	Q5t7s3 homo sapien
61	68	15.1	2233	2	Q4LE33_HUMAN	Q4le33 homo sapien
62	67.5	15.0	351	2	Q4WIU3_ASPFU	Q4wiu3 aspergillus
63	67.5	15.0	527	2	Q5NDL0_RAT	Q5ndl0 rattus norv
64	67.5	15.0	623	2	Q8JNB7_WSSV	Q8jnb7 white spot
65	67.5	15.0	623	2	Q91LN4_WSSV	Q91ln4 white spot
66	67.5	15.0	1282	2	Q6FRR1_CANGA	Q6frr1 candida gla
67	67	14.9	296	2	Q4ENI7_LISMO	Q4eni7 listeria mo
68	67	14.9	296	2	Q8Y8V0_LISMO	Q8y8v0 listeria mo
69	67	14.9	369	2	Q54B59_DICDI	Q54b59 dictyosteli
70	67	14.9	619	2	Q62701_RAT	Q62701 rattus norv
71	66.5	14.8	126	2	Q4I7X6_GIBZE	Q4i7x6 gibberella
72	66.5	14.8	296	2	Q4YGK5_PLABE	Q4ygk5 plasmodium
73	66.5	14.8	375	2	Q6LYB9_METMP	Q6lyb9 methanococc
74	66.5	14.8	926	2	Q6ZU11_HUMAN	Q6zu11 homo sapien
75	66	14.7	575	2	Q62657_RAT	Q62657 rattus norv
76	66	14.7	1131	2	Q54K42_DICDI	Q54k42 dictyosteli
77	66	14.7	1217	2	Q5W9G9_HUMAN	Q5w9g9 homo sapien
78	66	14.7	1324	2	Q8JKQ9_9VIRU	Q8jkq9 heliothis z
79	66	14.7	1425	2	Q5KHV2_CRYNE	Q5khv2 cryptococcu
80	66	14.7	1538	2	Q55UJ3_CRYNE	Q55uj3 cryptococcu
81	66	14.7	1538	2	Q5KHV3_CRYNE	Q5khv3 cryptococcu
82	65.5	14.6	252	2	Q46BP1_METBA	Q46bp1 methanosarc
83	65.5	14.6	413	2	Q4R5L1_MACFA	Q4r5l1 macaca fasc
84	65.5	14.6	620	2	Q9LXX4_ARATH	Q9lxx4 arabidopsis
85	65.5	14.6	695	2	Q4CH46_CLOTM	Q4ch46 clostridium
86	65.5	14.6	760	2	Q4IDC6_GIBZE	Q4idc6 gibberella
87	65.5	14.6	850	1	SEM1A_DROME	Q24322 drosophila
88	65.5	14.6	1043	2	Q55DW9_DICDI	Q55dw9 dictyosteli
89	65.5	14.6	1073	2	Q9W1T8_DROME	Q9w1t8 drosophila
90	65.5	14.6	1173	2	Q6NR54_DROME	Q6nr54 drosophila
91	65.5	14.6	1278	2	Q4Z391_PLABE	Q4z391 plasmodium
92	65.5	14.6	1342	2	Q2QS53_ORYSA	Q2qs53 oryza sativ
93	65.5	14.6	2113	2	Q46BK6_METBA	Q46bk6 methanosarc
94	65.5	14.6	2525	2	Q4Q184_LEIMA	Q4q184 leishmania
95	65	14.5	144	2	Q9J6E7_9HIV1	Q9j6e7 human immun
96	65	14.5	179	2	Q2J6B3_9ACTO	Q2j6b3 frankia sp.
97	65	14.5	193	2	Q6PI73_HUMAN	Q6pi73 homo sapien
98	65	14.5	389	2	Q4PFM5_USTMA	Q4pfm5 ustilago ma
99	65	14.5	493	2	Q65XF7_ORYSA	Q65xf7 oryza sativ
100	65	14.5	652	2	Q97MJ1_CLOAB	Q97mj1 clostridium
101	65	14.5	1612	2	Q5BFT6_EMENI	Q5bft6 aspergillus
102	64.5	14.4	343	2	Q54EK7_DICDI	Q54ek7 dictyosteli
103	64.5	14.4	350	2	Q6BNJ6_DEBHA	Q6bnj6 debaryomyce
104	64.5	14.4	383	2	Q396Q8_BURS3	Q396q8 burkholderi

105	64.5	14.4	387	2	P90905_CAEEL	P90905 caenorhabdi
106	64.5	14.4	460	2	Q61D03_CAEBR	Q61d03 caenorhabdi
107	64.5	14.4	461	2	P91197_CAEEL	P91197 caenorhabdi
108	64.5	14.4	468	2	Q52KU4_XENLA	Q52ku4 xenopus lae
109	64.5	14.4	475	1	AMO1_SCHPO	O74315 schizosacch
110	64.5	14.4	486	2	Q73CW4_BACC1	Q73cw4 bacillus ce
111	64.5	14.4	503	1	YEPA_SCHPO	O14470 schizosacch
112	64.5	14.4	505	2	Q3HLL6_9HIV2	Q3hll6 human immun
113	64.5	14.4	508	2	Q74118_9HIV2	Q74118 human immun
114	64.5	14.4	577	2	Q894E2_CLOTE	Q894e2 clostridium
115	64.5	14.4	754	2	Q8IBU4_PLAF7	Q8ibu4 plasmodium
116	64.5	14.4	764	2	O97343_SUBDO	O97343 suberites d
117	64.5	14.4	898	2	Q2QLI8_ORYSA	Q2qli8 oryza sativ
118	64.5	14.4	1163	1	LEPR_MACMU	Q9myl0 macaca mula
119	64	14.3	228	1	IF4E2_CAEEL	Q21693 caenorhabdi
120	64	14.3	252	2	Q6C9E9_YARLI	Q6c9e9 yarrowia li
121	64	14.3	660	2	Q484F0_COLP3	Q484f0 colwellia p
122	64	14.3	694	2	Q2QLJ8_ORYSA	Q2qlj8 oryza sativ
123	64	14.3	727	2	Q2S6T0_9GAMM	Q2s6t0 hahella che
124	64	14.3	798	2	Q86HW6_DICDI	Q86hw6 dictyosteli
125	64	14.3	802	2	Q55U46_CRYNE	Q55u46 cryptococcu
126	64	14.3	802	2	Q5KI96_CRYNE	Q5ki96 cryptococcu
127	64	14.3	819	2	Q55U47_CRYNE	Q55u47 cryptococcu
128	64	14.3	819	2	Q5KI97_CRYNE	Q5ki97 cryptococcu
129	64	14.3	881	2	Q8XSL4_RALSO	Q8xsl4 ralstonia s
130	64	14.3	935	2	Q2XDJ6_PSEPU	Q2xdj6 pseudomonas
131	64	14.3	992	1	PHS2_DICDI	P34114 dictyosteli
132	64	14.3	993	2	Q54F21_DICDI	Q54f21 dictyosteli
133	64	14.3	1500	2	O42080_9BETA	O42080 human herpe
134	64	14.3	1500	2	Q77Z83_HHV6U	Q77z83 human herpe
135	64	14.3	3056	2	Q8I639_PLAF7	Q8i639 plasmodium
136	64	14.3	5864	2	Q869L3_DICDI	Q86913 d similar t
137	63.5	14.1	341	2	Q5ACM8_CANAL	Q5acm8 candida alb
138	63.5	14.1	415	2	Q6INN9_XENLA	Q6inn9 xenopus lae
139	63.5	14.1	450	2	Q55DH3_DICDI	Q55dh3 dictyosteli
140	63.5	14.1	485	2	Q81HD7_BACCR	Q81hd7 bacillus ce
141	63.5	14.1	492	2	Q3ERW8_BACTI	Q3erw8 bacillus th
142	63.5	14.1	602	2	Q2PQS8_9HIV2	Q2pqs8 human immun
143	63.5	14.1	654	2	Q7TLW5_NPVCF	Q7tlw5 choristoneu
144	63.5	14.1	864	2	Q6BGY9_DEBHA	Q6bgy9 debaryomyce
145	63.5	14.1	886	2	Q622L7_CAEBR	Q622l7 caenorhabdi
146	63.5	14.1	906	2	Q93XS1_PRUPE	Q93xs1 prunus pers
147	63	14.0	229	2	Q5BWA1_SCHJA	Q5bwa1 schistosoma
148	63	14.0	231	2	Q8VRH7_AERHY	Q8vrh7 aeromonas h
149	63	14.0	299	2	Q6FD33_ACIAD	Q6fd33 acinetobact
150	63	14.0	366	2	Q2U5W6_ASPOR	Q2u5w6 aspergillus
151	63	14.0	418	1	NAC9_ARATH	Q9zvh0 arabidopsis
152	63	14.0	438	2	Q2UAS3_ASPOR	Q2uas3 aspergillus
153	63	14.0	467	2	Q660K0_BORGA	Q660k0 borrelia ga
154	63	14.0	577	2	Q9AUH9_PINTA	Q9auh9 pinus taeda
155	63	14.0	617	2	Q4YHS1_PLABE	Q4yhs1 plasmodium
156	63	14.0	655	2	Q38B78_9TRYP	Q38b78 trypanosoma
157	63	14.0	684	1	CDC4_CANAL	P53699 candida alb
158	63	14.0	737	2	Q6J3P9_SIVCZ	Q6j3p9 chimpanzee
159	63	14.0	742	2	Q55ZA4_CRYNE	Q55za4 cryptococcu
160	63	14.0	742	2	Q5KNL9_CRYNE	Q5knl9 cryptococcu
161	63	14.0	768	2	Q5A9A6_CANAL	Q5a9a6 candida alb
162	63	14.0	830	2	Q69565_9BETA	Q69565 human herpe
163	63	14.0	1080	2	Q6R7G6_9HERP	Q6r7g6 ostreid her
164	63	14.0	1081	2	Q4P8L6_USTMA	Q4p8l6 ustilago ma
165	63	14.0	1165	1	CHS3_YEAST	P29465 saccharomyc
166	63	14.0	1198	2	Q55E26_DICDI	Q55e26 dictyosteli
167	63	14.0	1198	2	Q2MCX4_DICDI	Q2mcx4 dictyosteli
168	63	14.0	1295	2	Q69471_9BETA	Q69471 human herpe
169	63	14.0	1447	2	Q6FLG8_CANGA	Q6flg8 candida gla
170	63	14.0	1570	2	Q9U0H8_PLAF7	Q9u0h8 plasmodium
171	63	14.0	1740	2	Q8IJK9_PLAF7	Q8ijk9 plasmodium
172	63	14.0	1931	2	Q7YYK9_CRYPV	Q7yyk9 cryptospori
173	63	14.0	2051	2	O96682_DROME	O96682 drosophila
174	63	14.0	2051	2	Q9V4A7_DROME	Q9v4a7 drosophila
175	62.5	13.9	151	2	Q3ZVI8_SPICI	Q3zvi8 spiroplasma
176	62.5	13.9	177	2	Q4Y2N4_PLACH	Q4y2n4 plasmodium
177	62.5	13.9	180	2	Q7RK89_PLAYO	Q7rk89 plasmodium
178	62.5	13.9	201	2	Q5AYF3_EMENI	Q5ayf3 aspergillus
179	62.5	13.9	210	2	Q4IR16_GIBZE	Q4ir16 gibberella
180	62.5	13.9	296	2	Q92DM8_LISIN	Q92dm8 listeria in
181	62.5	13.9	318	2	Q4WX16_ASPFU	Q4wx16 aspergillus
182	62.5	13.9	368	2	Q5JZR1_SOYBN	Q5jzr1 glycine max
183	62.5	13.9	412	1	AATC_HUMAN	P17174 homo sapien
184	62.5	13.9	413	2	Q2TU84_HUMAN	Q2tu84 homo sapien
185	62.5	13.9	413	2	Q5VW80_HUMAN	Q5vw80 homo sapien
186	62.5	13.9	561	2	Q8LM20_ORYSA	Q8lm20 oryza sativ
187	62.5	13.9	646	2	Q99071_USTHO	Q99071 ustilago ho
188	62.5	13.9	702	2	Q8SB54_ORYSA	Q8sb54 oryza sativ
189	62.5	13.9	826	2	Q8SXI1_DROME	Q8sxi1 drosophila
190	62.5	13.9	826	2	Q9VHN9_DROME	Q9vhn9 drosophila
191	62.5	13.9	851	2	Q4Y4G6_PLACH	Q4y4g6 plasmodium
192	62.5	13.9	879	2	Q45FW0_SIVCZ	Q45fw0 simian immu
193	62.5	13.9	911	2	Q7RJ02_PLAYO	Q7rj02 plasmodium
194	62.5	13.9	932	2	Q7VJK1_HELHP	Q7vjk1 helicobacte
195	62.5	13.9	1071	2	Q4HZT1_GIBZE	Q4hzt1 gibberella
196	62.5	13.9	1215	2	Q600C2_MYCH2	Q600c2 mycoplasma
197	62.5	13.9	1445	2	Q5CPT3_CRYPV	Q5cpt3 cryptospori
198	62.5	13.9	1630	2	Q6PCS0_MOUSE	Q6pcs0 mus musculu
199	62.5	13.9	1811	2	O36184_9VIRU	O36184 plautia sta
200	62.5	13.9	2222	2	Q4RY92_TETNG	Q4ry92 tetraodon n
201	62.5	13.9	3446	2	Q86AC8_DICDI	Q86ac8 dictyosteli
202	62	13.8	112	2	Q31E21_THICR	Q31e21 thiomicrosp
203	62	13.8	293	2	Q692Q5_9CLOS	Q692q5 citrus tris
204	62	13.8	293	2	Q692Q6_9CLOS	Q692q6 citrus tris
205	62	13.8	293	2	Q692Q8_9CLOS	Q692q8 citrus tris
206	62	13.8	293	2	Q692R0_9CLOS	Q692r0 citrus tris
207	62	13.8	293	2	Q692R2_9CLOS	Q692r2 citrus tris
208	62	13.8	327	2	Q5DD47_SCHJA	Q5dd47 schistosoma
209	62	13.8	382	2	Q83E23_COXBU	Q83e23 coxiella bu
210	62	13.8	404	2	Q2WQM4_CLOBE	Q2wqm4 clostridium
211	62	13.8	498	2	Q50MM6_ENTHI	Q50mm6 entamoeba h
212	62	13.8	508	2	Q74116_9HIV2	Q74116 human immun
213	62	13.8	537	1	ACEA_EMENI	P28298 emericella
214	62	13.8	592	2	Q5A4E1_CANAL	Q5a4e1 candida alb
215	62	13.8	862	2	Q74113_9HIV2	Q74113 human immun
216	62	13.8	864	2	Q6CD66_YARLI	Q6cd66 yarrowia li
217	62	13.8	868	2	Q54VT5_DICDI	Q54vt5 dictyosteli
218	62	13.8	924	2	Q9FIC2_ARATH	Q9fic2 arabidopsis
219	62	13.8	971	1	SEC5_YEAST	P89102 saccharomyc
220	62	13.8	1011	2	Q7RD67_PLAYO	Q7rd67 plasmodium
221	62	13.8	1339	2	Q3PID8_PARDE	Q3pid8 paracoccus
222	62	13.8	1466	2	Q8BB47_9BETA	Q8bb47 human herpe
223	62	13.8	1604	2	Q4UNE0_RICFE	Q4une0 rickettsia
224	62	13.8	1921	2	Q5X4P0_LEGPA	Q5x4p0 legionella
225	62	13.8	2179	2	Q7PDL7_PLAYO	Q7pdl7 plasmodium
226	62	13.8	2266	2	Q8WYP5_HUMAN	Q8wyp5 homo sapien
227	62	13.8	3115	2	Q9IFX0_9CLOS	Q9ifx0 citrus tris
228	61.5	13.7	240	2	Q33EW4_METHU	Q33ew4 methanospir
229	61.5	13.7	240	2	Q3PV22_NITHA	Q3pv22 nitrobacter
230	61.5	13.7	411	2	Q6NX26_XENTR	Q6nx26 xenopus tro
231	61.5	13.7	417	2	Q8YY26_ANASP	Q8yy26 anabaena sp
232	61.5	13.7	422	2	Q4HQ78_CAMUP	Q4hq78 campylobact
233	61.5	13.7	427	2	Q2NXH4_XANOR	Q2nxh4 xanthomonas
234	61.5	13.7	442	2	Q5CFX3_CRYHO	Q5cfx3 cryptospori
235	61.5	13.7	453	2	Q2U0N7_ASPOR	Q2u0n7 aspergillus
236	61.5	13.7	473	2	Q5GU60_XANOR	Q5gu60 xanthomonas
237	61.5	13.7	487	2	Q9P6E4_NEUCR	Q9p6e4 neurospora
238	61.5	13.7	493	2	Q4MWI7_BACCE	Q4mwi7 bacillus ce
239	61.5	13.7	512	2	Q6BH61_DEBHA	Q6bh61 debaryomyce
240	61.5	13.7	519	2	Q50ZA0_ENTHI	Q50za0 entamoeba h
241	61.5	13.7	536	2	Q2I8W8_9HIV1	Q2i8w8 human immun
242	61.5	13.7	544	2	Q4H3K1_CIOIN	Q4h3k1 ciona intes
243	61.5	13.7	556	2	Q6DEK7_BRARE	Q6dek7 brachydanio
244	61.5	13.7	590	2	Q2UBS6_ASPOR	Q2ubs6 aspergillus
245	61.5	13.7	647	2	Q99077_USTHO	Q99077 ustilago ho
246	61.5	13.7	686	2	Q4WKV2_ASPFU	Q4wkv2 aspergillus
247	61.5	13.7	825	2	Q9FK21_ARATH	Q9fk21 arabidopsis
248	61.5	13.7	889	2	Q6ZHH7_ORYSA	Q6zhh7 oryza sativ
249	61.5	13.7	1034	1	ULP2_YEAST	P40537 saccharomyc
250	61.5	13.7	1282	2	Q7Z8J6_USTMA	Q7z8j6 ustilago ma

251	61.5	13.7	1351	2	Q4RQD6_TETNG	Q4rqd6	tetraodon n
252	61.5	13.7	1413	2	Q9NBD3_CAEEL	Q9nbd3	caenorhabdi
253	61.5	13.7	1439	2	Q5CQG9_CRYPV	Q5cqg9	cryptospori
254	61.5	13.7	1493	2	Q9N5D3_CAEEL	Q9n5d3	caenorhabdi
255	61.5	13.7	1873	2	Q83044_9CLOS	Q83044	lettuce inf
256	61.5	13.7	3023	2	Q4P701_USTMA	Q4p701	ustilago ma
257	61.5	13.7	3462	1	RELN_RAT	P58751	rattus norv
258	61.5	13.7	3673	2	Q4DTY1_TRYCR	Q4dty1	trypanosoma
259	61	13.6	192	2	Q49390_MYCGE	Q49390	mycoplasma
260	61	13.6	204	1	RPC8_HUMAN	Q9y535	homo sapien
261	61	13.6	204	1	RPC8_MOUSE	Q9d2c6	mus musculu
262	61	13.6	204	2	Q5M7Y8_HUMAN	Q5m7y8	homo sapien
263	61	13.6	204	2	Q2T9X1_BOVIN	Q2t9x1	bos taurus
264	61	13.6	212	2	Q4Y2P3_PLACH	Q4y2p3	plasmodium
265	61	13.6	241	2	Q8AI21_9HIV1	Q8ai21	human immun
266	61	13.6	326	2	O23659_ARATH	O23659	arabidopsis
267	61	13.6	326	2	Q8H1N3_ARATH	Q8h1n3	arabidopsis
268	61	13.6	375	2	Q55S52_CRYNE	Q55s52	cryptococcu
269	61	13.6	375	2	Q5KGK4_CRYNE	Q5kgk4	cryptococcu
270	61	13.6	402	2	Q2UU41_ASPOR	Q2uu41	aspergillus
271	61	13.6	406	2	Q6ZC71_ORYSA	Q6zc71	oryza sativ
272	61	13.6	412	1	AATC_RAT	P13221	rattus norv
273	61	13.6	413	2	Q6P721_RAT	Q6p721	rattus norv
274	61	13.6	419	2	Q86M56_DROME	Q86m56	drosophila
275	61	13.6	449	2	Q2QQI8_ORYSA	Q2qqi8	oryza sativ
276	61	13.6	493	2	P94128_AERPU	P94128	aeromonas p
277	61	13.6	533	2	Q2TZ21_ASPOR	Q2tz21	aspergillus
278	61	13.6	574	2	Q8EC75_SHEON	Q8ec75	shewanella
279	61	13.6	642	2	Q75JG6_DICDI	Q75jg6	dictyosteli
280	61	13.6	681	2	Q552J1_DICDI	Q552j1	dictyosteli
281	61	13.6	687	2	Q8W3M2_CITUN	Q8w3m2	citrus unsh
282	61	13.6	715	2	Q59K73_CANAL	Q59k73	candida alb
283	61	13.6	725	2	Q8T124_DICDI	Q8t124	dictyosteli
284	61	13.6	729	2	Q59K69_CANAL	Q59k69	candida alb
285	61	13.6	771	2	Q8I5E1_PLAF7	Q8i5e1	plasmodium
286	61	13.6	788	2	Q9W4N2_DROME	Q9w4n2	drosophila
287	61	13.6	852	2	Q89607_9HIV2	Q89607	human immun
288	61	13.6	889	2	Q6ZC72_ORYSA	Q6zc72	oryza sativ
289	61	13.6	905	2	Q4XEF1_PLACH	Q4xef1	plasmodium
290	61	13.6	915	2	Q43042_PETHY	Q43042	petunia hyb
291	61	13.6	946	2	Q2UQZ7_ASPOR	Q2uqz7	aspergillus
292	61	13.6	1023	2	Q5CUV4_CRYPV	Q5cuv4	cryptospori
293	61	13.6	1109	2	Q6BWG1_DEBHA	Q6bwg1	debaryomyce
294	61	13.6	1203	2	Q55B98_DICDI	Q55b98	dictyosteli
295	61	13.6	1469	2	Q4P4A6_USTMA	Q4p4a6	ustilago ma
296	61	13.6	1550	2	O55601_9VIRU	O55601	garlic viru
297	61	13.6	1612	2	Q2UHC8_ASPOR	Q2uhc8	aspergillus
298	61	13.6	1668	2	Q4RUS6_TETNG	Q4rus6	tetraodon n
299	61	13.6	1714	2	Q90995_CHICK	Q90995	gallus gall
300	61	13.6	1808	1	TENA_CHICK	P10039	gallus gall
301	61	13.6	1810	2	Q90824_CHICK	Q90824	gallus gall
302	61	13.6	2019	2	Q64706_MOUSE	Q64706	mus musculu
303	61	13.6	2019	2	Q80YX2_MOUSE	Q80yx2	mus musculu
304	61	13.6	2110	2	Q80YX1_MOUSE	Q80yx1	mus musculu
305	61	13.6	4293	2	O08852_MOUSE	O08852	mus musculu
306	60.5	13.5	127	2	O18855_SHEEP	O18855	ovis aries
307	60.5	13.5	135	2	Q5TSF8_ANOGA	Q5tsf8	anopheles g
308	60.5	13.5	139	2	Q8LRP9_CRAMN	Q8lrp9	crataegus m
309	60.5	13.5	241	2	Q8AI44_9HIV1	Q8ai44	human immun
310	60.5	13.5	267	2	Q84HS5_RHIET	Q84hs5	rhizobium e
311	60.5	13.5	267	2	Q2K2Q6_RHIET	Q2k2q6	rhizobium e
312	60.5	13.5	343	2	Q7TU21_PROMP	Q7tu21	prochloroco
313	60.5	13.5	382	2	Q60U30_CAEBR	Q60u30	caenorhabdi
314	60.5	13.5	402	2	Q4V9H4_BRARE	Q4v9h4	brachydanio
315	60.5	13.5	444	2	Q97HP3_CLOAB	Q97hp3	clostridium
316	60.5	13.5	468	2	Q9XY08_BOMMO	Q9xy08	bombyx mori
317	60.5	13.5	502	2	Q6BKP6_DEBHA	Q6bkp6	debaryomyce
318	60.5	13.5	585	2	Q2U5T6_ASPOR	Q2u5t6	aspergillus
319	60.5	13.5	602	2	Q6MY96_ASPFU	Q6my96	aspergillus
320	60.5	13.5	612	2	Q7RGB3_PLAYO	Q7rgb3	plasmodium
321	60.5	13.5	661	1	INVB_DAUCA	P80065	daucus caro
322	60.5	13.5	668	2	Q6BYI7_DEBHA	Q6byi7	debaryomyce
323	60.5	13.5	740	2	Q5RD05_PONPY	Q5rd05	pongo pygma
324	60.5	13.5	747	2	Q9DSJ3_9HIV2	Q9dsj3	human immun
325	60.5	13.5	764	2	Q6BJR8_DEBHA	Q6bjr8	debaryomyce
326	60.5	13.5	780	2	Q5AWV0_EMENI	Q5awv0	aspergillus
327	60.5	13.5	785	2	Q54CE0_DICDI	Q54ce0	dictyosteli
328	60.5	13.5	913	2	Q6BIQ9_DEBHA	Q6biq9	debaryomyce
329	60.5	13.5	937	1	NUP98_RAT	P49793	rattus norv
330	60.5	13.5	941	2	Q6BZI3_DEBHA	Q6bzi3	debaryomyce
331	60.5	13.5	992	1	VPS41_YEAST	P38959	saccharomyc
332	60.5	13.5	1042	2	Q9NAL5_CAEEL	Q9nal5	caenorhabdi
333	60.5	13.5	1125	2	Q54H49_DICDI	Q54h49	dictyosteli
334	60.5	13.5	1168	2	Q5VH52_CIOIN	Q5vh52	ciona intes
335	60.5	13.5	1313	2	Q93UN0_HELPY	Q93un0	helicobacte
336	60.5	13.5	1335	2	Q4P846_USTMA	Q4p846	ustilago ma
337	60.5	13.5	1471	2	Q5CKX5_CRYHO	Q5ckx5	cryptospori
338	60.5	13.5	1736	2	Q86AT9_DICDI	Q86at9	dictyosteli
339	60.5	13.5	1736	2	Q95PH7_DICDI	Q95ph7	dictyosteli
340	60.5	13.5	4816	2	Q8T103_BOMMO	Q8t103	bombyx mori
341	60	13.4	71	2	Q3HFJ4_TRIER	Q3hfj4	trichodesmi
342	60	13.4	131	2	Q3NT45_SHEFR	Q3nt45	shewanella
343	60	13.4	145	2	Q3EPL0_BACTI	Q3epl0	bacillus th
344	60	13.4	162	2	Q91M77_9CLOS	Q91m77	citrus tris
345	60	13.4	162	2	Q91M85_9CLOS	Q91m85	citrus tris
346	60	13.4	182	2	Q4YF21_PLABE	Q4yf21	plasmodium
347	60	13.4	189	2	Q37XG9_SPHAR	Q37xg9	novosphingo
348	60	13.4	236	2	Q6GMW1_HUMAN	Q6gmw1	homo sapien
349	60	13.4	266	2	Q18362_CAEEL	Q18362	caenorhabdi
350	60	13.4	285	2	Q4AFP4_9CHLB	Q4afp4	chlorobium
351	60	13.4	286	2	Q3ZJ71_PSEAK	Q3zj71	pseudendocl
352	60	13.4	349	2	Q6LJ09_PHOPR	Q6lj09	photobacter
353	60	13.4	350	2	Q59WV1_CANAL	Q59wv1	candida alb
354	60	13.4	350	2	Q59XQ6_CANAL	Q59xq6	candida alb
355	60	13.4	353	2	Q2U8S1_ASPOR	Q2u8s1	aspergillus
356	60	13.4	362	2	Q9CNG0_PASMU	Q9cng0	pasteurella
357	60	13.4	365	2	Q4Z2P3_PLABE	Q4z2p3	plasmodium
358	60	13.4	372	2	Q61SF0_CAEBR	Q61sf0	caenorhabdi
359	60	13.4	442	2	Q30U90_THIDN	Q30u90	thiomicrosp
360	60	13.4	466	2	Q6CF22_YARLI	Q6cf22	yarrowia li
361	60	13.4	482	2	Q3TYP6_MOUSE	Q3typ6	mus musculu
362	60	13.4	482	2	Q4ZJM7_MOUSE	Q4zjm7	mus musculu
363	60	13.4	489	2	Q5L5H1_CHLAB	Q5l5h1	chlamydophi
364	60	13.4	507	2	Q74115_9HIV2	Q74115	human immun
365	60	13.4	514	1	G6PD_BOSIN	Q7ys37	bos indicus
366	60	13.4	518	2	Q9NJZ5_DROHE	Q9njz5	drosophila
367	60	13.4	577	2	O17165_CAEEL	O17165	caenorhabdi
368	60	13.4	613	2	Q60VC0_CAEBR	Q60vc0	caenorhabdi
369	60	13.4	667	2	Q7RLG1_PLAYO	Q7rlg1	plasmodium
370	60	13.4	682	2	Q8II15_PLAF7	Q8ii15	plasmodium
371	60	13.4	691	2	Q9NJZ4_DROHE	Q9njz4	drosophila
372	60	13.4	698	2	Q9NJZ3_DROHE	Q9njz3	drosophila
373	60	13.4	701	2	Q4RNN8_TETNG	Q4rnn8	tetraodon n
374	60	13.4	777	2	Q5R600_PONPY	Q5r600	pongo pygma
375	60	13.4	841	2	Q9NJY5_DROSL	Q9njy5	drosophila
376	60	13.4	841	2	Q9NJY9_DROHE	Q9njy9	drosophila
377	60	13.4	841	2	Q9NJZ6_DROHE	Q9njz6	drosophila
378	60	13.4	904	2	Q48NT4_PSE14	Q48nt4	pseudomonas
379	60	13.4	938	2	Q7N2M7_PHOLL	Q7n2m7	photorhabdu
380	60	13.4	947	2	Q4S557_TETNG	Q4s557	tetraodon n
381	60	13.4	955	2	Q54V91_DICDI	Q54v91	dictyosteli
382	60	13.4	1016	2	Q5ATD1_EMENI	Q5atd1	aspergillus
383	60	13.4	1148	1	AT8A2_MOUSE	P98200	mus musculu
384	60	13.4	1321	2	Q6A7F3_PROAC	Q6a7f3	propionibac
385	60	13.4	1336	2	Q6UK63_DICDI	Q6uk63	dictyosteli
386	60	13.4	1946	2	O97291_PLAF7	O97291	plasmodium
387	60	13.4	2504	2	Q54PL8_DICDI	Q54pl8	dictyosteli
388	60	13.4	3574	2	Q8IDA8_PLAF7	Q8ida8	plasmodium
389	60	13.4	4540	2	Q55EG2_DICDI	Q55eg2	dictyosteli
390	59.5	13.3	126	2	Q7S979_NEUCR	Q7s979	neurospora
391	59.5	13.3	187	2	Q4UKA1_RICFE	Q4uka1	rickettsia
392	59.5	13.3	195	2	Q2QSZ9_ORYSA	Q2qsz9	oryza sativ
393	59.5	13.3	208	2	Q60RG6_CAEBR	Q60rg6	caenorhabdi
394	59.5	13.3	236	2	Q2WPU7_CLOBE	Q2wpu7	clostridium
395	59.5	13.3	255	2	Q689Z6_9HYME	Q689z6	cotesia glo
396	59.5	13.3	297	2	Q6H970_ANTMA	Q6h970	antirrhinum

397	59.5	13.3	321	2	Q83AR3_COXBU	Q83ar3 coxiella bu
398	59.5	13.3	328	2	Q3NLW5_SHEFR	Q3nlw5 shewanella
399	59.5	13.3	368	2	Q5NVH2_PONPY	Q5nvh2 pongo pygma
400	59.5	13.3	379	2	Q8BH91_MOUSE	Q8bh91 m 10 days n
401	59.5	13.3	395	2	O69347_VIBSM	O69347 vibrio sp.
402	59.5	13.3	398	2	Q66LE0_9HIV1	Q66le0 human immun
403	59.5	13.3	413	2	Q5R524_PONPY	Q5r524 pongo pygma
404	59.5	13.3	413	2	Q5R691_PONPY	Q5r691 pongo pygma
405	59.5	13.3	420	2	Q68VY9_RICTY	Q68vy9 rickettsia
406	59.5	13.3	428	2	Q5CVC4_CRYPV	Q5cvc4 cryptospori
407	59.5	13.3	460	2	Q9M4V1_ELAGV	Q9m4v1 elaeis guin
408	59.5	13.3	482	2	Q49BF8_SCHMD	Q49bf8 schmidtea m
409	59.5	13.3	500	2	Q3UQ45_MOUSE	Q3uq45 m 15 days e
410	59.5	13.3	515	2	Q4PD21_USTMA	Q4pd21 ustilago ma
411	59.5	13.3	530	2	Q4YWN6_PLABE	Q4ywn6 plasmodium
412	59.5	13.3	555	2	Q9AUI0_PINTA	Q9aui0 pinus taeda
413	59.5	13.3	557	2	P94622_CLOCL	P94622 clostridium
414	59.5	13.3	627	2	Q8BXM6_MOUSE	Q8bxm6 mus musculu
415	59.5	13.3	628	2	Q8D349_WIGBR	Q8d349 wiggleswort
416	59.5	13.3	637	2	Q86B13_DICDI	Q86b13 dictyosteli
417	59.5	13.3	639	2	Q4WR68_ASPFU	Q4wr68 aspergillus
418	59.5	13.3	657	2	Q558W6_DICDI	Q558w6 dictyosteli
419	59.5	13.3	727	2	Q3UUG8_MOUSE	Q3uug8 mus musculu
420	59.5	13.3	740	2	Q86IH1_DICDI	Q86ih1 dictyosteli
421	59.5	13.3	821	2	P87237_SCHPO	P87237 schizosacch
422	59.5	13.3	832	2	Q6ZGD1_ORYSA	Q6zgd1 oryza sativ
423	59.5	13.3	862	2	Q76606_9HIV2	Q76606 human immun
424	59.5	13.3	862	2	Q9WLD7_9HIV2	Q9wld7 human immun
425	59.5	13.3	901	2	Q6H972_ANTMA	Q6h972 antirrhinum
426	59.5	13.3	902	2	Q4N4B5_THEPA	Q4n4b5 theileria p
427	59.5	13.3	905	2	Q88A43_PSESM	Q88a43 pseudomonas
428	59.5	13.3	1317	2	Q7RN19_PLAYO	Q7rn19 plasmodium
429	59.5	13.3	1330	2	Q9SXK5_9STRA	Q9sxk5 heterosigma
430	59.5	13.3	1357	2	Q8IKL1_PLAF7	Q8ikl1 plasmodium
431	59.5	13.3	1358	2	Q4RWU3_TETNG	Q4rwu3 tetraodon n
432	59.5	13.3	1361	2	Q7REY0_PLAYO	Q7rey0 plasmodium
433	59.5	13.3	1421	2	Q5CH19_CRYHO	Q5ch19 cryptospori
434	59.5	13.3	1707	2	Q2QVA9_ORYSA	Q2qva9 oryza sativ
435	59.5	13.3	1896	2	Q3UHK8_MOUSE	Q3uhk8 mus musculu
436	59.5	13.3	1962	1	TNR6A_HUMAN	Q8ndv7 homo sapien
437	59.5	13.3	4261	2	Q8IFP4_PLAF7	Q8ifp4 plasmodium
438	59.5	13.3	7716	2	Q7UWZ8_RHOBA	Q7uwz8 rhodopirell
439	59	13.1	119	2	Q84NA0_9FABA	Q84na0 anthyllis h
440	59	13.1	120	2	Q7RB16_PLAYO	Q7rb16 plasmodium
441	59	13.1	145	2	Q63FU8_BACCZ	Q63fu8 bacillus ce
442	59	13.1	145	2	Q6HNB8_BACHK	Q6hnb8 bacillus th
443	59	13.1	146	1	CYB5M_HUMAN	O43169 homo sapien
444	59	13.1	159	2	Q9JER3_9HIV1	Q9jer3 human immun
445	59	13.1	159	2	Q9JER6_9HIV1	Q9jer6 human immun
446	59	13.1	183	2	O46871_HUMAN	O46871 homo sapien
447	59	13.1	188	2	Q95466_HUMAN	Q95466 homo sapien
448	59	13.1	198	2	Q8GLI3_AERHY	Q8gli3 aeromonas h
449	59	13.1	201	2	Q519E5_ENTHI	Q519e5 entamoeba h
450	59	13.1	227	2	Q5SQ91_HUMAN	Q5sq91 homo sapien
451	59	13.1	231	2	Q8MGQ8_HUMAN	Q8mgq8 homo sapien
452	59	13.1	231	2	Q8VL68_AERHY	Q8vl68 aeromonas h
453	59	13.1	231	2	Q8VRH4_AERHY	Q8vrh4 aeromonas h
454	59	13.1	231	2	Q8VRH5_AERHY	Q8vrh5 aeromonas h
455	59	13.1	237	2	Q2UDL1_ASPOR	Q2udl1 aspergillus
456	59	13.1	254	2	Q5DFB4_SCHJA	Q5dfb4 schistosoma
457	59	13.1	256	2	Q5SQ92_HUMAN	Q5sq92 homo sapien
458	59	13.1	260	2	Q5JPL8_HUMAN	Q5jpl8 homo sapien
459	59	13.1	264	2	Q5SQ93_HUMAN	Q5sq93 homo sapien
460	59	13.1	272	2	Q7P0X1_CHRVO	Q7p0x1 chromobacte
461	59	13.1	275	2	Q5SQ90_HUMAN	Q5sq90 homo sapien
462	59	13.1	280	2	Q8IIK6_PLAF7	Q8iik6 plasmodium
463	59	13.1	284	2	O65499_ARATH	O65499 arabidopsis
464	59	13.1	289	2	Q4L968_STAHJ	Q4l968 staphylococ
465	59	13.1	295	1	METF_BUCBP	Q89b13 buchnera ap
466	59	13.1	324	2	Q4IG36_GIBZE	Q4ig36 gibberella
467	59	13.1	330	2	Q6GP91_XENLA	Q6gp91 xenopus lae
468	59	13.1	334	2	Q8RN80_AERHY	Q8rn80 aeromonas h
469	59	13.1	337	2	Q8RN84_AERHY	Q8rn84 aeromonas h
470	59	13.1	337	2	Q8RN87_AERHY	Q8rn87 aeromonas h
471	59	13.1	338	2	Q8RN88_AERHY	Q8rn88 aeromonas h
472	59	13.1	343	2	Q8RN78_AERHY	Q8rn78 aeromonas h
473	59	13.1	348	2	Q5LBM6_BACFN	Q5lbm6 bacteroides
474	59	13.1	366	2	Q8RN82_AERHY	Q8rn82 aeromonas h
475	59	13.1	367	2	Q8RN86_AERHY	Q8rn86 aeromonas h
476	59	13.1	369	2	Q8RN83_AERHY	Q8rn83 aeromonas h
477	59	13.1	369	2	Q8RN85_AERHY	Q8rn85 aeromonas h
478	59	13.1	371	2	Q8RJH3_AERHY	Q8rjh3 aeromonas h
479	59	13.1	375	2	Q7RIV1_PLAYO	Q7riv1 plasmodium
480	59	13.1	380	2	Q8RN77_AERHY	Q8rn77 aeromonas h
481	59	13.1	393	2	Q54R14_DICDI	Q54r14 dictyosteli
482	59	13.1	394	2	Q34835_KLULA	Q34835 kluyveromyc
483	59	13.1	396	2	Q6DN58_KLULA	Q6dn58 kluyveromyc
484	59	13.1	409	2	Q4YQC9_PLABE	Q4yqc9 plasmodium
485	59	13.1	410	2	Q7ZUW8_BRARE	Q7zuw8 brachydanio
486	59	13.1	412	1	AATC_HORSE	P08906 equus cabal
487	59	13.1	429	2	Q4QR59_XENLA	Q4qr59 xenopus lae
488	59	13.1	431	2	Q6DCR0_XENLA	Q6dcr0 xenopus lae
489	59	13.1	493	2	Q3LRX0_AERHY	Q3lrx0 aeromonas h
490	59	13.1	493	2	Q44063_AERHY	Q44063 aeromonas h
491	59	13.1	493	2	Q8GN63_AERHY	Q8gn63 aeromonas h
492	59	13.1	493	2	Q9S5D4_AERHY	Q9s5d4 aeromonas h
493	59	13.1	493	2	Q2MLU7_AERHY	Q2mlu7 aeromonas h
494	59	13.1	510	2	Q3SEW3_THIDA	Q3sew3 thiobacillu
495	59	13.1	517	2	Q559D0_DICDI	Q559d0 dictyosteli
496	59	13.1	518	2	Q9NJZ1_DROSL	Q9njz1 drosophila
497	59	13.1	554	2	Q9VDD5_DROME	Q9vdd5 drosophila
498	59	13.1	554	2	Q9LG03_ARATH	Q9lg03 arabidopsis
499	59	13.1	557	2	Q54IT7_DICDI	Q54it7 dictyosteli
500	59	13.1	575	2	Q4S208_TETNG	Q4s208 tetraodon n
501	59	13.1	605	2	Q6BK98_DEBHA	Q6bk98 debaryomyce
502	59	13.1	616	2	Q7SE17_NEUCR	Q7se17 neurospora
503	59	13.1	663	2	Q2KEJ3_MAGGR	Q2kej3 magnaporthe
504	59	13.1	677	2	Q7JFT7_RABIT	Q7jft7 oryctolagus
505	59	13.1	695	2	Q9NJZ2_DROSL	Q9njz2 drosophila
506	59	13.1	709	2	Q8TNF1_METAC	Q8tnf1 methanosarc
507	59	13.1	741	1	HOX1_HALRO	P28468 halocynthia
508	59	13.1	769	2	Q86IH4_DICDI	Q86ih4 dictyosteli
509	59	13.1	819	2	Q8I435_PLAF7	Q8i435 plasmodium
510	59	13.1	820	2	Q6CWX7_KLULA	Q6cwx7 kluyveromyc
511	59	13.1	838	2	Q9TXM3_CAEEL	Q9txm3 caenorhabdi
512	59	13.1	840	2	Q8I5X4_PLAF7	Q8i5x4 plasmodium
513	59	13.1	841	2	Q9NJZ0_DROSL	Q9njz0 drosophila
514	59	13.1	905	2	Q75AU7_ASHGO	Q75au7 ashbya goss
515	59	13.1	922	2	Q54H00_DICDI	Q54h00 dictyosteli
516	59	13.1	988	2	Q4P446_USTMA	Q4p446 ustilago ma
517	59	13.1	1006	2	O74458_SCHPO	O74458 schizosacch
518	59	13.1	1074	2	Q503K3_BRARE	Q503k3 brachydanio
519	59	13.1	1095	2	Q4XZ33_PLACH	Q4xz33 plasmodium
520	59	13.1	1515	2	Q95XK2_CAEEL	Q95xk2 caenorhabdi
521	59	13.1	1540	2	Q4XL97_PLACH	Q4xl97 plasmodium
522	59	13.1	1781	2	Q5SBL9_LACRE	Q5sbl9 lactobacill
523	59	13.1	1818	2	Q8EVF1_MYCPE	Q8evf1 mycoplasma
524	59	13.1	2352	1	MOK12_SCHPO	Q9uul4 schizosacch
525	59	13.1	2413	2	Q4S3T8_TETNG	Q4s3t8 tetraodon n
526	59	13.1	3001	2	Q8IL08_PLAF7	Q8il08 plasmodium
527	58.5	13.0	140	2	Q801D0_LATME	Q801d0 latimeria m
528	58.5	13.0	177	2	Q6NI13_CORDI	Q6ni13 corynebacte
529	58.5	13.0	179	2	Q6TGI5_PYRCO	Q6tgi5 pyrus commu
530	58.5	13.0	208	1	PORIM_HUMAN	Q8nl31 homo sapien
531	58.5	13.0	221	2	Q49FE3_9HIV1	Q49fe3 human immun
532	58.5	13.0	241	2	Q8AI13_9HIV1	Q8ai13 human immun
533	58.5	13.0	241	2	Q8AI14_9HIV1	Q8ai14 human immun
534	58.5	13.0	241	2	Q8AI18_9HIV1	Q8ai18 human immun
535	58.5	13.0	241	2	Q8AI24_9HIV1	Q8ai24 human immun
536	58.5	13.0	241	2	Q8AI27_9HIV1	Q8ai27 human immun
537	58.5	13.0	241	2	Q8AI28_9HIV1	Q8ai28 human immun
538	58.5	13.0	241	2	Q8AI30_9HIV1	Q8ai30 human immun
539	58.5	13.0	241	2	Q8AI31_9HIV1	Q8ai31 human immun
540	58.5	13.0	241	2	Q8AI32_9HIV1	Q8ai32 human immun
541	58.5	13.0	241	2	Q8AI33_9HIV1	Q8ai33 human immun
542	58.5	13.0	241	2	Q8AI34_9HIV1	Q8ai34 human immun

543	58.5	13.0	241	2	Q8AI36_9HIV1	Q8ai36 human immun
544	58.5	13.0	241	2	Q8AI37_9HIV1	Q8ai37 human immun
545	58.5	13.0	241	2	Q8AI38_9HIV1	Q8ai38 human immun
546	58.5	13.0	241	2	Q8AI39_9HIV1	Q8ai39 human immun
547	58.5	13.0	241	2	Q8AI42_9HIV1	Q8ai42 human immun
548	58.5	13.0	241	2	Q8AI43_9HIV1	Q8ai43 human immun
549	58.5	13.0	254	2	Q4Y1E7_PLACH	Q4y1e7 plasmodium
550	58.5	13.0	265	2	Q7S8J8_NEUCR	Q7s8j8 neurospora
551	58.5	13.0	272	2	Q7QIH5_ANOGA	Q7qih5 anopheles g
552	58.5	13.0	276	1	SLBP_DROME	Q9van6 drosophila
553	58.5	13.0	317	2	Q2S8K8_9GAMM	Q2s8k8 hahella che
554	58.5	13.0	328	1	EMB_RAT	O88775 rattus norv
555	58.5	13.0	332	2	Q4PIN4_USTMA	Q4pin4 ustilago ma
556	58.5	13.0	342	2	Q424M5_DESHA	Q424m5 desulfitoba
557	58.5	13.0	362	2	Q5B120_EMENI	Q5b120 aspergillus
558	58.5	13.0	376	2	Q95UP2_STYPU	Q95up2 stylonychia
559	58.5	13.0	405	2	Q8BMN8_MOUSE	Q8bmn8 mus musculu
560	58.5	13.0	421	2	Q9BIC9_TRISP	Q9bic9 trichinella
561	58.5	13.0	431	2	Q93227_CAEEL	Q93227 caenorhabdi
562	58.5	13.0	439	2	Q88928_WASMV	Q88928 watermelon
563	58.5	13.0	452	2	Q6GMG6_BRARE	Q6gmg6 brachydanio
564	58.5	13.0	526	2	Q517U8_ENTHI	Q517u8 entamoeba h
565	58.5	13.0	538	2	Q55JU4_CRYNE	Q55ju4 cryptococcu
566	58.5	13.0	538	2	Q5K9Q7_CRYNE	Q5k9q7 cryptococcu
567	58.5	13.0	555	2	Q9FSC9_POPTR	Q9fsc9 populus tri
568	58.5	13.0	555	2	Q9ZQW3_POPTR	Q9zqw3 populus tri
569	58.5	13.0	561	2	Q68FR5_RAT	Q68fr5 rattus norv
570	58.5	13.0	579	2	Q8T392_DUGJA	Q8t392 dugesia jap
571	58.5	13.0	588	2	Q4SGI2_TETNG	Q4sgi2 tetraodon n
572	58.5	13.0	595	2	Q4V721_DROME	Q4v721 drosophila
573	58.5	13.0	610	2	Q5L9Z2_BACFN	Q5l9z2 bacteroides
574	58.5	13.0	610	2	Q64Q99_BACFR	Q64q99 bacteroides
575	58.5	13.0	615	2	Q8BXX8_MOUSE	Q8bxx8 m 7 days ne
576	58.5	13.0	618	2	Q43X84_SOLUS	Q43x84 solibacter
577	58.5	13.0	624	2	Q9V789_DROME	Q9v789 drosophila
578	58.5	13.0	640	1	IGF1R_BOVIN	Q05688 b insulin-l
579	58.5	13.0	647	2	Q4N9M6_THEPA	Q4n9m6 theileria p
580	58.5	13.0	701	2	Q30TC3_THIDN	Q30tc3 thiomicrosp
581	58.5	13.0	744	2	Q3XB26_METFL	Q3xb26 methylobaci
582	58.5	13.0	762	2	Q55B06_DICDI	Q55b06 dictyosteli
583	58.5	13.0	782	2	Q55C90_DICDI	Q55c90 dictyosteli
584	58.5	13.0	789	2	Q8CFX1_MOUSE	Q8cfx1 mus musculu
585	58.5	13.0	797	2	Q8BLH1_MOUSE	Q8blh1 mus musculu
586	58.5	13.0	826	2	Q75JF0_DICDI	Q75jf0 dictyosteli
587	58.5	13.0	837	2	Q552H0_DICDI	Q552h0 dictyosteli
588	58.5	13.0	883	1	LMBL3_MOUSE	Q8blb7 mus musculu
589	58.5	13.0	885	2	Q5CGV6_CRYHO	Q5cgv6 cryptospori
590	58.5	13.0	932	2	Q7QB67_ANOGA	Q7qb67 anopheles g
591	58.5	13.0	961	2	Q8IC12_PLAF7	Q8ic12 plasmodium
592	58.5	13.0	966	2	Q55Y62_CRYNE	Q55y62 cryptococcu
593	58.5	13.0	996	2	Q67V89_ORYSA	Q67v89 oryza sativ
594	58.5	13.0	999	2	Q54BN8_DICDI	Q54bn8 dictyosteli
595	58.5	13.0	1003	2	Q4UIV2_THEAN	Q4uiv2 theileria a
596	58.5	13.0	1014	2	Q6BT63_DEBHA	Q6bt63 debaryomyce
597	58.5	13.0	1085	2	Q4XXA1_PLACH	Q4xxa1 plasmodium
598	58.5	13.0	1256	2	Q8I575_PLAF7	Q8i575 plasmodium
599	58.5	13.0	1315	2	Q8JKP9_9VIRU	Q8jkp9 heliothis z
600	58.5	13.0	1549	2	Q6MIW7_BDEBA	Q6miw7 bdellovibri
601	58.5	13.0	1615	1	LRP5_HUMAN	O75197 homo sapien
602	58.5	13.0	1615	2	Q9UES7_HUMAN	Q9ues7 homo sapien
603	58.5	13.0	1748	1	POLR_ELV	P35928 erysimum la
604	58.5	13.0	1748	2	Q549L0_ELV	Q54910 erysimum la
605	58.5	13.0	2251	2	Q5CJT6_CRYHO	Q5cjt6 cryptospori
606	58.5	13.0	2254	2	Q80N16_9PICO	Q80n16 ljungan vir
607	58.5	13.0	2269	2	Q5CWU1_CRYPV	Q5cwu1 cryptospori
608	58.5	13.0	2335	2	Q7YYR5_CRYPV	Q7yyr5 cryptospori
609	58.5	13.0	2522	2	Q7RK50_PLAYO	Q7rk50 plasmodium
610	58.5	13.0	2974	2	Q8I5L7_PLAF7	Q8i5l7 plasmodium
611	58.5	13.0	3597	2	Q8ILR5_PLAF7	Q8ilr5 plasmodium
612	58	12.9	145	2	Q4ML14_BACCE	Q4ml14 bacillus ce
613	58	12.9	145	2	Q5UIQ4_BACME	Q5uiq4 bacillus me
614	58	12.9	145	2	Q73DE6_BACC1	Q73de6 bacillus ce
615	58	12.9	146	1	CYB5M_PONPY	Q5rdj5 pongo pygma
616	58	12.9	187	2	Q7URC6_RHOBA	Q7urc6 rhodopirell
617	58	12.9	192	2	Q5C6W5_SCHJA	Q5c6w5 schistosoma
618	58	12.9	192	2	Q6UDN3_9HIV1	Q6udn3 human immun
619	58	12.9	194	2	Q4XAI8_PLACH	Q4xai8 plasmodium
620	58	12.9	209	2	Q7RKE4_PLAYO	Q7rke4 plasmodium
621	58	12.9	221	2	Q6VZR4_CNPV	Q6vzr4 canarypox v
622	58	12.9	229	2	Q29877_HUMAN	Q29877 homo sapien
623	58	12.9	229	2	Q30084_HUMAN	Q30084 homo sapien
624	58	12.9	232	2	Q4YF69_PLABE	Q4yf69 plasmodium
625	58	12.9	241	2	Q8AI20_9HIV1	Q8ai20 human immun
626	58	12.9	241	2	Q8AI22_9HIV1	Q8ai22 human immun
627	58	12.9	241	2	Q8AI23_9HIV1	Q8ai23 human immun
628	58	12.9	241	2	Q8AI25_9HIV1	Q8ai25 human immun
629	58	12.9	241	2	Q8AI29_9HIV1	Q8ai29 human immun
630	58	12.9	241	2	Q8AI35_9HIV1	Q8ai35 human immun
631	58	12.9	241	2	Q8AI40_9HIV1	Q8ai40 human immun
632	58	12.9	241	2	Q8AI41_9HIV1	Q8ai41 human immun
633	58	12.9	241	2	Q8AI45_9HIV1	Q8ai45 human immun
634	58	12.9	250	2	O19764_HUMAN	O19764 homo sapien
635	58	12.9	252	2	Q8WLZ6_BOVIN	Q8wlz6 bos taurus
636	58	12.9	261	1	KSGA_WIGBR	Q8d3i1 w dimethyla
637	58	12.9	261	2	Q30093_HUMAN	Q30093 homo sapien
638	58	12.9	261	2	Q5Y7B5_HUMAN	Q5y7b5 homo sapien
639	58	12.9	261	2	Q29884_HUMAN	Q29884 homo sapien
640	58	12.9	269	2	Q54NA1_DICDI	Q54na1 dictyosteli
641	58	12.9	271	2	Q3R0T0_XYLFA	Q3r0t0 xylella fas
642	58	12.9	278	2	Q4XTE6_PLACH	Q4xte6 plasmodium
643	58	12.9	290	2	Q6LGA0_PHOPR	Q6lga0 photobacter
644	58	12.9	299	2	Q5WXQ3_LEGPL	Q5wxq3 legionella
645	58	12.9	311	2	Q2U817_ASPOR	Q2u817 aspergillus
646	58	12.9	321	2	Q9L357_9PSED	Q9l357 pseudomonas
647	58	12.9	332	2	Q5BGD5_EMENI	Q5bgd5 aspergillus
648	58	12.9	333	2	Q2NF69_9EURY	Q2nf69 methanospha
649	58	12.9	361	2	Q7ZP61_9HIV1	Q7zp61 human immun
650	58	12.9	368	2	Q9YZ35_SIVCZ	Q9yz35 chimpanzee
651	58	12.9	375	1	AAT1_METJA	Q60317 methanococc
652	58	12.9	384	2	Q9S5K2_COMTE	Q9s5k2 comamonas t
653	58	12.9	386	2	Q2KHI2_MAGGR	Q2khi2 magnaporthe
654	58	12.9	405	2	Q9HUU4_PSEAE	Q9huu4 pseudomonas
655	58	12.9	406	2	Q4D1X8_TRYCR	Q4d1x8 trypanosoma
656	58	12.9	406	2	Q4DIA3_TRYCR	Q4dia3 trypanosoma
657	58	12.9	419	2	Q2K100_RHIET	Q2k100 rhizobium e
658	58	12.9	420	2	Q3ILV6_NATPD	Q3ilv6 natronomona
659	58	12.9	420	2	Q3ILX7_NATPD	Q3ilx7 natronomona
660	58	12.9	430	2	Q4CJD7_CLOTM	Q4cjd7 clostridium
661	58	12.9	439	1	MYC_MARMO	P22555 marmota mon
662	58	12.9	471	2	Q6UZ79_MEDTR	Q6uz79 medicago tr
663	58	12.9	471	2	Q3M9U0_ANAVT	Q3m9u0 anabaena va
664	58	12.9	471	2	Q5ZIJ5_CHICK	Q5zij5 gallus gall
665	58	12.9	475	2	Q4R7C6_MACFA	Q4r7c6 macaca fasc
666	58	12.9	476	2	Q68FX4_RAT	Q68fx4 rattus norv
667	58	12.9	479	2	Q4FKF0_9TRYP	Q4fkf0 trypanosoma
668	58	12.9	485	2	Q3SYW3_BOVIN	Q3syw3 bos taurus
669	58	12.9	486	1	HCLS1_HUMAN	P14317 homo sapien
670	58	12.9	486	1	HCLS1_MOUSE	P49710 mus musculu
671	58	12.9	486	2	Q53Y93_HUMAN	Q53y93 homo sapien
672	58	12.9	486	2	Q6IBK9_HUMAN	Q6ibk9 homo sapien
673	58	12.9	486	2	Q542G0_MOUSE	Q542g0 mus musculu
674	58	12.9	486	2	Q922I8_MOUSE	Q922i8 mus musculu
675	58	12.9	494	2	Q380W3_9TRYP	Q380w3 trypanosoma
676	58	12.9	497	1	G6PI_LEGPN	Q9rdy2 legionella
677	58	12.9	499	1	G6PI_LEGPA	Q5x6y8 legionella
678	58	12.9	499	1	G6PI_LEGPH	Q5zxh2 legionella
679	58	12.9	506	2	Q6D5R0_ERWCT	Q6d5r0 erwinia car
680	58	12.9	517	2	Q3RPL7_RALME	Q3rpl7 ralstonia m
681	58	12.9	520	2	Q61SJ3_CAEBR	Q61sj3 caenorhabdi
682	58	12.9	522	2	Q7SB58_NEUCR	Q7sb58 neurospora
683	58	12.9	528	1	YNH7_YEAST	P53940 saccharomyc
684	58	12.9	529	2	Q4Y555_PLACH	Q4y555 plasmodium
685	58	12.9	540	2	Q9S147_COMTE	Q9s147 comamonas t
686	58	12.9	573	2	Q4QHF2_LEIMA	Q4qhf2 leishmania
687	58	12.9	620	1	SYT_FUSNN	Q8rfs6 fusobacteri
688	58	12.9	628	2	Q41604_TULGE	Q41604 tulipa gesn

689	58	12.9	628	2	Q41605_TULGE	Q41605 tulipa gesn
690	58	12.9	628	2	Q3CNE9_ALTAT	Q3cne9 pseudoalter
691	58	12.9	758	2	O96037_CIOSA	O96037 ciona savig
692	58	12.9	769	2	Q37PB7_SPHAR	Q37pb7 novosphingo
693	58	12.9	795	2	O85889_SPHAR	O85889 sphingomona
694	58	12.9	858	2	Q74114_9HIV2	Q74114 human immun
695	58	12.9	926	2	Q4ZMG8_PSEU2	Q4zmg8 pseudomonas
696	58	12.9	985	2	Q617Z9_CAEBR	Q617z9 caenorhabdi
697	58	12.9	1025	2	Q8NDL1_HUMAN	Q8ndl1 homo sapien
698	58	12.9	1039	2	Q86NJ2_CAEEL	Q86nj2 caenorhabdi
699	58	12.9	1088	2	Q8I5S4_PLAF7	Q8i5s4 plasmodium
700	58	12.9	1114	2	Q63HQ7_HUMAN	Q63hq7 homo sapien
701	58	12.9	1114	2	Q9H0F1_HUMAN	Q9h0f1 homo sapien
702	58	12.9	1177	2	Q5AKV1_CANAL	Q5akv1 candida alb
703	58	12.9	1184	2	Q86NJ3_CAEEL	Q86nj3 caenorhabdi
704	58	12.9	1212	2	Q9U0L0_PLAF7	Q9u0l0 plasmodium
705	58	12.9	1307	2	Q4YVS2_PLABE	Q4yvs2 plasmodium
706	58	12.9	1318	2	Q8IDI3_PLAF7	Q8idi3 plasmodium
707	58	12.9	1331	2	Q8IBF6_PLAF7	Q8ibf6 plasmodium
708	58	12.9	1339	2	Q6NRS1_XENLA	Q6nrs1 xenopus lae
709	58	12.9	1354	2	O75183_HUMAN	O75183 homo sapien
710	58	12.9	1411	2	Q8JKS5_9VIRU	Q8jks5 heliothis z
711	58	12.9	1413	2	Q6YNQ7_9VIRU	Q6ynq7 botrytis vi
712	58	12.9	1419	2	Q86NJ4_CAEEL	Q86nj4 caenorhabdi
713	58	12.9	1605	2	Q8AYF1_XENLA	Q8ayf1 xenopus lae
714	58	12.9	1636	2	Q4XZZ6_PLACH	Q4xzz6 plasmodium
715	58	12.9	1658	2	Q9BIC1_CAEEL	Q9bic1 caenorhabdi
716	58	12.9	1666	2	Q9XY66_CAEEL	Q9xy66 caenorhabdi
717	58	12.9	1900	2	Q2KVT5_BORAV	Q2kvt5 bordetella
718	58	12.9	1917	2	Q4X570_PLACH	Q4x570 plasmodium
719	58	12.9	2655	2	Q6H7S8_ORYSA	Q6h7s8 oryza sativ
720	58	12.9	3869	2	Q86PQ3_CRYPV	Q86pq3 cryptospori
721	57.5	12.8	111	2	Q3UW30_MOUSE	Q3uw30 mus musculu
722	57.5	12.8	176	2	Q29969_HUMAN	Q29969 homo sapien
723	57.5	12.8	211	2	Q4YJZ8_PLABE	Q4yjz8 plasmodium
724	57.5	12.8	221	2	Q7ZMF2_9HIV1	Q7zmf2 human immun
725	57.5	12.8	229	2	Q30081_HUMAN	Q30081 homo sapien
726	57.5	12.8	237	2	Q30098_HUMAN	Q30098 homo sapien
727	57.5	12.8	243	2	Q2SPL5_9GAMM	Q2spl5 hahella che
728	57.5	12.8	255	2	O19506_HUMAN	O19506 homo sapien
729	57.5	12.8	261	2	Q5Y7B2_HUMAN	Q5y7b2 homo sapien
730	57.5	12.8	264	2	Q29970_HUMAN	Q29970 homo sapien
731	57.5	12.8	269	2	Q30155_HUMAN	Q30155 homo sapien
732	57.5	12.8	273	2	Q874V2_PODAN	Q874v2 podospora a
733	57.5	12.8	275	1	ICC_ECO57	P0aew5 escherichia
734	57.5	12.8	275	1	ICC_ECOLI	P0aew4 escherichia
735	57.5	12.8	275	2	Q31X00_SHIBS	Q31x00 shigella bo
736	57.5	12.8	275	2	Q32BT8_SHIDS	Q32bt8 shigella dy
737	57.5	12.8	275	2	Q3YXK8_SHISS	Q3yxk8 shigella so
738	57.5	12.8	275	2	Q2M9G8_ECOLI	Q2m9g8 escherichia
739	57.5	12.8	275	2	Q8FDI6_ECOL6	Q8fdi6 escherichia
740	57.5	12.8	275	2	Q83Q52_SHIFL	Q83q52 shigella fl
741	57.5	12.8	298	2	Q7R0G3_GIALA	Q7r0g3 giardia lam
742	57.5	12.8	338	2	Q53739_STRCH	Q53739 streptomyce
743	57.5	12.8	371	2	Q84U52_9ASPA	Q84u52 dendrobium
744	57.5	12.8	371	2	Q87648_SIVCZ	Q87648 chimpanzee
745	57.5	12.8	383	2	Q753G2_ASHGO	Q753g2 ashbya goss
746	57.5	12.8	392	2	Q6BNJ8_DEBHA	Q6bnj8 debaryomyce
747	57.5	12.8	400	2	Q4KP34_9MICR	Q4kp34 endoreticul
748	57.5	12.8	400	2	Q8XKD3_CLOPE	Q8xkd3 clostridium
749	57.5	12.8	413	2	Q01849_PHYCP	Q01849 phytophthor
750	57.5	12.8	420	2	Q8I499_CUPSA	Q8i499 cupiennius
751	57.5	12.8	425	2	Q06513_9HIV2	Q06513 human immun
752	57.5	12.8	442	2	Q5CPH5_CRYPV	Q5cph5 cryptospori
753	57.5	12.8	445	2	Q6FX91_CANGA	Q6fx91 candida gla
754	57.5	12.8	451	2	Q6IKU0_DROME	Q6iku0 drosophila
755	57.5	12.8	454	2	Q5KU75_GEOKA	Q5ku75 geobacillus
756	57.5	12.8	455	2	Q2PHK7_DAUCA	Q2phk7 daucus caro
757	57.5	12.8	458	2	Q7Z9Z5_9HYPO	Q7z9z5 uncultured
758	57.5	12.8	459	2	O78672_VICFA	O78672 vicia faba
759	57.5	12.8	462	2	Q2W5L4_MAGSA	Q2w5l4 magnetospir
760	57.5	12.8	485	2	Q9HEX8_PNECA	Q9hex8 pneumocysti
761	57.5	12.8	495	2	Q6FS46_CANGA	Q6fs46 candida gla
762	57.5	12.8	498	2	Q6KHT1_MYCMO	Q6kht1 mycoplasma
763	57.5	12.8	509	2	Q6JAH5_SORBI	Q6jah5 sorghum bic
764	57.5	12.8	509	2	Q3HLL8_9HIV2	Q3hll8 human immun
765	57.5	12.8	531	2	Q7W8D6_BORPA	Q7w8d6 bordetella
766	57.5	12.8	531	2	Q7WLZ5_BORBR	Q7wlz5 bordetella
767	57.5	12.8	550	2	P91263_CAEEL	P91263 caenorhabdi
768	57.5	12.8	559	2	Q8JR34_9CORO	Q8jr34 infectious
769	57.5	12.8	574	2	Q4ETL8_LISMO	Q4etl8 listeria mo
770	57.5	12.8	574	2	Q8Y3W3_LISMO	Q8y3w3 listeria mo
771	57.5	12.8	577	2	Q59RB2_CANAL	Q59rb2 candida alb
772	57.5	12.8	590	2	Q6TBR0_CRYPV	Q6tbr0 cryptospori
773	57.5	12.8	637	2	Q5CY08_CRYPV	Q5cy08 cryptospori
774	57.5	12.8	640	2	Q4WZB4_ASPFU	Q4wzb4 aspergillus
775	57.5	12.8	640	2	Q7XJM8_ARATH	Q7xjm8 arabidopsis
776	57.5	12.8	640	2	Q84WB1_ARATH	Q84wb1 arabidopsis
777	57.5	12.8	655	2	Q8I5P8_PLAF7	Q8i5p8 plasmodium
778	57.5	12.8	657	2	Q94H30_ORYSA	Q94h30 oryza sativ
779	57.5	12.8	659	2	Q4G138_HUMAN	Q4g138 homo sapien
780	57.5	12.8	664	2	Q9UVV2_ASPFU	Q9uvv2 aspergillus
781	57.5	12.8	667	2	Q6C222_YARLI	Q6c222 yarrowia li
782	57.5	12.8	667	2	Q6AQN1_DESPS	Q6aqn1 desulfotale
783	57.5	12.8	670	2	Q9DSI9_9HIV2	Q9dsi9 human immun
784	57.5	12.8	716	2	Q4JLB5_LACRE	Q4jlb5 lactobacill
785	57.5	12.8	722	1	DYRK2_DROME	Q9v3d5 drosophila
786	57.5	12.8	734	2	Q2SDA3_9GAMM	Q2sda3 hahella che
787	57.5	12.8	769	1	LYAM3_SHEEP	P98109 ovis aries
788	57.5	12.8	777	2	Q8IBA1_PLAF7	Q8iba1 plasmodium
789	57.5	12.8	783	2	Q5ZC02_ORYSA	Q5zc02 oryza sativ
790	57.5	12.8	785	2	Q6SLA6_GIBMO	Q6sla6 gibberella
791	57.5	12.8	795	2	Q7QW20_GIALA	Q7qw20 giardia lam
792	57.5	12.8	808	2	Q4P4V0_USTMA	Q4p4v0 ustilago ma
793	57.5	12.8	850	2	Q4WGA4_ASPFU	Q4wga4 aspergillus
794	57.5	12.8	852	2	Q6CMX0_KLULA	Q6cmx0 kluyveromyc
795	57.5	12.8	873	2	Q4JLK4_LACRE	Q4jlk4 lactobacill
796	57.5	12.8	877	2	Q83LZ9_SHIFL	Q83lz9 shigella fl
797	57.5	12.8	879	2	Q8C6Q7_MOUSE	Q8c6q7 mus musculu
798	57.5	12.8	886	2	Q90DC6_SIVCZ	Q90dc6 chimpanzee
799	57.5	12.8	895	2	Q5ZC03_ORYSA	Q5zc03 oryza sativ
800	57.5	12.8	902	2	Q91RC7_ADEO7	Q91rc7 ovine adeno
801	57.5	12.8	902	2	Q9Q3F8_9ADEN	Q9q3f8 goat adenov
802	57.5	12.8	971	1	AREA_GIBFU	P78688 gibberella
803	57.5	12.8	1003	2	Q60ZN8_CAEBR	Q60zn8 caenorhabdi
804	57.5	12.8	1012	2	Q727P3_DESVH	Q727p3 desulfovibr
805	57.5	12.8	1022	2	Q6CFZ0_YARLI	Q6cfz0 yarrowia li
806	57.5	12.8	1049	2	Q4Y187_PLACH	Q4y187 plasmodium
807	57.5	12.8	1051	2	Q6BHJ4_DEBHA	Q6bhj4 debaryomyce
808	57.5	12.8	1070	2	Q55ZN5_CRYNE	Q55zn5 cryptococcu
809	57.5	12.8	1070	2	Q5KNZ9_CRYNE	Q5knz9 cryptococcu
810	57.5	12.8	1123	2	Q4HXT0_GIBZE	Q4hxt0 gibberella
811	57.5	12.8	1130	2	Q3U382_MOUSE	Q3u382 mus musculu
812	57.5	12.8	1151	2	Q612U1_CAEBR	Q612u1 caenorhabdi
813	57.5	12.8	1165	1	LEPR_HUMAN	P48357 homo sapien
814	57.5	12.8	1173	2	Q7RAP3_PLAYO	Q7rap3 plasmodium
815	57.5	12.8	1272	2	O10243_CYVV	O10243 clover yell
816	57.5	12.8	1291	1	CD45_MOUSE	P06800 mus musculu
817	57.5	12.8	1298	2	Q5CSI8_CRYPV	Q5csi8 cryptospori
818	57.5	12.8	1317	2	Q5CQQ4_CRYPV	Q5cqq4 cryptospori
819	57.5	12.8	1329	2	Q3LWD4_CHLS6	Q3lwd4 chlorarachn
820	57.5	12.8	1343	2	Q64730_MOUSE	Q64730 mus musculu
821	57.5	12.8	1478	2	Q2UDH2_ASPOR	Q2udh2 aspergillus
822	57.5	12.8	1557	2	Q8QXW5_9VIRU	Q8qxw5 garlic viru
823	57.5	12.8	1773	2	Q55I70_CRYNE	Q55i70 cryptococcu
824	57.5	12.8	1774	2	Q8IAU8_PLAF7	Q8iau8 plasmodium
825	57.5	12.8	1807	1	ITB4_RAT	Q64632 rattus norv
826	57.5	12.8	1821	2	Q7PSP2_ANOGA	Q7psp2 anopheles g
827	57.5	12.8	1841	2	Q5K7Q5_CRYNE	Q5k7q5 cryptococcu
828	57.5	12.8	2048	2	Q4YRV4_PLABE	Q4yrv4 plasmodium
829	57.5	12.8	2118	2	Q8TI61_METAC	Q8ti61 methanosarc
830	57.5	12.8	2121	2	Q4KET1_PSEF5	Q4ket1 pseudomonas
831	57.5	12.8	2149	2	Q6CSU4_KLULA	Q6csu4 kluyveromyc
832	57.5	12.8	2214	2	Q2NEB8_9EURY	Q2neb8 methanospha
833	57.5	12.8	2280	2	Q8ILT4_PLAF7	Q8ilt4 plasmodium
834	57.5	12.8	2424	2	Q7RN73_PLAYO	Q7rn73 plasmodium

835	57.5	12.8	3072	2	O92645_CYVV	O92645 clover yell	908	57	12.7	631	2	Q9DSI6_9HIV2	Q9dsi6 human immun			
836	57.5	12.8	4260	2	Q4T3T2_TETNG	Q4t3t2 tetraodon n	909	57	12.7	639	2	Q6FYV9_BARQU	Q6fyv9 bartonella			
837	57.5	12.8	4590	2	Q54GY7_DICDI	Q54gy7 dictyosteli	910	57	12.7	644	2	Q5QLH2_ORYSA	Q5qlh2 oryza sativ			
838	57	12.7	51	2	Q8CKU4_YERPE	Q8cku4 yersinia pe	911	57	12.7	646	2	Q54YN7_DICDI	Q54yn7 dictyosteli			
839	57	12.7	93	2	Q7TCG1_9HEPC	Q7tcg1 hepatitis c	912	57	12.7	659	2	Q9DSL3_9HIV2	Q9dsl3 human immun			
840	57	12.7	94	2	Q31AM5_PROM9	Q31am5 prochloroco	913	57	12.7	660	2	Q5CSQ8_CRYPV	Q5csq8 cryptospori			
841	57	12.7	97	2	Q8UYQ5_9GEMI	Q8uyq5 tomato yell	914	57	12.7	678	2	Q643S1_CHICK	Q643s1 gallus gall			
842	57	12.7	99	2	Q6R4D0_9GEMI	Q6r4d0 tomato yell	915	57	12.7	706	2	Q18320_CAEEL	Q18320 caenorhabdi			
843	57	12.7	99	2	Q9J3M2_9GEMI	Q9j3m2 tomato yell	916	57	12.7	741	2	Q74107_9HIV2	Q74107 human immun			
844	57	12.7	111	2	Q54DQ1_DICDI	Q54dq1 dictyosteli	917	57	12.7	782	2	Q54XA6_DICDI	Q54xa6 dictyosteli			
845	57	12.7	130	2	Q6DUM8_FRAAN	Q6dum8 fragaria an	918	57	12.7	789	2	Q651Z3_ORYSA	Q651z3 oryza sativ			
846	57	12.7	140	2	Q5BY82_SCHJA	Q5by82 schistosoma	919	57	12.7	800	2	Q6AU80_ORYSA	Q6au80 oryza sativ			
847	57	12.7	145	2	Q81V07_BACAN	Q81v07 bacillus an	920	57	12.7	808	2	Q6N5H8_RHOPA	Q6n5h8 rhodopseudo			
848	57	12.7	149	2	Q5C5I4_SCHJA	Q5c5i4 schistosoma	921	57	12.7	812	2	Q73M73_TREDE	Q73m73 treponema d			
849	57	12.7	155	2	Q9NFW2_HYDAT	Q9nfw2 hydra atten	922	57	12.7	813	1	PMAX_ARATH	Q9t0e0 arabidopsis			
850	57	12.7	162	2	Q91M69_9CLOS	Q91m69 citrus tris	923	57	12.7	828	2	Q7XMR2_ORYSA	Q7xmr2 oryza sativ			
851	57	12.7	162	2	Q91M71_9CLOS	Q91m71 citrus tris	924	57	12.7	843	2	Q8I383_PLAF7	Q8i383 plasmodium			
852	57	12.7	162	2	Q91M74_9CLOS	Q91m74 citrus tris	925	57	12.7	846	2	Q7PDN1_PLAYO	Q7pdn1 plasmodium			
853	57	12.7	162	2	Q91M75_9CLOS	Q91m75 citrus tris	926	57	12.7	875	2	Q5CJ86_CRYHO	Q5cj86 cryptospori			
854	57	12.7	162	2	Q91M76_9CLOS	Q91m76 citrus tris	927	57	12.7	887	2	Q7ZBT2_SIVCZ	Q7zbt2 chimpanzee			
855	57	12.7	162	2	Q91M78_9CLOS	Q91m78 citrus tris	928	57	12.7	924	2	Q6FN63_CANGA	Q6fn63 candida gla			
856	57	12.7	162	2	Q91M79_9CLOS	Q91m79 citrus tris	929	57	12.7	943	2	Q4Z3B3_PLABE	Q4z3b3 plasmodium			
857	57	12.7	162	2	Q91M80_9CLOS	Q91m80 citrus tris	930	57	12.7	944	2	Q7RJ52_PLAYO	Q7rj52 plasmodium			
858	57	12.7	162	2	Q91M82_9CLOS	Q91m82 citrus tris	931	57	12.7	964	2	Q4I2C4_GIBZE	Q4i2c4 gibberella			
859	57	12.7	162	2	Q9J483_9CLOS	Q9j483 citrus tris	932	57	12.7	971	2	Q9VQB6_DROME	Q9vqb6 drosophila			
860	57	12.7	162	2	Q9J484_9CLOS	Q9j484 citrus tris	933	57	12.7	1007	2	Q9RIV8_STRCO	Q9riv8 streptomyce			
861	57	12.7	162	2	Q9J486_9CLOS	Q9j486 citrus tris	934	57	12.7	1020	2	Q4UH79_THEAN	Q4uh79 theileria a			
862	57	12.7	178	2	Q9QRN3_9HIV1	Q9qrn3 human immun	935	57	12.7	1026	2	Q6BY54_DEBHA	Q6by54 debaryomyce			
863	57	12.7	201	2	Q4Z445_PLABE	Q4z445 plasmodium	936	57	12.7	1042	1	LIN49_CAEEL	Q20318 caenorhabdi			
864	57	12.7	205	2	Q70QR2_9HIV1	Q70qr2 human immun	937	57	12.7	1076	2	Q8IL74_PLAF7	Q8il74 plasmodium			
865	57	12.7	221	2	Q49G33_9HIV1	Q49g33 human immun	938	57	12.7	1110	2	Q5CTI7_CRYPV	Q5cti7 cryptospori			
866	57	12.7	249	2	Q84V06_ARATH	Q84v06 arabidopsis	939	57	12.7	1133	2	Q7SA96_NEUCR	Q7sa96 neurospora			
867	57	12.7	266	2	Q387T1_9TRYP	Q387t1 trypanosoma	940	57	12.7	1157	2	Q5AX46_EMENI	Q5ax46 aspergillus			
868	57	12.7	272	2	Q462A1_9NUCL	Q462a1 trichoplusi	941	57	12.7	1233	1	MUC5A_HUMAN	P98088 homo sapien			
869	57	12.7	275	2	Q4YU78_PLABE	Q4yu78 plasmodium	942	57	12.7	1241	2	Q8SWK2_ENCCU	Q8swk2 encephalito			
870	57	12.7	275	2	Q7RHB0_PLAYO	Q7rhb0 plasmodium	943	57	12.7	1260	2	Q6C3I8_YARLI	Q6c3i8 yarrowia li			
871	57	12.7	278	2	Q64N94_BACFR	Q64n94 bacteroides	944	57	12.7	1316	2	Q8IAS8_PLAF7	Q8ias8 plasmodium			
872	57	12.7	281	2	Q4XDG0_PLACH	Q4xdg0 plasmodium	945	57	12.7	1336	2	Q5ZIR3_CHICK	Q5zir3 gallus gall			
873	57	12.7	301	2	Q8EVY9_MYCPE	Q8evy9 mycoplasma	946	57	12.7	1404	2	Q55DE9_DICDI	Q55de9 dictyosteli			
874	57	12.7	307	2	Q03632_PLAFA	Q03632 plasmodium	947	57	12.7	1411	1	ECM5_YEAST	Q03214 saccharomyc			
875	57	12.7	307	2	Q90Y79_BRARE	Q90y79 brachydanio	948	57	12.7	1428	2	Q4YU61_PLABE	Q4yu61 plasmodium			
876	57	12.7	307	2	Q90Z46_BRARE	Q90z46 brachydanio	949	57	12.7	1614	2	Q7RN98_PLAYO	Q7rn98 plasmodium			
877	57	12.7	314	2	Q73WZ5_MYCPA	Q73wz5 mycobacteri	950	57	12.7	1662	2	Q6BGS0_DEBHA	Q6bgs0 debaryomyce			
878	57	12.7	325	2	Q2S5H8_9SPHI	Q2s5h8 salinibacte	951	57	12.7	1828	2	Q8IIS4_PLAF7	Q8iis4 plasmodium			
879	57	12.7	334	2	Q4XJT9_PLACH	Q4xjt9 plasmodium	952	57	12.7	1884	2	Q7S737_NEUCR	Q7s737 neurospora			
880	57	12.7	336	2	Q46WP4_RALEJ	Q46wp4 ralstonia e	953	57	12.7	1921	2	Q5WW30_LEGPL	Q5ww30 legionella			
881	57	12.7	345	2	Q6CRH4_KLULA	Q6crh4 kluyveromyc	954	57	12.7	1921	2	Q5ZUX7_LEGPH	Q5zux7 legionella			
882	57	12.7	351	2	Q9FN76_ARATH	Q9fn76 arabidopsis	955	57	12.7	2379	2	Q8IJW3_PLAF7	Q8ijw3 plasmodium			
883	57	12.7	387	2	Q9RM35_ENTFC	Q9rm35 enterococcu	956	57	12.7	2515	2	Q4S220_TETNG	Q4s220 tetraodon n			
884	57	12.7	399	2	Q5HZM7_XENLA	Q5hzm7 xenopus lae	957	57	12.7	2761	2	Q19522_CAEEL	Q19522 caenorhabdi			
885	57	12.7	403	2	Q8C214_MOUSE	Q8c214 mus musculu	958	57	12.7	3115	2	Q9WID7_9CLOS	Q9wid7 citrus tris			
886	57	12.7	426	2	Q5XMM5_9HEPC	Q5xmm5 hepatitis c	959	57	12.7	3869	2	Q7WRN5_9NOST	Q7wrn5 anabaena ci			
887	57	12.7	438	2	Q8CDY5_MOUSE	Q8cdy5 mus musculu	960	56.5	12.6	128	2	Q6S8L5_PLAFA	Q6s815 plasmodium			
888	57	12.7	439	2	Q2I0F6_9VIRU	Q2i0f6 capsicum ch	961	56.5	12.6	169	2	Q9U2W1_CAEEL	Q9u2w1 caenorhabdi			
889	57	12.7	446	2	Q9SKE9_ARATH	Q9ske9 arabidopsis	962	56.5	12.6	192	2	Q5PF60_SALPA	Q5pf60 salmonella			
890	57	12.7	453	2	Q80ZM2_MOUSE	Q80zm2 mus musculu	963	56.5	12.6	199	2	Q6S303_9HIV1	Q6s303 human immun			
891	57	12.7	454	2	Q58L93_PSEPO	Q58l93 pseudechis	964	56.5	12.6	203	2	Q6S317_9HIV1	Q6s317 human immun			
892	57	12.7	458	2	Q4XSJ3_PLACH	Q4xsj3 plasmodium	965	56.5	12.6	220	2	Q49D32_9HIV1	Q49d32 human immun			
893	57	12.7	460	2	Q7UXM5_RHOBA	Q7uxm5 rhodopirell	966	56.5	12.6	222	2	Q49FD9_9HIV1	Q49fd9 human immun			
894	57	12.7	471	2	Q8Z0Q8_ANASP	Q8z0q8 anabaena sp	967	56.5	12.6	232	2	Q98J31_RHILO	Q98j31 rhizobium l			
895	57	12.7	485	1	OC90_MOUSE	Q9z0l3 mus musculu	968	56.5	12.6	235	2	Q76H40_9CAUD	Q76h40 salmonella			
896	57	12.7	499	1	G6PI_LEGPL	Q5wye0 legionella	969	56.5	12.6	235	2	Q8HAH5_BPST6	Q8hah5 bacteriopha			
897	57	12.7	560	2	Q80WQ3_MOUSE	Q80wq3 mus musculu	970	56.5	12.6	243	2	Q4WP42_ASPFU	Q4wp42 aspergillus			
898	57	12.7	561	2	Q8BP02_MOUSE	Q8bp02 mus musculu	971	56.5	12.6	246	2	Q9BK03_TRICA	Q9bk03 tribolium c			
899	57	12.7	561	2	Q8BRG8_MOUSE	Q8brg8 mus musculu	972	56.5	12.6	246	2	Q3SVU0_NITWN	Q3svu0 nitrobacter			
900	57	12.7	562	2	Q4A1B9_SACBA	Q4a1b9 saccharomyc	973	56.5	12.6	251	1	YMV5_CAEEL	P34507 caenorhabdi			
901	57	12.7	577	2	Q7RSE4_PLAYO	Q7rse4 plasmodium	974	56.5	12.6	263	2	Q9SCR3_ARATH	Q9scr3 arabidopsis			
902	57	12.7	583	1	AP1_KLULA	P56095 kluyveromyc	975	56.5	12.6	265	2	Q9F5C6_AGRRH	Q9f5c6 agrobacteri			
903	57	12.7	599	2	Q4IJM7_GIBZE	Q4ijm7 gibberella	976	56.5	12.6	273	2	Q3RSV7_RALME	Q3rsv7 ralstonia m			
904	57	12.7	619	1	LAC1_NEUCR	P06811 neurospora	977	56.5	12.6	276	2	Q8RY28_ARATH	Q8ry28 arabidopsis			
905	57	12.7	619	1	LAC2_NEUCR	P10574 neurospora	978	56.5	12.6	276	2	Q5XPN1_ACICA	Q5xpn1 acinetobact			
906	57	12.7	619	2	Q7RV60_NEUCR	Q7rv60 neurospora	979	56.5	12.6	276	2	Q83WC8_ACICA	Q83wc8 acinetobact			
907	57	12.7	622	2	Q8C202_MOUSE	Q8c202 mus musculu	980	56.5	12.6	291	1	NANK2_ECOL6	Q8fdu8 escherichia			

981	56.5	12.6	291	2	Q6KCZ0_ECOLI	Q6kcz0 escherichia
982	56.5	12.6	293	2	Q9GPT0_DICDI	Q9gpt0 dictyosteli
983	56.5	12.6	308	2	Q5FWS0_XENTR	Q5fws0 xenopus tro
984	56.5	12.6	318	2	Q6MM59_BDEBA	Q6mm59 bdellovibri
985	56.5	12.6	324	2	Q4QKL3_HAEI8	Q4qkl3 haemophilus
986	56.5	12.6	328	2	Q87673_SIVCZ	Q87673 chimpanzee
987	56.5	12.6	339	2	Q53QF1_HUMAN	Q53qf1 homo sapien
988	56.5	12.6	340	2	Q6NLV9_ARATH	Q6nlv9 arabidopsis
989	56.5	12.6	351	2	Q9W2V8_DROME	Q9w2v8 drosophila
990	56.5	12.6	356	2	Q83FR9_TROWT	Q83fr9 tropheryma
991	56.5	12.6	356	2	Q83HE7_TROW8	Q83he7 tropheryma
992	56.5	12.6	381	2	Q4P151_USTMA	Q4p151 ustilago ma
993	56.5	12.6	395	2	Q2U1F1_ASPOR	Q2u1f1 aspergillus
994	56.5	12.6	396	2	O78673_9ROSI	O78673 cucurbita f
995	56.5	12.6	411	2	Q54RK8_DICDI	Q54rk8 dictyosteli
996	56.5	12.6	432	2	Q4Z345_PLABE	Q4z345 plasmodium
997	56.5	12.6	448	2	Q58ED3_BRARE	Q58ed3 brachydanio
998	56.5	12.6	457	1	PLSB_PEA	P30706 pisum sativ
999	56.5	12.6	470	2	Q8S342_CAPAN	Q8s342 capsicum an
1000	56.5	12.6	476	2	Q3RU81_RALME	Q3ru81 ralstonia m
1001	56.5	12.6	480	2	Q4CP76_TRYCR	Q4cp76 trypanosoma
1002	56.5	12.6	480	2	Q37QK8_SPHAR	Q37qk8 novosphingo
1003	56.5	12.6	481	2	Q84XU5_ELAGV	Q84xu5 elaeis guin
1004	56.5	12.6	516	2	Q4UGS7_THEAN	Q4ugs7 theileria a
1005	56.5	12.6	523	2	Q3E893_ARATH	Q3e893 arabidopsis
1006	56.5	12.6	548	2	Q4Z7R6_PLABE	Q4z7r6 plasmodium
1007	56.5	12.6	563	2	Q4Z1E3_PLABE	Q4z1e3 plasmodium
1008	56.5	12.6	569	2	Q9ZPY2_ARATH	Q9zpy2 arabidopsis
1009	56.5	12.6	571	2	Q4WD61_ASPFU	Q4wd61 aspergillus
1010	56.5	12.6	572	2	Q4HZG2_GIBZE	Q4hzg2 gibberella
1011	56.5	12.6	577	2	O96756_DUGTI	O96756 dugesia tig
1012	56.5	12.6	605	2	Q00292_ASPTE	Q00292 aspergillus
1013	56.5	12.6	617	2	Q4X364_PLACH	Q4x364 plasmodium
1014	56.5	12.6	629	2	Q8NA79_HUMAN	Q8na79 homo sapien
1015	56.5	12.6	630	2	Q4Z6L0_PLABE	Q4z610 plasmodium
1016	56.5	12.6	649	2	Q502K2_BRARE	Q502k2 brachydanio
1017	56.5	12.6	682	2	Q5VSN1_HUMAN	Q5vsn1 homo sapien
1018	56.5	12.6	686	2	Q8ND65_HUMAN	Q8nd65 homo sapien
1019	56.5	12.6	687	2	Q3VKX0_9CHLB	Q3vkx0 pelodictyon
1020	56.5	12.6	724	2	Q37QI0_SPHAR	Q37qi0 novosphingo
1021	56.5	12.6	739	2	Q3R700_XYLFA	Q3r700 xylella fas
1022	56.5	12.6	739	2	Q3RHT6_XYLFA	Q3rht6 xylella fas
1023	56.5	12.6	740	2	Q3RA42_XYLFA	Q3ra42 xylella fas
1024	56.5	12.6	740	2	Q87B20_XYLFT	Q87b20 xylella fas
1025	56.5	12.6	740	2	Q9PG63_XYLFA	Q9pg63 xylella fas
1026	56.5	12.6	789	2	Q8QRR9_9CORO	Q8qrr9 transmissib
1027	56.5	12.6	789	2	Q8QRS3_9CORO	Q8qrs3 transmissib
1028	56.5	12.6	790	2	Q8QRS1_9CORO	Q8qrs1 transmissib
1029	56.5	12.6	790	2	Q8QRS2_9CORO	Q8qrs2 transmissib
1030	56.5	12.6	803	2	Q8ND63_HUMAN	Q8nd63 homo sapien
1031	56.5	12.6	808	2	Q9QRQ0_9CORO	Q9qrq0 canine coro
1032	56.5	12.6	811	2	Q8NSE2_CORGL	Q8nse2 corynebacte
1033	56.5	12.6	825	2	Q5AUT1_EMENI	Q5aut1 aspergillus
1034	56.5	12.6	838	2	Q54GJ1_DICDI	Q54gj1 dictyosteli
1035	56.5	12.6	852	2	Q6UFH8_9HIV1	Q6ufh8 human immun
1036	56.5	12.6	856	1	ENV_HV2NZ	P05883 human immun
1037	56.5	12.6	868	2	Q75KG8_ORYSA	Q75kg8 oryza sativ
1038	56.5	12.6	874	2	Q8YQH8_ANASP	Q8yqh8 anabaena sp
1039	56.5	12.6	879	1	YL088_MIMIV	Q5upf8 mimivirus.
1040	56.5	12.6	882	2	Q7SKF3_9HIV2	Q7skf3 human immun
1041	56.5	12.6	891	1	NIA7_HORVU	P27968 hordeum vul
1042	56.5	12.6	902	2	Q9Q3G0_9ADEN	Q9q3g0 bovine aden
1043	56.5	12.6	910	2	O71149_ADEB4	O71149 bovine aden
1044	56.5	12.6	952	2	Q55M05_CRYNE	Q55m05 cryptococcu
1045	56.5	12.6	952	2	Q5K8R4_CRYNE	Q5k8r4 cryptococcu
1046	56.5	12.6	974	2	Q7QC91_ANOGA	Q7qc91 anopheles g
1047	56.5	12.6	986	2	Q4RQJ2_TETNG	Q4rqj2 tetraodon n
1048	56.5	12.6	1018	2	O61295_9DIPT	O61295 chymomyza c
1049	56.5	12.6	1065	2	Q4UE85_THEAN	Q4ue85 theileria a
1050	56.5	12.6	1068	2	Q7QU18_GIALA	Q7qu18 giardia lam
1051	56.5	12.6	1117	2	Q652W3_ORYSA	Q652w3 oryza sativ
1052	56.5	12.6	1125	1	TEA3_SCHPO	O14248 schizosacch
1053	56.5	12.6	1158	2	Q6KIC5_MYCMO	Q6kic5 mycoplasma
1054	56.5	12.6	1173	2	Q8IEM5_PLAF7	Q8iem5 plasmodium
1055	56.5	12.6	1201	2	Q9C0W2_SCHPO	Q9c0w2 schizosacch
1056	56.5	12.6	1208	2	Q54WZ1_DICDI	Q54wz1 dictyosteli
1057	56.5	12.6	1241	2	O13617_SCHPO	O13617 schizosacch
1058	56.5	12.6	1263	2	Q4X3J2_PLACH	Q4x3j2 plasmodium
1059	56.5	12.6	1291	2	Q6BZ89_DEBHA	Q6bz89 debaryomyce
1060	56.5	12.6	1312	2	Q7RNR7_PLAYO	Q7rnr7 plasmodium
1061	56.5	12.6	1360	2	Q5VQS0_ORYSA	Q5vqs0 oryza sativ
1062	56.5	12.6	1447	1	SPIKE_CVPPU	P07946 porcine tra
1063	56.5	12.6	1447	1	SPIKE_CVPRT	Q01977 porcine tra
1064	56.5	12.6	1447	2	Q8QQW0_9CORO	Q8qqw0 transmissib
1065	56.5	12.6	1447	2	Q9IW04_9CORO	Q9iw04 transmissib
1066	56.5	12.6	1472	2	Q4YAV8_PLABE	Q4yav8 plasmodium
1067	56.5	12.6	1496	2	Q7RJE3_PLAYO	Q7rje3 plasmodium
1068	56.5	12.6	1577	2	Q7F2I6_ORYSA	Q7f2i6 oryza sativ
1069	56.5	12.6	1713	2	Q54B29_DICDI	Q54b29 dictyosteli
1070	56.5	12.6	1735	2	Q8VIG2_RAT	Q8vig2 rattus norv
1071	56.5	12.6	1748	2	Q54FL9_DICDI	Q54fl9 dictyosteli
1072	56.5	12.6	1750	2	Q4CPP9_TRYCR	Q4cpp9 trypanosoma
1073	56.5	12.6	1918	2	Q7RLT6_PLAYO	Q7rlt6 plasmodium
1074	56.5	12.6	2122	2	Q54R92_DICDI	Q54r92 dictyosteli
1075	56.5	12.6	2157	2	Q60T97_CAEBR	Q60t97 caenorhabdi
1076	56.5	12.6	2413	2	P71401_HAEIN	P71401 haemophilus
1077	56.5	12.6	2413	2	Q4KTX9_HAEIN	Q4ktx9 haemophilus
1078	56.5	12.6	3005	1	ZFH2_DROME	P28167 drosophila
1079	56.5	12.6	3005	2	Q4SHP3_TETNG	Q4shp3 tetraodon n
1080	56.5	12.6	3240	2	Q54DT4_DICDI	Q54dt4 dictyosteli
1081	56.5	12.6	4351	1	FAT2_RAT	O88277 rattus norv
1082	56.5	12.6	5138	2	Q9ZW94_ARATH	Q9zw94 arabidopsis
1083	56	12.5	94	2	Q74HF7_LACJO	Q74hf7 lactobacill
1084	56	12.5	100	2	Q84N94_9FABA	Q84n94 indigofera
1085	56	12.5	130	2	Q2VJP9_DROMU	Q2vjp9 drosophila
1086	56	12.5	131	2	Q5DPK0_9HIV1	Q5dpk0 human immun
1087	56	12.5	133	2	Q7VBS5_PROMA	Q7vbs5 prochloroco
1088	56	12.5	145	2	Q81HT9_BACCR	Q81ht9 bacillus ce
1089	56	12.5	162	2	Q91M84_9CLOS	Q91m84 citrus tris
1090	56	12.5	162	2	Q9J482_9CLOS	Q9j482 citrus tris
1091	56	12.5	162	2	Q9J487_9CLOS	Q9j487 citrus tris
1092	56	12.5	162	2	Q9J488_9CLOS	Q9j488 citrus tris
1093	56	12.5	162	2	Q9J489_9CLOS	Q9j489 citrus tris
1094	56	12.5	162	2	Q9J494_9CLOS	Q9j494 citrus tris
1095	56	12.5	164	1	Y461_MYCMS	Q6mte7 mycoplasma
1096	56	12.5	164	2	Q87KK8_VIBPA	Q87kk8 vibrio para
1097	56	12.5	169	2	Q7VX98_BORPE	Q7vx98 bordetella
1098	56	12.5	169	2	Q7W864_BORPA	Q7w864 bordetella
1099	56	12.5	169	2	Q7WLL2_BORBR	Q7wll2 bordetella
1100	56	12.5	175	2	Q8WLZ8_BOVIN	Q8wlz8 bos taurus
1101	56	12.5	181	2	Q2WLW2_CLOBE	Q2wlw2 clostridium
1102	56	12.5	181	2	Q5Y2L7_9HIV1	Q5y217 human immun
1103	56	12.5	191	2	Q5C6Q9_SCHJA	Q5c6q9 schistosoma
1104	56	12.5	191	2	Q9DVE9_9HIV1	Q9dve9 human immun
1105	56	12.5	199	2	Q31312_APHCE	Q31312 aphelocoma
1106	56	12.5	203	2	Q86S73_CAEEL	Q86s73 caenorhabdi
1107	56	12.5	203	2	Q4S9X1_TETNG	Q4s9x1 tetraodon n
1108	56	12.5	207	2	Q6S319_9HIV1	Q6s319 human immun
1109	56	12.5	207	2	Q6S320_9HIV1	Q6s320 human immun
1110	56	12.5	214	2	Q7MIT2_VIBVY	Q7mit2 vibrio vuln
1111	56	12.5	214	2	Q8DB41_VIBVU	Q8db41 vibrio vuln
1112	56	12.5	220	2	Q4RRZ2_TETNG	Q4rrz2 tetraodon n
1113	56	12.5	221	2	Q49G40_9HIV1	Q49g40 human immun
1114	56	12.5	229	2	Q30080_HUMAN	Q30080 homo sapien
1115	56	12.5	231	2	Q8VRH6_AERHY	Q8vrh6 aeromonas h
1116	56	12.5	233	2	Q67AJ5_HUMAN	Q67aj5 homo sapien
1117	56	12.5	233	2	Q7MZT9_PHOLL	Q7mzt9 photorhabdu
1118	56	12.5	234	2	Q67AJ6_HUMAN	Q67aj6 homo sapien
1119	56	12.5	237	2	Q30097_HUMAN	Q30097 homo sapien
1120	56	12.5	240	2	Q30305_BOVIN	Q30305 bos taurus
1121	56	12.5	247	2	Q30310_BOVIN	Q30310 bos taurus
1122	56	12.5	248	2	Q5DWG2_CRYJA	Q5dwg2 cryptomeria
1123	56	12.5	250	2	O19709_HUMAN	O19709 homo sapien
1124	56	12.5	259	1	YG31_YEAST	P53269 saccharomyc
1125	56	12.5	261	1	HB22_HUMAN	P01919 homo sapien
1126	56	12.5	261	2	Q5Y7D0_HUMAN	Q5y7d0 homo sapien

1127	56	12.5	261	2	Q5Y7F1_HUMAN	Q5y7f1 homo sapien
1128	56	12.5	261	2	Q5XWC9_BOVIN	Q5xwc9 bos taurus
1129	56	12.5	261	2	Q30266_BOVIN	Q30266 bos taurus
1130	56	12.5	261	2	Q3ZC29_BOVIN	Q3zc29 bos taurus
1131	56	12.5	270	2	O24347_SECCE	O24347 secale cere
1132	56	12.5	278	2	Q5L813_BACFN	Q5l813 bacteroides
1133	56	12.5	296	2	Q60ZQ3_CAEBR	Q60zq3 caenorhabdi
1134	56	12.5	302	1	HXC1A_BRARE	Q98sh9 brachydanio
1135	56	12.5	302	2	Q4WIA4_ASPFU	Q4wia4 aspergillus
1136	56	12.5	309	2	Q4XHV1_PLACH	Q4xhv1 plasmodium
1137	56	12.5	331	2	Q5CLY4_CRYHO	Q5cly4 cryptospori
1138	56	12.5	343	2	Q6MK57_BDEBA	Q6mk57 bdellovibri
1139	56	12.5	359	2	Q6PD87_BRARE	Q6pd87 brachydanio
1140	56	12.5	386	2	Q3H9A6_TRIER	Q3h9a6 trichodesmi
1141	56	12.5	386	2	Q7U9X0_SYNPX	Q7u9x0 synechococc
1142	56	12.5	402	2	Q54PK7_DICDI	Q54pk7 dictyosteli
1143	56	12.5	409	2	Q8A5X6_BACTN	Q8a5x6 bacteroides
1144	56	12.5	411	2	O45534_CAEEL	O45534 caenorhabdi
1145	56	12.5	413	2	Q4YTQ8_PLABE	Q4ytq8 plasmodium
1146	56	12.5	447	2	Q9SJX4_ARATH	Q9sjx4 arabidopsis
1147	56	12.5	453	1	TBA1_NEUCR	P38668 neurospora
1148	56	12.5	454	2	Q60AU0_METCA	Q60au0 methylococc
1149	56	12.5	458	2	Q84TK1_ARATH	Q84tk1 arabidopsis
1150	56	12.5	470	2	Q8IIT0_PLAF7	Q8iit0 plasmodium
1151	56	12.5	481	2	O18471_HELVI	O18471 heliothis v
1152	56	12.5	484	2	Q7R8T2_PLAYO	Q7r8t2 plasmodium
1153	56	12.5	492	1	AER3_AERHY	Q06305 aeromonas h
1154	56	12.5	492	1	AER4_AERHY	Q06303 aeromonas h
1155	56	12.5	499	2	Q21528_CAEEL	Q21528 caenorhabdi
1156	56	12.5	501	2	Q7XG89_ORYSA	Q7xg89 oryza sativ
1157	56	12.5	501	2	Q8SB08_ORYSA	Q8sb08 oryza sativ
1158	56	12.5	512	2	Q7RQG1_PLAYO	Q7rqg1 plasmodium
1159	56	12.5	513	2	Q52572_PSESP	Q52572 pseudomonas
1160	56	12.5	514	2	Q9EZP3_BURCE	Q9ezp3 burkholderi
1161	56	12.5	550	2	Q41QP1_FERAC	Q41qp1 ferroplasma
1162	56	12.5	555	2	Q9I3A5_PSEAE	Q9i3a5 pseudomonas
1163	56	12.5	570	2	Q5ARB0_EMENI	Q5arb0 aspergillus
1164	56	12.5	578	2	Q8RYC7_ARATH	Q8ryc7 arabidopsis
1165	56	12.5	596	2	Q5ATH5_EMENI	Q5ath5 aspergillus
1166	56	12.5	610	2	Q4UG81_THEAN	Q4ug81 theileria a
1167	56	12.5	631	1	LIRB3_HUMAN	O75022 homo sapien
1168	56	12.5	632	2	Q96KV2_HUMAN	Q96kv2 homo sapien
1169	56	12.5	635	2	Q9Y3H6_HUMAN	Q9y3h6 homo sapien
1170	56	12.5	637	1	SYT_LEGPL	Q5wt82 legionella
1171	56	12.5	648	2	Q9LQV6_ARATH	Q9lqv6 arabidopsis
1172	56	12.5	651	2	Q6ZV26_HUMAN	Q6zv26 homo sapien
1173	56	12.5	654	2	Q2WLW3_CLOBE	Q2wlw3 clostridium
1174	56	12.5	657	2	Q8IYS7_HUMAN	Q8iys7 homo sapien
1175	56	12.5	664	2	Q5SLK8_THET8	Q5slk8 thermus the
1176	56	12.5	670	2	Q840Y5_NEIME	Q840y5 neisseria m
1177	56	12.5	674	2	Q7Q378_ANOGA	Q7q378 anopheles g
1178	56	12.5	677	2	Q6LEX4_PLAF7	Q6lex4 plasmodium
1179	56	12.5	695	2	Q6ZNP7_HUMAN	Q6znp7 homo sapien
1180	56	12.5	703	2	Q4AL42_9CHLB	Q4al42 chlorobium
1181	56	12.5	703	2	Q97DW8_CLOAB	Q97dw8 clostridium
1182	56	12.5	704	2	Q4YCC1_PLABE	Q4ycc1 plasmodium
1183	56	12.5	711	2	Q9KBE8_BACHD	Q9kbe8 bacillus ha
1184	56	12.5	714	1	RGD2_YEAST	P43556 saccharomyc
1185	56	12.5	731	1	YJI2_YEAST	P47031 saccharomyc
1186	56	12.5	731	2	Q7PUQ1_ANOGA	Q7puq1 anopheles g
1187	56	12.5	756	2	Q2WHE1_CLOBE	Q2whe1 clostridium
1188	56	12.5	759	2	Q2SJL2_9GAMM	Q2sjl2 hahella che
1189	56	12.5	766	2	Q7RKM1_PLAYO	Q7rkm1 plasmodium
1190	56	12.5	789	2	Q8QRR7_9CORO	Q8qrr7 transmissib
1191	56	12.5	791	2	Q8I299_PLAF7	Q8i299 plasmodium
1192	56	12.5	805	2	Q6DXS0_GOSHI	Q6dxs0 gossypium h
1193	56	12.5	857	2	Q4D509_TRYCR	Q4d509 trypanosoma
1194	56	12.5	857	2	Q4DP85_TRYCR	Q4dp85 trypanosoma
1195	56	12.5	857	2	Q5U897_9HIV1	Q5u897 human immun
1196	56	12.5	904	1	ABRU_DROME	Q24174 drosophila
1197	56	12.5	930	2	Q5CIA6_CRYHO	Q5cia6 cryptospori
1198	56	12.5	932	2	Q5CSP4_CRYPV	Q5csp4 cryptospori
1199	56	12.5	944	2	Q58T20_ARATH	Q58t20 arabidopsis
1200	56	12.5	949	2	Q6CU98_KLULA	Q6cu98 kluyveromyc
1201	56	12.5	953	1	LUMI_ARATH	Q38796 arabidopsis
1202	56	12.5	955	2	Q20829_CAEEL	Q20829 caenorhabdi
1203	56	12.5	968	2	Q6ZU25_HUMAN	Q6zu25 homo sapien
1204	56	12.5	972	2	Q9VSA5_DROME	Q9vsa5 drosophila
1205	56	12.5	1019	2	Q4YU89_PLABE	Q4yu89 plasmodium
1206	56	12.5	1022	2	Q6IP11_XENLA	Q6ip11 xenopus lae
1207	56	12.5	1059	2	Q9VVC6_DROME	Q9vvc6 drosophila
1208	56	12.5	1089	2	Q8I605_PLAF7	Q8i605 plasmodium
1209	56	12.5	1125	2	Q54C71_DICDI	Q54c71 dictyosteli
1210	56	12.5	1147	1	DPO3A_BORBU	O51526 borrelia bu
1211	56	12.5	1148	1	AT8A2_HUMAN	Q9nti2 homo sapien
1212	56	12.5	1155	2	Q8WPH2_BOMMO	Q8wph2 bombyx mori
1213	56	12.5	1188	2	Q6ZSP3_HUMAN	Q6zsp3 homo sapien
1214	56	12.5	1296	2	Q61EL9_CAEBR	Q61el9 caenorhabdi
1215	56	12.5	1297	2	Q759H0_ASHGO	Q759h0 ashbya goss
1216	56	12.5	1308	1	YTX2_XENLA	P14381 xenopus lae
1217	56	12.5	1328	2	Q4RKW3_TETNG	Q4rkw3 tetraodon n
1218	56	12.5	1356	2	Q6LFA0_PLAF7	Q6lfa0 plasmodium
1219	56	12.5	1418	2	Q7PVG3_ANOGA	Q7pvg3 anopheles g
1220	56	12.5	1447	2	Q5CFG8_CRYHO	Q5cfg8 cryptospori
1221	56	12.5	1506	2	Q5CW39_CRYPV	Q5cw39 cryptospori
1222	56	12.5	1527	2	Q54CY2_DICDI	Q54cy2 dictyosteli
1223	56	12.5	1616	2	Q5ZKF9_CHICK	Q5zkf9 gallus gall
1224	56	12.5	1765	2	Q54WL2_DICDI	Q54wl2 dictyosteli
1225	56	12.5	1772	2	Q5SBN0_LACRE	Q5sbn0 lactobacill
1226	56	12.5	1779	2	Q9HCK1_HUMAN	Q9hck1 homo sapien
1227	56	12.5	2147	2	Q54CA8_DICDI	Q54ca8 dictyosteli
1228	56	12.5	2319	2	Q4RT87_TETNG	Q4rt87 tetraodon n
1229	56	12.5	2402	2	Q6LFK0_PLAF7	Q6lfk0 plasmodium
1230	56	12.5	2441	2	Q54F71_DICDI	Q54f71 dictyosteli
1231	56	12.5	2558	2	Q5CWM7_CRYPV	Q5cwm7 cryptospori
1232	56	12.5	2564	2	Q7YZ64_CRYPV	Q7yz64 cryptospori
1233	56	12.5	2603	2	Q5TRL4_ANOGA	Q5trl4 anopheles g
1234	56	12.5	2773	2	Q8IBF4_PLAF7	Q8ibf4 plasmodium
1235	56	12.5	3570	2	Q7Q737_ANOGA	Q7q737 anopheles g
1236	56	12.5	3758	2	Q4QEN3_LEIMA	Q4qen3 leishmania
1237	55.5	12.4	79	2	Q33H02_METHU	Q33h02 methanospir
1238	55.5	12.4	94	2	Q4E1E2_TRYCR	Q4e1e2 trypanosoma
1239	55.5	12.4	100	2	Q8FGG2_ECOL6	Q8fgg2 escherichia
1240	55.5	12.4	101	2	Q84N77_LUPNA	Q84n77 lupinus nan
1241	55.5	12.4	103	2	Q5XGH4_XENTR	Q5xgh4 xenopus tro
1242	55.5	12.4	109	2	Q6U5M4_KLEPN	Q6u5m4 klebsiella
1243	55.5	12.4	151	2	Q54EC0_DICDI	Q54ec0 dictyosteli
1244	55.5	12.4	160	1	CHLL_POLAC	P36439 polystichum
1245	55.5	12.4	160	2	Q7KR83_DROME	Q7kr83 drosophila
1246	55.5	12.4	161	2	Q28606_SHEEP	Q28606 ovis aries
1247	55.5	12.4	162	2	Q707F0_ECOLI	Q707f0 escherichia
1248	55.5	12.4	189	2	Q2W1K6_MAGSA	Q2w1k6 magnetospir
1249	55.5	12.4	201	2	Q3RT69_RALME	Q3rt69 ralstonia m
1250	55.5	12.4	207	2	Q2U5U6_ASPOR	Q2u5u6 aspergillus
1251	55.5	12.4	208	2	Q6ZTV0_HUMAN	Q6ztv0 homo sapien
1252	55.5	12.4	214	2	Q2MDZ4_9HIV1	Q2mdz4 human immun
1253	55.5	12.4	218	1	CTFA_CLOAB	P33752 clostridium
1254	55.5	12.4	219	2	Q4TYX8_ARATH	Q4tyx8 arabidopsis
1255	55.5	12.4	222	2	Q49D56_9HIV1	Q49d56 human immun
1256	55.5	12.4	222	2	Q49D58_9HIV1	Q49d58 human immun
1257	55.5	12.4	222	2	Q49D60_9HIV1	Q49d60 human immun
1258	55.5	12.4	222	2	Q49D61_9HIV1	Q49d61 human immun
1259	55.5	12.4	222	2	Q49D62_9HIV1	Q49d62 human immun
1260	55.5	12.4	224	2	Q5D8L0_SCHJA	Q5d8l0 schistosoma
1261	55.5	12.4	226	2	Q59PT7_CANAL	Q59pt7 candida alb
1262	55.5	12.4	226	2	Q5WN15_CAEBR	Q5wn15 caenorhabdi
1263	55.5	12.4	230	2	Q9Y0S2_LYMDI	Q9y0s2 lymantria d
1264	55.5	12.4	230	2	Q2V2Z8_ARATH	Q2v2z8 arabidopsis
1265	55.5	12.4	243	2	Q9FK29_ARATH	Q9fk29 arabidopsis
1266	55.5	12.4	246	2	Q3IC17_PSEHT	Q3ic17 pseudoalter
1267	55.5	12.4	251	2	Q4ZBU8_9CAUD	Q4zbu8 bacteriopha
1268	55.5	12.4	251	2	Q4ZCW8_9CAUD	Q4zcw8 bacteriopha
1269	55.5	12.4	251	2	Q2YTU4_STAAB	Q2ytu4 staphylococ
1270	55.5	12.4	261	2	Q4YTC9_PLABE	Q4ytc9 plasmodium
1271	55.5	12.4	267	2	Q93UX0_9RHIZ	Q93ux0 agrobacteri
1272	55.5	12.4	276	2	O28774_ARCFU	O28774 archaeoglob

1273	55.5	12.4	288	2	Q98S12_GUITH	Q98s12 guillardia
1274	55.5	12.4	296	2	Q5PQA4_XENLA	Q5pqa4 xenopus lae
1275	55.5	12.4	300	2	Q5CUS1_CRYPV	Q5cus1 cryptospori
1276	55.5	12.4	301	2	Q7RJR8_PLAYO	Q7rjr8 plasmodium
1277	55.5	12.4	302	2	Q5HQB3_STAEQ	Q5hqb3 staphylococ
1278	55.5	12.4	302	2	Q8CT32_STAES	Q8ct32 staphylococ
1279	55.5	12.4	304	2	Q5BJ68_XENTR	Q5bj68 xenopus tro
1280	55.5	12.4	306	2	Q7RA21_PLAYO	Q7ra21 plasmodium
1281	55.5	12.4	326	2	Q7X9F6_9FABA	Q7x9f6 galega orie
1282	55.5	12.4	326	2	Q451M2_9BURK	Q451m2 burkholderi
1283	55.5	12.4	326	2	Q4LTC7_9BURK	Q4ltc7 burkholderi
1284	55.5	12.4	337	2	Q8KFB1_CHLTE	Q8kfb1 chlorobium
1285	55.5	12.4	338	2	O45821_CAEEL	O45821 caenorhabdi
1286	55.5	12.4	345	2	Q50UY8_ENTHI	Q50uy8 entamoeba h
1287	55.5	12.4	350	2	Q4SH30_TETNG	Q4sh30 tetraodon n
1288	55.5	12.4	354	2	Q7PYJ0_ANOGA	Q7pyj0 anopheles g
1289	55.5	12.4	358	2	Q9V4M3_DROME	Q9v4m3 drosophila
1290	55.5	12.4	359	2	Q71049_9HIV1	Q71049 human immun
1291	55.5	12.4	373	2	Q7R9L3_PLAYO	Q7r9l3 plasmodium
1292	55.5	12.4	374	2	Q3TP40_MOUSE	Q3tp40 mus musculu
1293	55.5	12.4	382	2	Q6ATE2_ORYSA	Q6ate2 oryza sativ
1294	55.5	12.4	391	2	Q3C811_9CLOT	Q3c811 alkaliphilu
1295	55.5	12.4	393	2	Q50Z47_ENTHI	Q50z47 entamoeba h
1296	55.5	12.4	403	2	Q50HW5_LOTJA	Q50hw5 lotus japon
1297	55.5	12.4	415	2	Q3KP74_MOUSE	Q3kp74 mus musculu
1298	55.5	12.4	417	2	Q97FA3_CLOAB	Q97fa3 clostridium
1299	55.5	12.4	427	2	Q8W3G2_ORYSA	Q8w3g2 oryza sativ
1300	55.5	12.4	427	2	Q8PQY4_XANAC	Q8pqy4 xanthomonas
1301	55.5	12.4	441	1	TBA_ENCCU	Q8sri6 encephalito
1302	55.5	12.4	441	1	VA39_VACCV	P24764 vaccinia vi
1303	55.5	12.4	443	2	Q6P985_HUMAN	Q6p985 homo sapien
1304	55.5	12.4	446	2	Q7Z9L9_COPCI	Q7z9l9 coprinus ci
1305	55.5	12.4	449	1	TBA_GIBZE	Q5i2j3 gibberella
1306	55.5	12.4	459	2	Q6MZY0_HUMAN	Q6mzy0 homo sapien
1307	55.5	12.4	462	2	Q683B7_ARATH	Q683b7 arabidopsis
1308	55.5	12.4	470	2	Q76BF8_ORYLA	Q76bf8 oryzias lat
1309	55.5	12.4	477	2	Q683F9_ARATH	Q683f9 arabidopsis
1310	55.5	12.4	482	2	Q2TXG0_ASPOR	Q2txg0 aspergillus
1311	55.5	12.4	486	2	Q87R02_VIBPA	Q87r02 vibrio para
1312	55.5	12.4	488	2	Q67X97_ARATH	Q67x97 arabidopsis
1313	55.5	12.4	488	2	Q67ZA2_ARATH	Q67za2 arabidopsis
1314	55.5	12.4	488	2	Q94CC6_ARATH	Q94cc6 arabidopsis
1315	55.5	12.4	492	2	Q61BF5_CAEBR	Q61bf5 caenorhabdi
1316	55.5	12.4	497	2	Q48T10_STRPM	Q48t10 streptococc
1317	55.5	12.4	497	2	Q5XBP8_STRP6	Q5xbp8 streptococc
1318	55.5	12.4	497	2	Q8K751_STRP3	Q8k751 streptococc
1319	55.5	12.4	497	2	Q8P0K6_STRP8	Q8p0k6 streptococc
1320	55.5	12.4	497	2	Q99ZC2_STRP1	Q99zc2 streptococc
1321	55.5	12.4	498	1	ZN271_HUMAN	Q14591 homo sapien
1322	55.5	12.4	501	2	Q43265_MAIZE	Q43265 zea mays (m
1323	55.5	12.4	504	2	Q6TKQ2_HELTI	Q6tkq2 helisoma tr
1324	55.5	12.4	509	2	Q6BYN6_DEBHA	Q6byn6 debaryomyce
1325	55.5	12.4	514	2	Q6CK27_KLULA	Q6ck27 kluyveromyc
1326	55.5	12.4	514	2	Q4G339_9PERO	Q4g339 rhabdosargu
1327	55.5	12.4	516	1	NACH_DROAN	O61370 drosophila
1328	55.5	12.4	527	2	Q5NDL2_HUMAN	Q5ndl2 homo sapien
1329	55.5	12.4	527	2	Q5NDL1_PANTR	Q5ndl1 pan troglod
1330	55.5	12.4	527	2	Q5NDL9_CANFA	Q5ndl9 canis famil
1331	55.5	12.4	537	2	Q5CS03_CRYPV	Q5cs03 cryptospori
1332	55.5	12.4	544	2	Q97M46_CLOAB	Q97m46 clostridium
1333	55.5	12.4	557	2	Q4Z552_PLABE	Q4z552 plasmodium
1334	55.5	12.4	561	2	Q61K34_CAEBR	Q61k34 caenorhabdi
1335	55.5	12.4	568	1	MMP21_MOUSE	Q8k3f2 mus musculu
1336	55.5	12.4	568	2	Q3KP73_MOUSE	Q3kp73 mus musculu
1337	55.5	12.4	569	2	Q6ZQ53_MOUSE	Q6zq53 mus musculu
1338	55.5	12.4	578	2	Q4R7H1_MACFA	Q4r7h1 macaca fasc
1339	55.5	12.4	586	2	Q551C4_DICDI	Q551c4 dictyosteli
1340	55.5	12.4	588	2	Q2PAI9_MAIZE	Q2pai9 zea mays (m
1341	55.5	12.4	602	2	Q66UC5_9DIPT	Q66uc5 culicoides
1342	55.5	12.4	623	2	Q6FIM0_CANGA	Q6fim0 candida gla
1343	55.5	12.4	643	2	Q6BSN4_DEBHA	Q6bsn4 debaryomyce
1344	55.5	12.4	646	1	LYAM3_BOVIN	P42201 bos taurus
1345	55.5	12.4	649	2	Q28657_RABIT	Q28657 oryctolagus
1346	55.5	12.4	662	2	Q8IAW6_PLAF7	Q8iaw6 plasmodium
1347	55.5	12.4	676	2	Q9H5A7_HUMAN	Q9h5a7 homo sapien
1348	55.5	12.4	683	2	O36401_9GAMA	O36401 alcelaphine
1349	55.5	12.4	688	2	Q7S3U0_NEUCR	Q7s3u0 neurospora
1350	55.5	12.4	697	2	Q2UHZ4_ASPOR	Q2uhz4 aspergillus
1351	55.5	12.4	702	2	Q4SRR8_TETNG	Q4srr8 tetraodon n
1352	55.5	12.4	704	1	MSN2_YEAST	P33748 saccharomyc
1353	55.5	12.4	707	2	Q5CRK5_CRYPV	Q5crk5 cryptospori
1354	55.5	12.4	710	2	Q4RRG6_TETNG	Q4rrg6 tetraodon n
1355	55.5	12.4	718	2	Q8CS09_STAES	Q8cs09 staphylococ
1356	55.5	12.4	729	2	Q54HB7_DICDI	Q54hb7 dictyosteli
1357	55.5	12.4	789	2	Q8QRS0_9CORO	Q8qrs0 transmissib
1358	55.5	12.4	798	1	ITB1_FELCA	P53713 felis silve
1359	55.5	12.4	798	2	Q8SQC0_BOVIN	Q8sqc0 bos taurus
1360	55.5	12.4	804	2	Q35W08_9GAMM	Q35w08 shewanella
1361	55.5	12.4	805	2	Q6DXT4_GOSHI	Q6dxt4 gossypium h
1362	55.5	12.4	841	2	Q4ICM6_GIBZE	Q4icm6 gibberella
1363	55.5	12.4	858	1	CYAG_DICDI	Q03101 dictyosteli
1364	55.5	12.4	858	2	Q86A89_DICDI	Q86a89 dictyosteli
1365	55.5	12.4	860	1	ENV_HV2BE	P18094 human immun
1366	55.5	12.4	861	2	Q3TPG3_MOUSE	Q3tpg3 mus musculu
1367	55.5	12.4	861	2	Q9IUZ4_9HIV1	Q9iuz4 human immun
1368	55.5	12.4	875	2	O48930_SOYBN	O48930 glycine max
1369	55.5	12.4	875	2	Q5H1L0_XANOR	Q5h1l0 xanthomonas
1370	55.5	12.4	877	2	Q8PMQ7_XANAC	Q8pmq7 xanthomonas
1371	55.5	12.4	879	2	Q88028_SIVCZ	Q88028 chimpanzee
1372	55.5	12.4	885	2	Q2U6U9_ASPOR	Q2u6u9 aspergillus
1373	55.5	12.4	885	2	Q3FUF3_9BURK	Q3fuf3 rhodoferax
1374	55.5	12.4	886	1	NIA1_SOYBN	P54233 glycine max
1375	55.5	12.4	890	1	NIA2_SOYBN	P39870 glycine max
1376	55.5	12.4	890	2	Q9SYR0_SOYBN	Q9syr0 glycine max
1377	55.5	12.4	911	2	Q83905_ADEO7	Q83905 ovine adeno
1378	55.5	12.4	912	1	NIA2_HORVU	P27969 hordeum vul
1379	55.5	12.4	914	2	Q3TKT7_MOUSE	Q3tkt7 mus musculu
1380	55.5	12.4	915	1	NIA1_HORVU	P27967 hordeum vul
1381	55.5	12.4	916	2	Q60BP0_METCA	Q60bp0 methylococc
1382	55.5	12.4	917	2	Q873D8_NEUCR	Q873d8 neurospora
1383	55.5	12.4	940	2	Q3HJG6_TRIER	Q3hjg6 trichodesmi
1384	55.5	12.4	984	2	Q3UJE5_MOUSE	Q3uje5 mus musculu
1385	55.5	12.4	987	2	Q5QF51_9CAUD	Q5qf51 pseudomonas
1386	55.5	12.4	992	2	Q4Z6U8_PLABE	Q4z6u8 plasmodium
1387	55.5	12.4	992	2	Q7TT14_MOUSE	Q7tt14 mus musculu
1388	55.5	12.4	1002	1	RBM12_MOUSE	Q8r4x3 mus musculu
1389	55.5	12.4	1004	2	Q8IBA4_PLAF7	Q8iba4 plasmodium
1390	55.5	12.4	1016	2	O61296_9DIPT	O61296 chymomyza c
1391	55.5	12.4	1060	2	Q86T73_HUMAN	Q86t73 homo sapien
1392	55.5	12.4	1074	2	Q4XPJ3_PLACH	Q4xpj3 plasmodium
1393	55.5	12.4	1099	2	Q9U9K8_DICDI	Q9u9k8 dictyosteli
1394	55.5	12.4	1130	2	Q6R7G2_9HERP	Q6r7g2 ostreid her
1395	55.5	12.4	1157	2	Q54U88_DICDI	Q54u88 dictyosteli
1396	55.5	12.4	1187	2	Q6PFD9_MOUSE	Q6pfd9 mus musculu
1397	55.5	12.4	1225	2	Q4L4Y3_STAHJ	Q4l4y3 staphylococ
1398	55.5	12.4	1245	2	Q5CKS9_CRYHO	Q5cks9 cryptospori
1399	55.5	12.4	1352	2	Q55T02_CRYNE	Q55t02 cryptococcu
1400	55.5	12.4	1439	2	Q5CPF4_CRYPV	Q5cpf4 cryptospori
1401	55.5	12.4	1501	2	Q75JS9_DICDI	Q75js9 dictyosteli
1402	55.5	12.4	1540	2	Q559R8_DICDI	Q559r8 dictyosteli
1403	55.5	12.4	1582	2	Q60ST0_CAEBR	Q60st0 caenorhabdi
1404	55.5	12.4	1608	2	Q54VR7_DICDI	Q54vr7 dictyosteli
1405	55.5	12.4	1710	2	Q54YG2_DICDI	Q54yg2 dictyosteli
1406	55.5	12.4	1729	1	NUP98_HUMAN	P52948 homo sapien
1407	55.5	12.4	1848	2	Q4S113_TETNG	Q4s113 tetraodon n
1408	55.5	12.4	1873	2	Q6S003_DICDI	Q6s003 dictyosteli
1409	55.5	12.4	1874	1	POLR_KYMVJ	P36304 kennedya ye
1410	55.5	12.4	1918	2	Q47XT7_COLP3	Q47xt7 colwellia p
1411	55.5	12.4	1919	2	Q4DX29_TRYCR	Q4dx29 trypanosoma
1412	55.5	12.4	1946	2	Q4N6K9_THEPA	Q4n6k9 theileria p
1413	55.5	12.4	5432	2	Q7RPX5_PLAYO	Q7rpx5 plasmodium
1414	55.5	12.4	8647	2	Q7KQP5_DROME	Q7kqp5 drosophila
1415	55.5	12.4	8648	2	Q7KQP6_DROME	Q7kqp6 drosophila
1416	55.5	12.4	8930	2	Q7KQP7_DROME	Q7kqp7 drosophila
1417	55.5	12.4	8943	2	Q9V4F7_DROME	Q9v4f7 drosophila
1418	55.5	12.4	9341	2	Q8I3N9_PLAF7	Q8i3n9 plasmodium

1419	55	12.2	89	2	Q4XAV4_PLACH	Q4xav4 plasmodium
1420	55	12.2	95	2	Q4XCI0_PLACH	Q4xci0 plasmodium
1421	55	12.2	96	2	O07160_MYCLE	O07160 mycobacteri
1422	55	12.2	97	2	Q6R4D6_9GEMI	Q6r4d6 tomato yell
1423	55	12.2	102	2	Q7TAS6_ICMV	Q7tas6 indian cass
1424	55	12.2	132	2	Q4RTY3_TETNG	Q4rty3 tetraodon n
1425	55	12.2	133	2	Q2U4T3_ASPOR	Q2u4t3 aspergillus
1426	55	12.2	136	2	Q6NG01_CORDI	Q6ng01 corynebacte
1427	55	12.2	140	2	Q6CAM9_YARLI	Q6cam9 yarrowia li
1428	55	12.2	148	2	Q6ZNP2_HUMAN	Q6znp2 homo sapien
1429	55	12.2	150	2	Q84FW6_ECOLI	Q84fw6 escherichia
1430	55	12.2	150	2	Q2I7Q1_VIBCH	Q2i7q1 vibrio chol
1431	55	12.2	155	2	Q54CV7_DICDI	Q54cv7 dictyosteli
1432	55	12.2	162	2	Q91M68_9CLOS	Q91m68 citrus tris
1433	55	12.2	164	2	Q2SRY2_MYCCA	Q2sry2 mycoplasma
1434	55	12.2	165	2	Q8WYU1_HUMAN	Q8wyu1 homo sapien
1435	55	12.2	165	2	O32551_ECOLI	O32551 escherichia
1436	55	12.2	165	2	Q2Q017_KLETE	Q2q017 klebsiella
1437	55	12.2	165	2	Q2Q0A3_ENTCL	Q2q0a3 enterobacte
1438	55	12.2	165	2	Q3HYB2_PSEAE	Q3hyb2 pseudomonas
1439	55	12.2	165	2	Q3LUG1_ACIBA	Q3lug1 acinetobact
1440	55	12.2	165	2	Q6DVP0_SHISO	Q6dvp0 shigella so
1441	55	12.2	168	2	Q2W7W7_MAGSA	Q2w7w7 magnetospir
1442	55	12.2	175	2	Q8WLZ7_BOVIN	Q8wlz7 bos taurus
1443	55	12.2	176	2	Q70R01_9HIV1	Q70r01 human immun
1444	55	12.2	179	2	Q7XJ29_PYRCO	Q7xj29 pyrus commu
1445	55	12.2	183	2	O19715_HUMAN	O19715 homo sapien
1446	55	12.2	183	2	Q29922_HUMAN	Q29922 homo sapien
1447	55	12.2	183	2	Q30090_HUMAN	Q30090 homo sapien
1448	55	12.2	183	2	Q30102_HUMAN	Q30102 homo sapien
1449	55	12.2	183	2	Q7YP69_HUMAN	Q7yp69 homo sapien
1450	55	12.2	186	2	Q7PQY2_ANOGA	Q7pqy2 anopheles g
1451	55	12.2	188	2	Q5ZB19_ORYSA	Q5zb19 oryza sativ
1452	55	12.2	205	2	Q4Y0H4_PLACH	Q4y0h4 plasmodium
1453	55	12.2	208	2	Q2INC9_9DELT	Q2inc9 anaeromyxob
1454	55	12.2	218	1	RPE_TREPA	O66107 treponema p
1455	55	12.2	218	2	Q9N490_CAEEL	Q9n490 caenorhabdi
1456	55	12.2	220	2	Q67AK0_HUMAN	Q67ak0 homo sapien
1457	55	12.2	224	2	Q5SP12_HUMAN	Q5sp12 homo sapien
1458	55	12.2	224	2	Q29967_HUMAN	Q29967 homo sapien
1459	55	12.2	224	2	Q8SZB7_DROME	Q8szb7 drosophila
1460	55	12.2	224	2	Q2KC13_RHIET	Q2kc13 rhizobium e
1461	55	12.2	227	2	Q67AJ9_HUMAN	Q67aj9 homo sapien
1462	55	12.2	228	2	P79526_HUMAN	P79526 homo sapien
1463	55	12.2	229	2	Q30075_HUMAN	Q30075 homo sapien
1464	55	12.2	229	2	Q30076_HUMAN	Q30076 homo sapien
1465	55	12.2	229	2	Q30077_HUMAN	Q30077 homo sapien
1466	55	12.2	229	2	Q30078_HUMAN	Q30078 homo sapien
1467	55	12.2	229	2	Q30079_HUMAN	Q30079 homo sapien
1468	55	12.2	229	2	O19707_HUMAN	O19707 homo sapien
1469	55	12.2	229	2	O19712_HUMAN	O19712 homo sapien
1470	55	12.2	229	2	Q9MYH2_HUMAN	Q9myh2 homo sapien
1471	55	12.2	230	2	Q30132_HUMAN	Q30132 homo sapien
1472	55	12.2	230	2	Q4YVZ6_PLABE	Q4yvz6 plasmodium
1473	55	12.2	230	2	Q9LJG5_ARATH	Q9ljg5 arabidopsis
1474	55	12.2	233	2	Q67AK3_HUMAN	Q67ak3 homo sapien
1475	55	12.2	233	2	Q67AK4_HUMAN	Q67ak4 homo sapien
1476	55	12.2	233	2	Q67AK5_HUMAN	Q67ak5 homo sapien
1477	55	12.2	233	2	Q9I607_PSEAE	Q9i607 pseudomonas
1478	55	12.2	234	2	Q67AJ7_HUMAN	Q67aj7 homo sapien
1479	55	12.2	234	2	Q67AJ8_HUMAN	Q67aj8 homo sapien
1480	55	12.2	234	2	Q67AK1_HUMAN	Q67ak1 homo sapien
1481	55	12.2	234	2	Q67AK2_HUMAN	Q67ak2 homo sapien
1482	55	12.2	234	2	Q67AK6_HUMAN	Q67ak6 homo sapien
1483	55	12.2	234	2	Q67AK7_HUMAN	Q67ak7 homo sapien
1484	55	12.2	234	2	Q67AK8_HUMAN	Q67ak8 homo sapien
1485	55	12.2	234	2	Q67AK9_HUMAN	Q67ak9 homo sapien
1486	55	12.2	234	2	Q67AL0_HUMAN	Q67al0 homo sapien
1487	55	12.2	234	2	Q67AL1_HUMAN	Q67al1 homo sapien
1488	55	12.2	234	2	Q67AL2_HUMAN	Q67al2 homo sapien
1489	55	12.2	234	2	Q67AL3_HUMAN	Q67al3 homo sapien
1490	55	12.2	234	2	Q67AL4_HUMAN	Q67al4 homo sapien
1491	55	12.2	234	2	Q67AL5_HUMAN	Q67al5 homo sapien
1492	55	12.2	234	2	Q67AL8_HUMAN	Q67al8 homo sapien
1493	55	12.2	235	2	Q67AJ3_HUMAN	Q67aj3 homo sapien
1494	55	12.2	235	2	Q67AJ4_HUMAN	Q67aj4 homo sapien
1495	55	12.2	240	2	Q45FY0_HUMAN	Q45fy0 homo sapien
1496	55	12.2	248	2	Q2M0J0_DROPS	Q2m0j0 drosophila
1497	55	12.2	249	2	Q5FF04_EHRRG	Q5ff04 ehrlichia r
1498	55	12.2	249	2	Q5HCF5_EHRRW	Q5hcf5 ehrlichia r
1499	55	12.2	250	2	O19711_HUMAN	O19711 homo sapien
1500	55	12.2	250	2	O19714_HUMAN	O19714 homo sapien

ALIGNMENTS

RESULT 1
Q53R12_HUMAN
ID Q53R12_HUMAN PRELIMINARY; PRT; 229 AA.
AC Q53R12;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein FLJ22800.
GN Name=FLJ22800;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Nguyen C., Harris A., Meyer R.;
RT "The sequence of Homo sapiens BAC clone RP11-563C6.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.H.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Wilson R.K.;
RL Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
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CC ---
DR EMBL; AC097662; AAY24253.1; -; Genomic_DNA.
DR Ensembl; ENSG00000168955; Homo sapiens.
DR GO; GO:0016021; C:integral to membrane; IEA.
KW Hypothetical protein.
SQ SEQUENCE 229 AA; 25075 MW; 1718E0594997A1A1 CRC64;

Query Match 100.0%; Score 449; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.6e-42;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 KGPLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGW 60
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Db        111 KGPLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGW 170

Qy         61 RASSFHFDSEENKHRLIHFS 80
              ||||||||||||||||||||
Db        171 RASSFHFDSEENKHRLIHFS 190
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RESULT 2
Q5U609_HUMAN
ID Q5U609_HUMAN PRELIMINARY; PRT; 229 AA.
AC Q5U609;
DT 07-DEC-2004, integrated into UniProtKB/TrEMBL.

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DT   07-DEC-2004, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   TM4SF20 protein.
GN   Name=TM4SF20;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Colon;
RG   NIH MGC Project;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; BC035754; AAH35754.1; -; mRNA.
DR   Ensembl; ENSG00000168955; Homo sapiens.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR008661; L6_membrane.
DR   Pfam; PF05805; L6_membrane; 1.
SQ   SEQUENCE   229 AA;  25137 MW;  B750504AFD7C247D CRC64;

  Query Match            100.0%;  Score 449;  DB 2;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.6e-42;
  Matches   80;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KGPLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 KGPLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGW 170

Qy         61 RASSFHFDSEENKHRLIHFS 80
              ||||||||||||||||||||
Db        171 RASSFHFDSEENKHRLIHFS 190


RESULT 3
Q6UWS1_HUMAN
ID   Q6UWS1_HUMAN   PRELIMINARY;   PRT;   229 AA.
AC   Q6UWS1;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   TCCE518.
GN   ORFNames=UNQ518;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA   Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA   Wood W.I., Godowski P.J., Gray A.M.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY358671; AAQ89034.1; -; mRNA.
DR   Ensembl; ENSG00000168955; Homo sapiens.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR008661; L6_membrane.
DR   Pfam; PF05805; L6_membrane; 1.
SQ   SEQUENCE   229 AA;  25109 MW;  1718ED342C58C903 CRC64;

  Query Match            100.0%;  Score 449;  DB 2;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 4.6e-42;
  Matches   80;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KGPLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 KGPLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGW 170

Qy         61 RASSFHFDSEENKHRLIHFS 80
              ||||||||||||||||||||
Db        171 RASSFHFDSEENKHRLIHFS 190


RESULT 4
Q9H5X9_HUMAN
ID   Q9H5X9_HUMAN   PRELIMINARY;   PRT;   229 AA.
AC   Q9H5X9;
DT   01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2001, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Hypothetical protein FLJ22800.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Ileal mucosa;
RA   Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
RA   Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
RA   Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,
RA   Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
RA   Isogai T., Sugano S.;
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AK026453; BAB15488.1; -; mRNA.
DR   Ensembl; ENSG00000168955; Homo sapiens.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR008661; L6_membrane.
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DR   Pfam; PF05805; L6_membrane; 1.
SQ   SEQUENCE   229 AA;  25103 MW;  B7505D2798B34CDF CRC64;

  Query Match             100.0%;  Score 449;  DB 2;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-42;
  Matches   80;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KGPLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 KGPLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGW 170

Qy         61 RASSFHFDSEENKHRLIHFS 80
              ||||||||||||||||||||
Db        171 RASSFHFDSEENKHRLIHFS 190


RESULT 5
Q3T0Z4_BOVIN
ID   Q3T0Z4_BOVIN   PRELIMINARY;   PRT;   230 AA.
AC   Q3T0Z4;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-MAR-2006, entry version 4.
DE   Hypothetical protein.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Crossbred x Angus; TISSUE=Ileum;
RA   Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,
RA   Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C.,
RA   Wagner L., Bala M., Barbazuk S., Barber S., Babakaiff R., Beland J.,
RA   Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,
RA   Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D.,
RA   Siddiqui A., Holt R., Jones S.J., Marra M.A.;
RL   Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; BC102196; AAI02197.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR008661; L6_membrane.
DR   Pfam; PF05805; L6_membrane; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   230 AA;  25214 MW;  FF48895B0B2F6932 CRC64;

  Query Match              58.8%;  Score 264;  DB 2;  Length 230;
  Best Local Similarity    56.2%;  Pred. No. 2.9e-21;
  Matches   45;  Conservative   16;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 KGPLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGW 60
              :|||:||| ||: ::|||||||::  : |||:|||| ||| | |  | |:  :| |: |
Db        111 EGPLICNSQSNTTSSCEFSLKNLTANYKESFDLQWFFEDSCVPHTDSNNPSITNTTANNW 170

Qy         61 RASSFHFDSEENKHRLIHFS 80
              |  : ||:| ||:||:||||
Db        171 RVYNLHFNSIENQHRIIHFS 190


RESULT 6
Q9CQY8_MOUSE
ID   Q9CQY8_MOUSE   PRELIMINARY;   PRT;   226 AA.
AC   Q9CQY8;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 20.
DE   11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length
DE   enriched library, clone:5033426G15 product:similar to CDNA: FLJ22800
DE   FIS, CLONE KAIA2630 (10 day old male pancreas cDNA, RIKEN full-length
DE   enriched library, clone:1810018L02 product:similar to CDNA: FLJ22800
DE   FIS, CLONE KAIA2630).
GN   Name=Tm4sf20;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
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RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AK017195; BAB30629.1; -; mRNA.
DR   EMBL; AK007532; BAB25093.1; -; mRNA.
DR   Ensembl; ENSMUSG00000026149; Mus musculus.
DR   MGI; MGI:1913511; Tm4sf20.
DR   GO; GO:0005615; C:extracellular space; RCA.
DR   GO; GO:0016021; C:integral to membrane; RCA.
DR   InterPro; IPR008661; L6_membrane.
DR   Pfam; PF05805; L6_membrane; 1.
SQ   SEQUENCE   226 AA;  24760 MW;  3FE6BA1C6A335EAD CRC64;

  Query Match            52.9%;  Score 237.5;  DB 2;  Length 226;
  Best Local Similarity  53.8%;  Pred. No. 2.7e-18;
  Matches   43;  Conservative   13;  Mismatches   21;  Indels    3;  Gaps    2;

Qy          1 KGPLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGW 60
              :|||:||: :||   |||||||:|   |||||| |||| :|  || |  || |: | | |
Db        111 EGPLICNTQANSTVTCEFSLKNLSKFDPESFNLLWFFNGTCVSPTDFKNPTINN-MVSNW 169

Qy         61 RASSFHFDSEENKHRLIHFS 80
                 :   : :|||::||: |||
Db        170 KIP--NSNSEEDRHRIFHFS 187


RESULT 7
Q9D3R0_MOUSE
ID   Q9D3R0_MOUSE   PRELIMINARY;   PRT;   226 AA.
AC   Q9D3R0;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 21.
DE   11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length
DE   enriched library, clone:5033405M13 product:similar to CDNA: FLJ22800
DE   FIS, CLONE KAIA2630.
GN   Name=Tm4sf20; Synonyms=1810018L02Rik;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
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RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
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RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
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RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
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RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
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RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
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RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
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RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
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RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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CC ---
DR EMBL; AK017154; BAB30618.1; -; mRNA.
DR Ensembl; ENSMUSG00000026149; Mus musculus.
DR MGI; MGI:1913511; 1810018L02Rik.
DR MGI; MGI:1913511; Tm4sf20.

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DR   GO; GO:0005615; C:extracellular space; RCA.
DR   GO; GO:0016021; C:integral to membrane; RCA.
DR   InterPro; IPR008661; L6_membrane.
DR   Pfam; PF05805; L6_membrane; 1.
SQ   SEQUENCE   226 AA;  24714 MW;  8BE6BE5C2D1EDDC0 CRC64;

  Query Match             52.9%;  Score 237.5;  DB 2;  Length 226;
  Best Local Similarity   53.8%;  Pred. No. 2.7e-18;
  Matches   43;  Conservative   13;  Mismatches   21;  Indels    3;  Gaps    2;

Qy          1 KGPLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGW 60
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Qy         61 RASSFHFDSEENKHRLIHFS 80
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Db        170 KIP--NSNSEEDRHRIFHFS 187


RESULT 8
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ID   Q9D3Q0_MOUSE   PRELIMINARY;   PRT;   226 AA.
AC   Q9D3Q0;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 21.
DE   11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length
DE   enriched library, clone:5033430P14 product:similar to CDNA: FLJ22800
DE   FIS, CLONE KAIA2630.
GN   Name=Tm4sf20; Synonyms=1810018L02Rik;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
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RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
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RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
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RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AK017209; BAB30635.1; -; mRNA.
DR   Ensembl; ENSMUSG00000026149; Mus musculus.
DR   MGI; MGI:1913511; 1810018L02Rik.
DR   MGI; MGI:1913511; Tm4sf20.
DR   GO; GO:0005615; C:extracellular space; RCA.
DR   GO; GO:0016021; C:integral to membrane; RCA.
DR   InterPro; IPR008661; L6_membrane.
DR   Pfam; PF05805; L6_membrane; 1.
SQ   SEQUENCE   226 AA;  24786 MW;  3FE6BA06703344B7 CRC64;

  Query Match             51.6%;  Score 231.5;  DB 2;  Length 226;
  Best Local Similarity   52.5%;  Pred. No. 1.3e-17;
  Matches   42;  Conservative   13;  Mismatches   22;  Indels    3;  Gaps    2;

Qy          1 KGPLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGW 60
              :|||:||: :||   |||||||:|   |||||| |||| :|  || |  || |: |   |
Db        111 EGPLICNTQANSTVTCEFSLKNLSKFDPESFNLLWFFNGTCVSPTDFKNPTINN-MVINW 169

Qy         61 RASSFHFDSEENKHRLIHFS 80
              :    : :|||::||: |||
Db        170 KIP--NSNSEEDRHRIFHFS 187


RESULT 9
Q4KL96_XENLA
ID   Q4KL96_XENLA   PRELIMINARY;   PRT;   242 AA.
AC   Q4KL96;
DT   02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT   02-AUG-2005, sequence version 1.
DT   07-FEB-2006, entry version 2.
DE   Hypothetical protein (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; BC099340; AAH99340.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
KW   Hypothetical protein.
FT   NON_TER       1       1
SQ   SEQUENCE   242 AA;  25805 MW;  286B61472781616E CRC64;

  Query Match             20.7%;  Score 93;  DB 2;  Length 242;
  Best Local Similarity   37.8%;  Pred. No. 0.052;
  Matches   17;  Conservative   10;  Mismatches   16;  Indels    2;  Gaps    1;

Qy          1 KGPLMCNSPSNSNANCEFSLKNIS--DIHPESFNLQWFFNDSCAP 43
              ||||:| : ||  ::|:::| |:|         |:| |  | :| |
Db        125 KGPLICETGSNELSSCDYTLANLSSNSFKELQFDLAWLRNTTCIP 169


RESULT 10
Q66S52_9UROC
ID   Q66S52_9UROC   PRELIMINARY;   PRT;   277 AA.
AC   Q66S52;
DT   11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2004, sequence version 1.
DT   07-FEB-2006, entry version 12.
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DE   Chymotrypsin B-like protein.
GN   ORFNames=008-07;
OS   Oikopleura dioica.
OC   Eukaryota; Metazoa; Chordata; Urochordata; Appendicularia;
OC   Oikopleuridae; Oikopleura.
OX   NCBI_TaxID=34765;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15343333; DOI=10.1038/nature02709;
RA   Seo H.C., Edvardsen R.B., Maeland A.D., Bjordal M., Jensen M.F.,
RA   Hansen A., Flaat M., Weissenbach J., Lehrach H., Wincker P.,
RA   Reinhardt R., Chourrout D.;
RT   "Hox cluster disintegration with persistent anteroposterior order of
RT   expression in Oikopleura dioica.";
RL   Nature 431:67-71(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15649342; DOI=10.1016/j.cub.2004.12.010;
RA   Edvardsen R.B., Seo H.C., Jensen M.F., Mialon A., Mikhaleva J.,
RA   Bjordal M., Cartry J., Reinhardt R., Weissenbach J., Wincker P.,
RA   Chourrout D.;
RT   "Remodelling of the homeobox gene complement in the tunicate
RT   Oikopleura dioica.";
RL   Curr. Biol. 15:R12-R13(2005).
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CC   ---------------------------------------------------------------------
DR   EMBL; AY613856; AAT47850.1; -; Genomic_DNA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis; IEA.
DR   InterPro; IPR001254; Peptidase_S1_S6.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   Pfam; PF00089; Trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Protease; Serine protease.
SQ   SEQUENCE   277 AA;  30581 MW;  2BC4FEBA5AA27C8C CRC64;

  Query Match            18.6%;  Score 83.5;  DB 2;  Length 277;
  Best Local Similarity  32.8%;  Pred. No. 0.71;
  Matches   22;  Conservative    9;  Mismatches   23;  Indels   13;  Gaps    3;

Qy          2 GPLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDSCAP--PTGFNKPTSNDTMASG 59
              |||:| : |: | |  | :  :|          :   || |  |||| |    : : |
Db        214 GPLVC-ARSSGNMNTRFEISGVSS----------WSGQSCYPANPTGFMKGPIRNKLKSC 262

Qy         60 WRASSFH 66
              :| | ||
Db        263 YRFSDFH 269


RESULT 11
Q9PT67_XENLA
ID   Q9PT67_XENLA   PRELIMINARY;   PRT;   342 AA.
AC   Q9PT67;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT   01-MAY-2000, sequence version 1.
DT   07-FEB-2006, entry version 25.
DE   XFD-12'' protein.
GN   Name=xfd-12'';
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20025545; PubMed=10559492; DOI=10.1016/S0925-4773(99)00195-1;
RA   Soelter M., Koester M., Hollemann T., Brey A., Pieler T., Knoechel W.;
RT   "Characterization of a subfamily of related winged helix genes, XFD-
RT   12/12'/12'' (XFLIP), during Xenopus embryogensis.";
RL   Mech. Dev. 89:161-165(1999).
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ242678; CAB44730.1; -; mRNA.
DR   HSSP; Q63245; 2HDC.
DR   SMR; Q9PT67; 96-192.
DR   TRANSFAC; T04174; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0006350; P:transcription; IEA.
DR   InterPro; IPR001766; TF_Fork_head.
DR   InterPro; IPR011991; Wing_hlx_DNA_bd.
DR   Pfam; PF00250; Fork_head; 1.
DR   PRINTS; PR00053; FORKHEAD.
DR   ProDom; PD000425; TF_Fork_head; 1.
DR   SMART; SM00339; FH; 1.
DR   PROSITE; PS00657; FORK_HEAD_1; 1.
DR   PROSITE; PS00658; FORK_HEAD_2; 1.
DR   PROSITE; PS50039; FORK_HEAD_3; 1.
KW   DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SQ   SEQUENCE   342 AA;  38498 MW;  665D66F09F27F4FD CRC64;

  Query Match            18.5%;  Score 83;  DB 2;  Length 342;
  Best Local Similarity  36.5%;  Pred. No. 1;
  Matches   19;  Conservative    7;  Mismatches   14;  Indels   12;  Gaps    2;

Qy          7 NSPSNSNANCEFSLKNI------SDIHPESFNLQWFFND------SCAPPTG 46
              | ||||:: | ||::||      : |  |||  | :|        |  |:|
Db        270 NHPSNSHSKCSFSIENIMGETKEPEKHLTSFNQNWNYNHLLQSSRLCLLPSG 321


RESULT 12
Q695C3_PICMA
ID   Q695C3_PICMA   PRELIMINARY;   PRT;   142 AA.
AC   Q695C3;
DT   13-SEP-2004, integrated into UniProtKB/TrEMBL.
DT   13-SEP-2004, sequence version 1.
DT   07-FEB-2006, entry version 8.
DE   NAM protein (Fragment).
GN   Name=Sb29;
OS   Picea mariana (Black spruce).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX   NCBI_TaxID=3335;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Bouille M., Bousquet J.;
RT   "Trans-species shared polymorphisms at orthologous nuclear gene loci
RT   among distant species in the conifer Picea (Pinaceae): implications
RT   for the long-term maintenance of genetic diversity in trees.";
RL   Am. J. Bot. 91:63-73(2005).
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CC   ---------------------------------------------------------------------
DR   EMBL; AY611037; AAT88035.1; -; Genomic_DNA.
FT   NON_TER       1      1
SQ   SEQUENCE   142 AA;  15972 MW;  96380ADB9E498344 CRC64;

  Query Match            18.3%;  Score 82;  DB 2;  Length 142;
  Best Local Similarity  29.7%;  Pred. No. 0.48;
  Matches   30;  Conservative   14;  Mismatches   27;  Indels   30;  Gaps    7;

Qy          5 MCNSPSNSNANCEFSLKNISD----------IHP--ESFNLQW----------FFND- 39
              :| || |||  |  :|   ||          :|   | | ||              ||
Db         14 LCVSPMNSNI-CLQNLDFFSDSTLKAPVQNTAFNPIYSSINHQWTNCNSTDLMSGLHNDS 72
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Qy          40 SCAPPTGFNKPTS-NDTMASGWRASSFHFDSEENKHRLIHF 79
               ||: |: |::| |  : : | :|  :|   |:| :  | :|
Db          73 SCSKPSSFSEPISEKEEVQSSFRLENF---SQEQQQSLFNF 110


RESULT 13
O65095_PICMA
ID   O65095_PICMA   PRELIMINARY;   PRT;   148 AA.
AC   O65095;
DT   01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT   01-AUG-1998, sequence version 1.
DT   07-FEB-2006, entry version 17.
DE   ATAF1-like protein (Fragment).
GN   Name=Sb29;
OS   Picea mariana (Black spruce).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX   NCBI_TaxID=3335;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98278823; PubMed=9611216;
RA   Perry D.J., Bousquet J.;
RT   "Sequence-tagged-site (STS) markers of arbitrary genes: development,
RT   characterization and analysis of linkage in black spruce.";
RL   Genetics 149:1089-1098(1998).
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CC   ---------------------------------------------------------------------
DR   EMBL; AF051748; AAC32165.1; -; Genomic_DNA.
FT   NON_TER       1       1
SQ   SEQUENCE   148 AA;  16658 MW;  78091616816D081A CRC64;

  Query Match             18.3%;  Score 82;  DB 2;  Length 148;
  Best Local Similarity   29.7%;  Pred. No. 0.5;
  Matches   30;  Conservative   14;  Mismatches   27;  Indels   30;  Gaps    7;

Qy           5 MCNSPSNSNANCEFSLKNISD-----------IHP--ESFNLQW-----------FFND- 39
               :| || ||| |  :|   ||            :|   | | ||             ||
Db          20 LCVSPMNSNI-CLQNLDFFSDSTLKAPVQNTAFNPIYSSINHQWTNCNSTDLMSGLHNDS 78

Qy          40 SCAPPTGFNKPTS-NDTMASGWRASSFHFDSEENKHRLIHF 79
               ||: |: |::| |  : : | :|  :|   |:| :  | :|
Db          79 SCSKPSSFSEPISEKEEVQSSFRLENF---SQEQQQSLFNF 116


RESULT 14
Q9PRJ8_XENLA
ID   Q9PRJ8_XENLA   PRELIMINARY;   PRT;   352 AA.
AC   Q9PRJ8;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT   01-MAY-2000, sequence version 1.
DT   07-FEB-2006, entry version 26.
DE   XFD-12 protein (Fox protein) (Winged helix protein).
GN   Name=xfd-12; Synonyms=FoxD5a, foxD5a;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20025545; PubMed=10559492; DOI=10.1016/S0925-4773(99)00195-1;
RA   Soelter M., Koester M., Hollemann T., Brey A., Pieler T., Knoechel W.;
RT   "Characterization of a subfamily of related winged helix genes, XFD-
RT   12/12''/12'' (XFLIP), during Xenopus embryogensis.";
RL   Mech. Dev. 89:161-165(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15555577; DOI=10.1016/j.bbrc.2004.10.177;
RA   Schon C., Koster M., Knochel W.;
RT   "A downstream enhancer is essential for Xenopus FoxD5 transcription.";
RL   Biochem. Biophys. Res. Commun. 325:1360-1366(2004).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21294976; PubMed=11401404; DOI=10.1006/dbio.2001.0191;
RA   Sullivan S.A., Akers L., Moody S.A.;
RT   "foxD5a, a Xenopus winged helix gene, maintains an immature neural
RT   ectoderm via transcriptional repression that is dependent on the C-
RT   terminal domain.";
RL   Dev. Biol. 232:439-457(2001).
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ242676; CAB44728.1; -; mRNA.
DR   EMBL; AJ850135; CAH64537.1; -; Genomic_DNA.
DR   EMBL; AF162782; AAD47811.1; -; mRNA.
DR   HSSP; Q63245; 2HDC.
DR   SMR; Q9PRJ8; 96-192.
DR   TRANSFAC; T04172; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0006350; P:transcription; IEA.
DR   InterPro; IPR001766; TF_Fork_head.
DR   InterPro; IPR011991; Wing_hlx_DNA_bd.
DR   Pfam; PF00250; Fork_head; 1.
DR   PRINTS; PR00053; FORKHEAD.
DR   ProDom; PD000425; TF_Fork_head; 1.
DR   SMART; SM00339; FH; 1.
DR   PROSITE; PS00657; FORK_HEAD_1; 1.
DR   PROSITE; PS00658; FORK_HEAD_2; 1.
DR   PROSITE; PS50039; FORK_HEAD_3; 1.
KW   DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SQ   SEQUENCE   352 AA;  39719 MW;  24F3DA0EA2A6891C CRC64;

  Query Match             17.8%;  Score 80;  DB 2;  Length 352;
  Best Local Similarity   33.3%;  Pred. No. 2.3;
  Matches   19;  Conservative    8;  Mismatches   18;  Indels   12;  Gaps    2;

Qy           7 NSPSNSNANCEFSLKNI------SDIHPESFNLQWFFN------DSCAPPTGFNKPT 51
               | |:|| : | ||::||       : : :|||  | :|       ||  |   |  |
Db         274 NHPNNSQSKCSFSIENIMRKPKEPEPNIQSFNSHWNYNHVFQRPSSCLLPAVLNLST 330


RESULT 15
Q70W02_CIOIN
ID   Q70W02_CIOIN   PRELIMINARY;   PRT;   808 AA.
AC   Q70W02;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   SoxE protein (Fragment).
GN   Name=soxE;
OS   Ciona intestinalis.
OC   Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC   Phlebobranchia; Cionidae; Ciona.
OX   NCBI_TaxID=7719;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Leveugle M., Prat K., Popovici C., Birnbaum D., Coulier F.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AJ534323; CAD58841.1; -; mRNA.
DR   Ensembl; ENSCING00000001019; Ciona intestinalis.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 1.
DR   SMART; SM00398; HMG; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 1.
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FT   NON_TER       1      1
SQ   SEQUENCE   808 AA;  89828 MW;  41DE23173A877B5E CRC64;

  Query Match             17.6%;  Score 79;  DB 2;  Length 808;
  Best Local Similarity   32.2%;  Pred. No. 8;
  Matches   29;  Conservative   13;  Mismatches   26;  Indels   22;  Gaps    6;

Qy          5 MCNSPSNSNANCEFSLKNISDI-HPESFNLQWFFNDS------CAPPTGFN-----KPTS 52
              :|:|||| :   : |: || :: | |    |  ::||      |:|||  |     || |
Db        351 VCHSPSNQSPPHQGSITNIYEVMHRE----QRGYHDSPDATVPCSPPTAINMDESKKPHS 406

Qy         53 -----NDTMAS-GWRASSFHFDSEENKHRL 76
                    | :  |   | ||    || : | :
Db        407 TLHSRNSSFGSKQQRGSSIDLTSECSSHSM 436


Search completed: November 21, 2006, 20:10:18
Job time : 166.187 secs
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OM protein - protein search, using sw model
Run on:         November 21, 2006, 20:10:39 ; Search time 20.367 Seconds
                                        (without alignments)
                                        404.080 Million cell updates/sec
Title:          US-10-063-553-48_COPY_32_49
Perfect score:  93
Sequence:       1 VSLVEEDQFSQNPISCFE 18
Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5
Searched:       2589679 seqs, 457216429 residues
Total number of hits satisfying chosen parameters:      2589679
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries
Database :       A_Geneseq_8:*
                1:  geneseqp1980s:*
                2:  geneseqp1990s:*
                3:  geneseqp2000s:*
                4:  geneseqp2001s:*
                5:  geneseqp2002s:*
                6:  geneseqp2003as:*
                7:  geneseqp2003bs:*
                8:  geneseqp2004s:*
     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.
                                SUMMARIES
  No.   Score  Match Length DB  ID                          Description
RESULT 1
ID   AAY66703 standard; protein; 229 AA.
DE   Membrane-bound protein PRO994.
PN   WO9963088-A2.
PD   09-DEC-1999.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 3;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 2
ID   AAU29122 standard; protein; 229 AA.
DE   Human PRO polypeptide sequence #99.
PN   WO200168848-A2.
PD   20-SEP-2001.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 4;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 3
ID   AAB87549 standard; protein; 229 AA.
DE   Human PRO994.
PN   WO200116318-A2.
PD   08-MAR-2001.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 4;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 4
ID   AAB65226 standard; protein; 229 AA.
DE   Human PRO994 (UNQ518) protein sequence SEQ ID NO:258.
PN   WO200073454-A1.
PD   07-DEC-2000.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 4;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 5
ID   ABG95874 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein PRO994.
PN   US2002119130-A1.
PD   29-AUG-2002.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 5;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 6
ID   ABU58498 standard; protein; 229 AA.
DE   Human PRO polypeptide #99.
PN   US2003027272-A1.
PD   06-FEB-2003.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 7
ID   ABU88046 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003032127-A1.
PD   13-FEB-2003.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 8
ID   ABU84361 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003032112-A1.
PD   13-FEB-2003.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 9
ID   ABR66235 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003027278-A1.
PD   06-FEB-2003.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 10
ID   ABR65625 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003036159-A1.
PD   20-FEB-2003.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 11
ID   ABU99565 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003040070-A1.
PD   27-FEB-2003.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 12
ID   ABU58041 standard; protein; 229 AA.
DE   Human PRO polypeptide #73.
PN   US2003027163-A1.
PD   06-FEB-2003.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 13
ID   ABU59119 standard; protein; 229 AA.
DE   Novel human secreted or transmembrane protein PRO994.
PN   US2002132252-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 14
ID   ABU82631 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein PRO994.
PN   US2003032023-A1.
PD   13-FEB-2003.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 15
ID   ABU82804 standard; protein; 229 AA.
DE   Human PRO polypeptide #99.
PN   US2003032113-A1.
PD   13-FEB-2003.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 16
ID   ABU89925 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003036147-A1.
PD   20-FEB-2003.
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Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 17
ID ABR68174 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 18
ID ABU60550 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, #103.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 19
ID ABU96227 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 20
ID ABU92658 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 21
ID ABO08735 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 22
ID ABO02787 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 23
ID ABR74941 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 24
ID ABR94703 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 25
ID ABU13932 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 26
ID ABU85676 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 27
ID ABU98836 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 28
ID ABU98051 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 29
ID ABU91757 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 30
ID ABU89450 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 31
ID ABU86291 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 32
ID ABU67504 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 33
ID ABU80532 standard; protein; 229 AA.
DE Human PRO protein #99.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 34
ID ABU72517 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 35
ID ABU90899 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 36
ID ABO33958 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.

PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 37
ID ABR99450 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 38
ID ABR98840 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 39
ID ABO16363 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 40
ID ABR92263 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 41
ID ABO18904 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 42
ID ABR78325 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 43
ID ABU71975 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 44
ID ABU85061 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 45
ID ABO00200 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 46
ID ABO11532 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 47
ID ABO02177 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 48
ID ABU88751 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 49
ID ABU83446 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 50
ID ABO06247 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 51
ID ABR59283 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 52
ID ABO09345 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 53
ID ABO19209 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 54
ID ABO11227 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 55
ID ABR66845 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 56
ID ABO16058 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040060-A1.
PD 27-FEB-2003.

Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 57
ID ABO13764 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 58
ID ABU71529 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 59
ID ABU65667 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, SEQ ID 198.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 60
ID ABO07515 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 61
ID ABO03702 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 62
ID ABR67150 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 63
ID ABO15753 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 64
ID ABU56034 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, PRO994.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 65
ID ABU72310 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 66
ID ABU65362 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 67
ID ABU95307 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 68
ID ABU71210 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 69
ID ABO07820 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 70
ID ABR70061 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 71
ID ABR69394 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 72
ID ABO01535 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 73
ID ABU81337 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 74
ID ABR60134 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 75
ID ABU90983 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 76
ID ABR67869 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027269-A1.
PD 06-FEB-2003.

Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 77
ID ABR65257 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 78
ID ABR68479 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 79
ID ABR71891 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 80
ID ABU59266 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, #103.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 81
ID ABU85371 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 82
ID ABU89061 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 83
ID ABU83141 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 84
ID ABU94997 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 85
ID ABU90545 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 86
ID ABU84056 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 87
ID ABU93707 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 88
ID ABO25963 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 89
ID ABR64952 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 90
ID ABO27304 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO994.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 91
ID ABR68784 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 92
ID ABO06600 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 93
ID ABR99145 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 94
ID ABU57029 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 95
ID ABU85981 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 96
ID ABU82268 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;

RESULT 97
ID ABU87279 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 98
ID ABU83751 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 99
ID ABO08125 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 100
ID ABU92499 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 101
ID ABU81836 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 102
ID ABU66000 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 103
ID ABU81169 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 104
ID ABR59829 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 105
ID ABU94017 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 106
ID ABU99870 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 107
ID ABR66540 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 108
ID ABR90958 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 109
ID ABO53284 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 110
ID ABU58972 standard; protein; 229 AA.
DE Human sectreted/transmembrane protein, #103.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 111
ID ABU94385 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 112
ID ABU79267 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 113
ID ABU86596 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 114
ID ABU86901 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 115
ID ABU94690 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 116
ID ABO04617 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 117

ID ABR70366 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 118
ID ABU92350 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 119
ID ABU98531 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 120
ID ABR65930 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 121
ID ABR64647 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 122
ID ABU59415 standard; protein; 229 AA.
DE Novel human secreted or transmembrane protein PRO812.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 123
ID ABU79572 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 124
ID ABU92963 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 125
ID ABU95922 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 126
ID ABU91142 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 127
ID ABU90235 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 128
ID ABO09650 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 129
ID ABO10922 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 130
ID ABR70976 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 131
ID ABU98286 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 132
ID ABU87584 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 133
ID ABU91452 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 134
ID ABU89291 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 135
ID ABU84666 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 136
ID ABR69756 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 137
ID ABU80133 standard; protein; 229 AA.
DE Human PRO protein #99.
PN US2003036139-A1.

PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 138
ID ABU82498 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 139
ID ABU92181 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 140
ID ABU93402 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 141
ID ABO09955 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 142
ID ABO09040 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 143
ID ABU96462 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 144
ID ABU10887 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 145
ID ABU10608 standard; protein; 229 AA.
DE Human secreted/transmembrane protein #99.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 146
ID ABU81639 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 147
ID ABU72132 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 148
ID ABU95617 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 149
ID ABU96826 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 150
ID ABR70671 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 151
ID ABO05022 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 152
ID ABO08430 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 153
ID ABU88578 standard; protein; 229 AA.
DE Human secreted and transmembrane polypeptide PRO994.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 154
ID ABO34092 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 155
ID ABO05637 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 156
ID ABR74026 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 157

ID ABR95618 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 158
ID ABR80915 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 159
ID ABR81220 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 160
ID ABM00916 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 161
ID ABR88518 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 162
ID ABM77339 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 163
ID ABO28823 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 164
ID ABO31568 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 165
ID ABM07985 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 166
ID ABO40465 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 167
ID ABO35890 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 168
ID ABO44029 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 169
ID ADA77950 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 170
ID ABM24824 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 171
ID ABO03092 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 172
ID ABR90348 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 173
ID ABM17262 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 174
ID ABR95008 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 175
ID ABR95313 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;

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  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 176
ID   ADB17105 standard; protein; 229 AA.
DE   Human transmembrane PRO polypeptide (SeqID 48).
PN   US2003050462-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 177
ID   ABO21551 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003054471-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 178
ID   ABR97815 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003064452-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 179
ID   ABR87603 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068705-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 180
ID   ABM77644 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003054473-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 181
ID   ABM27874 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003064440-A1.
PD   03-APR-2003.
  Query Match             100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 182
ID   ABM06155 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068704-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 183
ID   ABM03661 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068722-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 184
ID   ABM35112 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003073183-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 185
ID   ABM26349 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003104549-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 186
ID   ABO48131 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003049749-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 187
ID   ABR92873 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003064462-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 188
ID   ABO24634 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003065159-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 189
ID   ADA37769 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein PRO994.
PN   US2003008297-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 190
ID   ABM11645 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003064447-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 191
ID   ABM02746 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003073184-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 192
ID   ABM16042 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003064463-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 193
ID   ABO27603 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003064451-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 194
ID   ABM29094 standard; protein; 229 AA.
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DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068721-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 195
ID   ABM07070 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068699-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 196
ID   ABM21164 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068707-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 197
ID   ABM09510 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003073175-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 198
ID   ABO41380 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003068695-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 199
ID   ABO36195 standard; protein; 229 AA.
DE   Human PRO polypeptide #99.
PN   US2003068703-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 200
ID   ABO43724 standard; protein; 229 AA.
DE   Human PRO polypeptide #99.
PN   US2003068732-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 201
ID   ABM76424 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003082717-A1.
PD   01-MAY-2003.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 202
ID   ABM76120 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003104548-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 203
ID   ABM25739 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003104542-A1.
PD   05-JUN-2003.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 204
ID   ABM26044 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003104543-A1.
PD   05-JUN-2003.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 205
ID   ADA21455 standard; protein; 229 AA.
DE   Human secreted/transmembrane polypeptide PRO994.
PN   US2003054404-A1.
PD   20-MAR-2003.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 206
ID   ABO03397 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003036127-A1.
PD   20-FEB-2003.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 207
ID   ABQ02482 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003040061-A1.
PD   27-FEB-2003.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 208
ID   ABO44262 standard; protein; 229 AA.
DE   Human secreted/transmembrane polypeptide PRO 994.
PN   US2003018172-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 209
ID   ABR90653 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003036130-A1.
PD   20-FEB-2003.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 210
ID   ABR73721 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003054468-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 211
ID   ABO16973 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003054470-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 212
ID   ABR94398 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003044917-A1.
PD   06-MAR-2003.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 213
ID   ABR75905 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003044929-A1.
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PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 214
ID ABR71281 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 215
ID ABR93178 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 216
ID ABR93483 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 217
ID ADA10242 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, PRO994.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 218
ID ABR87908 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 219
ID ABO27908 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 220
ID ABO30043 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 221
ID ABO33252 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 222
ID ABM04940 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 223
ID ABM08900 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 224
ID ABO36500 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 225
ID ABO35585 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 226
ID ABO39550 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 227
ID ABM10425 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 228
ID ABM11950 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 229
ID ABO52096 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 230
ID ABO52401 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 231
ID ADA19910 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;

RESULT 232
ID ABO23719 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 233
ID ADB17293 standard; protein; 229 AA.
DE Human transmembrane PRO polypeptide (SeqID 48).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 234
ID ADA17786 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 235
ID ABR97205 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 236
ID ABR86993 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 237
ID ABM11035 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 238
ID ABM28179 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 239
ID ABO32178 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 240
ID ABM15305 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 241
ID ABM06460 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 242
ID ABM04271 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 243
ID ABM22384 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 244
ID ABM07680 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 245
ID ABO40770 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 246
ID ABM35417 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 247
ID ABM33180 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 248
ID ABO52706 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 249
ID ABO50266 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 250
ID ABU99260 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040055-A1.
PD 27-FEB-2003.

Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 251
ID ABO04312 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 252
ID ABO05942 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 253
ID ABM18482 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 254
ID ADA27894 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 255
ID ABR97510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 256
ID ABR80610 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 257
ID ABM01221 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 258
ID ABR88823 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 259
ID ABM13475 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 260
ID ABM20859 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 261
ID ABO41990 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 262
ID ABO42600 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 263
ID ABM10120 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 264
ID ABO38635 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 265
ID ABM32875 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 266
ID ABM22689 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 267
ID ABM74900 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 268
ID ADA79742 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 269
ID ABR96290 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;

RESULT 270
ID ABM02441 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 271
ID ABR86383 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 272
ID ABR86688 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 273
ID ABM16652 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 274
ID ABM29704 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 275
ID ABO29128 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 276
ID ABM23909 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 277
ID ABM23299 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 278
ID ABM22079 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 279
ID ABO37720 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 280
ID ABM28484 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 281
ID ABM28789 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 282
ID ABM66433 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 283
ID ABM75815 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 284
ID ABM34095 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 285
ID ABM34400 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 286
ID ABO20331 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 287
ID ABO21246 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 288
ID ABO22161 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

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  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 289
ID   ADA20082 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003055222-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 290
ID   ABO34190 standard; protein; 229 AA.
DE   Human secreted/transmembrane polypeptide PRO 994.
PN   US2003060601-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 291
ID   ABR96595 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003054460-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 292
ID   ADA94474 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein PRO994.
PN   US2003059832-A1.
PD   27-MAR-2003.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 293
ID   ABR85773 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003049753-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 294
ID   ABR99755 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003049763-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 295
ID   ABM00306 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003073172-A1.
PD   17-APR-2003.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 296
ID   ABM00611 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003073172-A1.
PD   17-APR-2003.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 297
ID   ABO29738 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003068700-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 298
ID   ABM23604 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068736-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 299
ID   ABM29399 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068679-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 300
ID   ABO38330 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003068767-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 301
ID   ABO45630 standard; protein; 229 AA.
DE   Human PRO polypeptide #99.
PN   US2003073182-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 302
ID   ABM20554 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003104557-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 303
ID   ADA81469 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003092121-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 304
ID   ABO16668 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003027276-A1.
PD   06-FEB-2003.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 305
ID   ABO18294 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003044920-A1.
PD   06-MAR-2003.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 306
ID   ABO22721 standard; protein; 229 AA.
DE   Human PRO polypeptide #99.
PN   US2003027265-A1.
PD   06-FEB-2003.
  Query Match           100.0%;  Score 93;  DB 6;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 307
ID   ABO23026 standard; protein; 229 AA.
DE   Human PRO polypeptide #99.
PN   US2003054461-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
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Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 308
ID ABR92568 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 309
ID ABR81525 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 310
ID ABM77949 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 311
ID ABR89738 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 312
ID ABM26654 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 313
ID ABM13780 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 314
ID ABO28518 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 315
ID ABO30348 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 316
ID ABM07375 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 317
ID ABM03966 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 318
ID ABO37110 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 319
ID ABO41685 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 320
ID ABO35280 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 321
ID ABM25129 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 322
ID ABO47521 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 323
ID ABO47826 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 324
ID ABO48436 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 325
ID ABO51486 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 326
ID ABO51791 standard; protein; 229 AA.
DE Human PRO polypeptide #99.

PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 327
ID ABO50571 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 328
ID ABR79695 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 329
ID ABM16957 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 330
ID ABO17989 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 331
ID ABO20941 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 332
ID ABR96900 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 333
ID ADA38699 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 334
ID ABM12255 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 335
ID ABM16347 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 336
ID ABM24214 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 337
ID ABM14695 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 338
ID ABM04576 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 339
ID ABM06765 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 340
ID ABM09205 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 341
ID ABO39245 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 342
ID ABM75510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US20031045545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 343
ID ABM25434 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US20031045541-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 344
ID ABM19944 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US20031045554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 345
ID ABO46850 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049762-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 346
ID ABO47155 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 347
ID ADA83267 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 348
ID ABR71586 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 349
ID ABR72196 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 350
ID ABR98535 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 351
ID ABO06905 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 352
ID ABR84858 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 353
ID ABR73416 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 354
ID ABR76510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 355
ID ABR73111 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 356
ID ABM18177 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 357
ID ABO20636 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 358
ID ABO25379 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 359
ID ABO25684 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 360
ID ABR94093 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 361
ID ADA92820 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 362
ID ABR80000 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 363
ID ABM11340 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 364
ID ABO32947 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;

RESULT 365
ID ABO30653 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 366
ID ABO30958 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 367
ID ABM27264 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 368
ID ABM30009 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 369
ID ABM05545 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 370
ID ABM15610 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 371
ID ABM08595 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 372
ID ABO42295 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 373
ID ABO38025 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 374
ID ABO45935 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 375
ID ABM66738 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 376
ID ADB20310 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 377
ID ABM19639 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 378
ID ABO49351 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 379
ID ABO49656 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 380
ID ADA78562 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 381
ID ABR88213 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 382
ID ADA00379 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO 994.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 383
ID ABM26959 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.

PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 384
ID ABM03356 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 385
ID ABO39855 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 386
ID ABO49961 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 387
ID ABO50876 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 388
ID ABO05332 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 389
ID ABR74636 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 390
ID ABR77115 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 391
ID ABM17872 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 392
ID ABR95923 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 393
ID ABO21856 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 394
ID ABO20026 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 395
ID ABO24329 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 396
ID ABR86078 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 397
ID ABM10730 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 398
ID ABM76729 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 399
ID ABR89433 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 400
ID ABM12560 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 401
ID ABM05850 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 402
ID ABO34975 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068728-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 403
ID ABM03051 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 404
ID ABM19029 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 405
ID ABM19334 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 406
ID ABO46545 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 407
ID ABO49046 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 408
ID ABR69089 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 409
ID ABR89128 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 410
ID ABR72501 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 411
ID ABR74331 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;

RESULT 412
ID ABO18599 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 413
ID ABR80305 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 414
ID ABM01526 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 415
ID ABM02136 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 416
ID ABR87298 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 417
ID ABM12865 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 418
ID ABM30619 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 419
ID ABM24519 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 420
ID ABO29433 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 421
ID ABO31263 standard; protein; 229 AA.

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DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003068710-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 422
ID   ABM14390 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068686-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 423
ID   ABM09815 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003073178-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 424
ID   ABO38940 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003068774-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 425
ID   ABM34705 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003104538-A1.
PD   05-JUN-2003.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 426
ID   ABO51181 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003049781-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 427
ID   ABO04007 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003036158-A1.
PD   20-FEB-2003.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 428
ID   ABO10477 standard; protein; 229 AA.
DE   Human PRO polypeptide #99.
PN   US2003036151-A1.
PD   20-FEB-2003.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 429
ID   ABO53178 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein PRO994.
PN   US2003044806-A1.
PD   06-MAR-2003.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 430
ID   ABR77720 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003040067-A1.
PD   27-FEB-2003.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 431
ID   ABR78930 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003054456-A1.
PD   20-MAR-2003.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 432
ID   ABO24024 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003054482-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 433
ID   ABR93788 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003054457-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 434
ID   ABM01831 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003059883-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 435
ID   ABM78254 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003049764-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 436
ID   ABR90043 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003073177-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 437
ID   ADA22381 standard; protein; 229 AA.
DE   Human secreted/transmembrane polypeptide PRO994.
PN   US2003040473-A1.
PD   27-FEB-2003.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 438
ID   ABM27569 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003064442-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 439
ID   ABM13170 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003064450-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-07;
RESULT 440
ID   ABO31873 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
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PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 441
ID ABM14085 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 442
ID ABM08290 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 443
ID ABO40160 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 444
ID ABM74595 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 445
ID ABM33790 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 446
ID ABM20249 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 447
ID ABO48741 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 448
ID ABO22548 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 449
ID ABR72806 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;

RESULT 450
ID ABO15448 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 451
ID ABR85163 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 452
ID ABO15143 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 453
ID ABO17278 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 454
ID ABM17567 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 455
ID ADA06547 standard; protein; 229 AA.
DE Human secreted/transmembrane PRO polypeptide #73.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 456
ID ADA39240 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 457
ID ABR85468 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 458
ID ABM77034 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 459
ID ABO28213 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;

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  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 460
ID   ABM22994 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068757-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 461
ID   ABM30314 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068723-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 462
ID   ABM21774 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068741-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 463
ID   ABM21469 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068744-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 464
ID   ABM15000 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068766-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 465
ID   ABO41075 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003068694-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 466
ID   ABO36805 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003068715-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 467
ID   ABO37415 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003068726-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 468
ID   ABM75205 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003104544-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 469
ID   ABM33485 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003096357-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 470
ID   ABO46240 standard; protein; 229 AA.
DE   Human PRO polypeptide #99.
PN   US2003049760-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 471
ID   ADA82633 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003049755-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 472
ID   ADB85621 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2003049735-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 473
ID   ADB96266 standard; protein; 229 AA.
DE   Human PRO polypeptide #73.
PN   US2003054403-A1.
PD   20-MAR-2003.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 474
ID   ABM31839 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068680-A1.
PD   10-APR-2003.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 475
ID   ABM31229 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068762-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 476
ID   ADB85941 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein (PRO) #99.
PN   US2003054472-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 477
ID   ABM32144 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
PN   US2003068708-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 7;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 478
ID   ABM32449 standard; protein; 229 AA.
DE   Human secreted polypeptide PRO994, SEQ ID NO:198.
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PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 479
ID ADB68300 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 480
ID ADB68107 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 481
ID ABM31534 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 482
ID ABM30924 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 483
ID ADB90924 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 484
ID ADC57738 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 485
ID ADC55102 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 486
ID ADC11969 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 487
ID ADC07004 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 488
ID ADC56391 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 489
ID ADC17183 standard; protein; 229 AA.
DE Mammalian PRO polypeptide (SeqID 48).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 490
ID ADC07446 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 491
ID ADC11436 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 492
ID ADC14881 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 493
ID ADC52376 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 494
ID ADC14558 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 495
ID ADD08090 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 496
ID ADC81915 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 497
ID ADD07557 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 498
ID ADC82448 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 499
ID ADD05671 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 500
ID ADD08628 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 501
ID ADD06877 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 502
ID ADC83124 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 503
ID ADD55231 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 504
ID ADD36052 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 505
ID ADD56189 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 506
ID ADD54627 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 507
ID ADE26781 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 508
ID ADE26248 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 509
ID ADF67185 standard; protein; 229 AA.
DE Human PRO994 amino acid sequence SEQ ID NO:258.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 510
ID ADG01053 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 511
ID ADG08606 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 512
ID ADG02666 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 513
ID ADG01373 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 514
ID ADF95548 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 515
ID ADF95227 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 516
ID ADG12363 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;

RESULT 517
ID ADH24080 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 518
ID ADH34106 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 519
ID ADH29939 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 520
ID ADH23910 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 521
ID ADH09023 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 522
ID ADG85314 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 523
ID ADH24590 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 524
ID ADH37446 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 525
ID ADH02035 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 526
ID ADH37616 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 527
ID ADG85654 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 528
ID ADH24250 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 529
ID ADH38544 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 530
ID ADG83665 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 531
ID ADH29473 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 532
ID ADH27589 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 533
ID ADH37786 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 534
ID ADH37963 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 535
ID ADH57383 standard; protein; 229 AA.

DE Novel human secreted and transmembrane protein PRO994.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 536
ID ADH53525 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 537
ID ADH53695 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 538
ID ADH52031 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 539
ID ADH49886 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 540
ID ADI25396 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 541
ID ADH90189 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 542
ID ADI25566 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 543
ID ADH97740 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 544
ID ADI35439 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 545
ID ADI03588 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 546
ID ADI11945 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 547
ID ADH90019 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 548
ID ADH99931 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 549
ID ADH98420 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 550
ID ADI11095 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 551
ID ADI11605 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 552
ID ADH98250 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 553
ID ADH98590 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 554
ID ADH98080 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 555
ID ADI05068 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 556
ID ADI03418 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 557
ID ADI04813 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 558
ID ADH78267 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 559
ID ADI19611 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 560
ID ADH90359 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 561
ID ADI03078 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 562
ID ADH77927 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 563
ID ADH97910 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 564
ID ADI01295 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 565
ID ADI01990 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 566
ID ADI03248 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 567
ID ADI11435 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 568
ID ADI02337 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 569
ID ADI11775 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 570
ID ADI05412 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 571
ID ADH79484 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;

RESULT 572
ID ADI19441 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 573
ID ADI05242 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 574
ID ADH79654 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 575
ID ADI01480 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 576
ID ADI01650 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 577
ID ADI01820 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 578
ID ADH79824 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 579
ID ADI04642 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 580
ID ADI02778 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 581
ID ADH78097 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 582
ID ADI25736 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 583
ID ADI25906 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 584
ID ADK65418 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 585
ID ADH98760 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 586
ID ADH80001 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 587
ID ADL32804 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 588
ID ADM30338 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 589
ID ADL93732 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 590
ID ABM85217 standard; protein; 229 AA.

DE Human protein sequence hCP1734062.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 591
ID ADC52186 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 592
ID ADE74335 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 593
ID ADE74947 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 594
ID ADF35384 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 595
ID ADG11634 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 596
ID ADF96160 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 597
ID ADG04431 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 598
ID ADG00591 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 599
ID ADH06618 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 600
ID ADH06448 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 601
ID ADG68869 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 602
ID ADH27759 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 603
ID ADH25100 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 604
ID ADH33732 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 605
ID ADG82847 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 606
ID ADH02375 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 607
ID ADH07982 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 608
ID ADG69379 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;

RESULT 609
ID ADH39200 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 610
ID ADH26128 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 611
ID ADG83940 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 612
ID ADH19504 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 613
ID ADG85484 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 614
ID ADH06278 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 615
ID ADH30108 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 616
ID ADH24420 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 617
ID ADH33097 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 618
ID ADG69549 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 619
ID ADH07812 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 620
ID ADG85824 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 621
ID ADH39370 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 622
ID ADH33562 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 623
ID ADH33902 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 624
ID ADH01112 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 625
ID ADG69719 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 626
ID ADH20997 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 627
ID ADH02205 standard; protein; 229 AA.
DE Human PRO polypeptide #24.

PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 628
ID ADG69209 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 629
ID ADG85994 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 630
ID ADH24930 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 631
ID ADH39547 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 632
ID ADH20037 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 633
ID ADH02545 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 634
ID ADG69039 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 635
ID ADH07642 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 636
ID ADG86164 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 637
ID ADH24760 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 638
ID ADH25808 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 639
ID ADH38374 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 640
ID ADH57213 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 641
ID ADH52201 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 642
ID ADH49567 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 643
ID ADH90529 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 644
ID ADI11265 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 645
ID ADH98930 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003190698-A1.
PD 09-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 646
ID ADI02160 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 647
ID ADH90699 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 648
ID ADJ54836 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 649
ID ADJ98574 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 650
ID ADJ98744 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 651
ID ADH78903 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 652
ID ADJ99137 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 653
ID ADJ99307 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 654
ID ADJ98925 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 655
ID ADH79073 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 656
ID ADK00933 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 657
ID ADK14454 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 658
ID ADJ64607 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 659
ID ADM31503 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 660
ID ADM36550 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 661
ID ADM40355 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 662
ID ADM80903 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
RESULT 663
ID ADN37963 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;

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  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 664
ID   ADR14507 standard; protein; 229 AA.
DE   Human NF-kappaB pathway-associated protein SeqID508.
PN   WO2004065577-A2.
PD   05-AUG-2004.
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
  Query Match           100.0%;  Score 93;  DB 8;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 665
ID   ADY77743 standard; protein; 229 AA.
DE   Neoplastic disease detection protein PRO994.
PN   US2005059102-A1.
PD   17-MAR-2005.
PA   (EATO/) EATON D L.
PA   (FILV/) FILVAROFF E.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GRIM/) GRIMALDI J C.
PA   (GURN/) GURNEY A L.
PA   (WATA/) WATANABE C K.
PA   (WOOD/) WOOD W I.
  Query Match           100.0%;  Score 93;  DB 9;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 666
ID   AEA38511 standard; protein; 229 AA.
DE   Human secreted/transmembrane protein, #141.
PN   US2005112725-A1.
PD   26-MAY-2005.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 9;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 667
ID   AED50193 standard; protein; 229 AA.
DE   Novel human secreted and transmembrane protein PRO994.
PN   US2005163766-A1.
PD   28-JUL-2005.
  Query Match           100.0%;  Score 93;  DB 9;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 668
ID   AEF12574 standard; protein; 229 AA.
DE   Human PRO994 protein SEQ ID NO:48.
PN   US2006008901-A1.
PD   12-JAN-2006.
PA   (GETH ) GENENTECH INC.
  Query Match           100.0%;  Score 93;  DB 10;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 669
ID   AEF74263 standard; protein; 229 AA.
DE   Human PRO994 protein SEQ ID NO:48.
PN   US2005260647-A1.
PD   24-NOV-2005.
PA   (EATO/) EATON D L.
PA   (FILV/) FILVAROFF E.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GRIM/) GRIMALDI J C.
PA   (GURN/) GURNEY A L.
PA   (WATA/) WATANABE C K.
PA   (WOOD/) WOOD W L.
  Query Match           100.0%;  Score 93;  DB 10;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
RESULT 670
ID   ABM85216 standard; protein; 230 AA.
DE   Mouse protein sequence mCP5099.
PN   WO2003073826-A2.
PD   12-SEP-2003.
PA   (SAGR-) SAGRES DISCOVERY.
  Query Match           75.3%;  Score 70;  DB 7;  Length 230;
  Best Local Similarity   72.2%;  Pred. No. 0.0019;
RESULT 671
ID   ABB60457 standard; protein; 410 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 8163.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
  Query Match           48.4%;  Score 45;  DB 4;  Length 410;
  Best Local Similarity   53.3%;  Pred. No. 72;
RESULT 672
ID   AAW15074 standard; protein; 420 AA.
DE   M. leprae gyrase intein.
PN   FR2739859-A1.
PD   18-APR-1997.
PA   (INSP ) INST PASTEUR.
  Query Match           47.3%;  Score 44;  DB 2;  Length 420;
  Best Local Similarity   46.7%;  Pred. No. 1.1e+02;
RESULT 673
ID   ABU35713 standard; protein; 1249 AA.
DE   Protein encoded by Prokaryotic essential gene #21240.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
  Query Match           47.3%;  Score 44;  DB 6;  Length 1249;
  Best Local Similarity   46.7%;  Pred. No. 3.8e+02;
RESULT 674
ID   AAW15078 standard; protein; 1273 AA.
DE   M. leprae gyrA precursor.
PN   FR2739859-A1.
PD   18-APR-1997.
PA   (INSP ) INST PASTEUR.
  Query Match           47.3%;  Score 44;  DB 2;  Length 1273;
  Best Local Similarity   46.7%;  Pred. No. 3.8e+02;
RESULT 675
ID   ABO00725 standard; protein; 232 AA.
DE   Novel human polypeptide #312.
PN   WO2003023013-A2.
PD   20-MAR-2003.
PA   (HYSE-) HYSEQ INC.
  Query Match           46.2%;  Score 43;  DB 6;  Length 232;
  Best Local Similarity   66.7%;  Pred. No. 82;
RESULT 676
ID   AAU31159 standard; protein; 1058 AA.
DE   Novel human secreted protein #1650.
PN   WO200179449-A2.
PD   25-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match           46.2%;  Score 43;  DB 4;  Length 1058;
  Best Local Similarity   69.2%;  Pred. No. 4.6e+02;
RESULT 677
ID   AAR71333 standard; protein; 1110 AA.
DE   Deduced sequence encoded by Wilson's disease gene cDNA.
PN   WO9506714-A1.
PD   09-MAR-1995.
PA   (UYCO ) UNIV COLUMBIA NEW YORK.
PA   (GEHO ) GEN HOSPITAL CORP.
  Query Match           46.2%;  Score 43;  DB 2;  Length 1110;
  Best Local Similarity   69.2%;  Pred. No. 4.9e+02;
RESULT 678
ID   AAE36368 standard; protein; 149 AA.
DE   Human neuron-restrictive silencer factor repressor splice variant.
PN   WO200297044-A2.
PD   05-DEC-2002.
PA   (UYJE-) UNIV JEFFERSON THOMAS.
  Query Match           45.2%;  Score 42;  DB 6;  Length 149;
  Best Local Similarity   53.3%;  Pred. No. 74;
RESULT 679
ID   AAM58345 standard; protein; 222 AA.
DE   Human brain expressed single exon probe encoded protein SEQ ID NO: 30450.
PN   WO200157275-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
  Query Match           45.2%;  Score 42;  DB 4;  Length 222;
  Best Local Similarity   46.7%;  Pred. No. 1.2e+02;
RESULT 680
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ID ABU03573 standard; protein; 222 AA.
DE Human expressed protein tag (EPT) #239.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 222;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
RESULT 681
ID AAR99364 standard; protein; 252 AA.
DE Human REST protein DNA binding domain.
PN WO9629433-A1.
PD 26-SEP-1996.
PA (UYNY) UNIV NEW YORK STATE RES FOUND.
Query Match 45.2%; Score 42; DB 2; Length 252;
Best Local Similarity 53.3%; Pred. No. 1.3e+02;
RESULT 682
ID AAR99388 standard; protein; 428 AA.
DE Human REST protein (aa9-436).
PN WO9629433-A1.
PD 26-SEP-1996.
PA (UYNY) UNIV NEW YORK STATE RES FOUND.
Query Match 45.2%; Score 42; DB 2; Length 428;
Best Local Similarity 53.3%; Pred. No. 2.5e+02;
RESULT 683
ID AAR99367 standard; protein; 468 AA.
DE Human REST protein partial sequence (aa73-540).
PN WO9629433-A1.
PD 26-SEP-1996.
PA (UYNY) UNIV NEW YORK STATE RES FOUND.
Query Match 45.2%; Score 42; DB 2; Length 468;
Best Local Similarity 53.3%; Pred. No. 2.7e+02;
RESULT 684
ID AAR99387 standard; protein; 487 AA.
DE Human REST protein (aa41-527).
PN WO9629433-A1.
PD 26-SEP-1996.
PA (UYNY) UNIV NEW YORK STATE RES FOUND.
Query Match 45.2%; Score 42; DB 2; Length 487;
Best Local Similarity 53.3%; Pred. No. 2.8e+02;
RESULT 685
ID AAR99370 standard; protein; 538 AA.
DE Human REST protein partial sequence (aa1-538).
PN WO9629433-A1.
PD 26-SEP-1996.
PA (UYNY) UNIV NEW YORK STATE RES FOUND.
Query Match 45.2%; Score 42; DB 2; Length 538;
Best Local Similarity 53.3%; Pred. No. 3.2e+02;
RESULT 686
ID AEC08930 standard; protein; 564 AA.
DE REST-transactivator protein.
PN WO2005076981-A2.
PD 25-AUG-2005.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 45.2%; Score 42; DB 9; Length 564;
Best Local Similarity 53.3%; Pred. No. 3.4e+02;
RESULT 687
ID AAW02288 standard; protein; 678 AA.
DE Human neuron restrictive silencer factor (partial sequence).
PN WO9627665-A2.
PD 12-SEP-1996.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 45.2%; Score 42; DB 2; Length 678;
Best Local Similarity 53.3%; Pred. No. 4.1e+02;
RESULT 688
ID ABG19842 standard; protein; 875 AA.
DE Novel human diagnostic protein #19833.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 45.2%; Score 42; DB 4; Length 875;
Best Local Similarity 46.7%; Pred. No. 5.5e+02;
RESULT 689
ID AEC08928 standard; protein; 926 AA.
DE REST-transactivator protein.
PN WO2005076981-A2.
PD 25-AUG-2005.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 45.2%; Score 42; DB 9; Length 926;
Best Local Similarity 53.3%; Pred. No. 5.9e+02;
RESULT 690
ID AAW02289 standard; protein; 976 AA.
DE Mouse neuron restrictive silencer factor.
PN WO9627665-A2.
PD 12-SEP-1996.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 45.2%; Score 42; DB 2; Length 976;
Best Local Similarity 53.3%; Pred. No. 6.2e+02;
RESULT 691
ID ADU80835 standard; protein; 1082 AA.
DE Murine NRSF protein.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1082;
Best Local Similarity 53.3%; Pred. No. 7e+02;
RESULT 692
ID AAR99365 standard; protein; 1097 AA.
DE Human REST protein.
PN WO9629433-A1.
PD 26-SEP-1996.
PA (UYNY) UNIV NEW YORK STATE RES FOUND.
Query Match 45.2%; Score 42; DB 2; Length 1097;
Best Local Similarity 53.3%; Pred. No. 7.1e+02;
RESULT 693
ID ADU80860 standard; protein; 1097 AA.
DE Human NRSF protein finger 4 variant F4v6.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 7.1e+02;
RESULT 694
ID ADU80870 standard; protein; 1097 AA.
DE Human NRSF protein finger 5 variant F5v8.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 7.1e+02;
RESULT 695
ID ADU80863 standard; protein; 1097 AA.
DE Human NRSF protein finger 5 variant F5v1.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 7.1e+02;
RESULT 696
ID ADU80868 standard; protein; 1097 AA.
DE Human NRSF protein finger 5 variant F5v6.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 7.1e+02;
RESULT 697
ID ADU80867 standard; protein; 1097 AA.
DE Human NRSF protein finger 5 variant F5v5.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 7.1e+02;
RESULT 698
ID ADU80861 standard; protein; 1097 AA.
DE Human NRSF protein finger 4 variant F4v7.

PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 7.1e+02;
RESULT 699
ID ADU80866 standard; protein; 1097 AA.
DE Human NRSF protein finger 5 variant F5v4.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 7.1e+02;
RESULT 700
ID ADU80859 standard; protein; 1097 AA.
DE Human NRSF protein finger 4 variant F4v5.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 7.1e+02;
RESULT 701
ID ADU80862 standard; protein; 1097 AA.
DE Human NRSF protein finger 4 variant F4v8.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 7.1e+02;
RESULT 702
ID ADU80869 standard; protein; 1097 AA.
DE Human NRSF protein finger 5 variant F5v7.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 7.1e+02;
RESULT 703
ID ADU80858 standard; protein; 1097 AA.
DE Human NRSF protein finger 4 variant F4v4.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 7.1e+02;
RESULT 704
ID ADU80864 standard; protein; 1097 AA.
DE Human NRSF protein finger 5 variant F5v2.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 7.1e+02;
RESULT 705
ID ADU80833 standard; protein; 1097 AA.
DE Human NRSF protein.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 7.1e+02;
RESULT 706
ID ADU80857 standard; protein; 1097 AA.
DE Human NRSF protein finger 4 variant F4v1.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 7.1e+02;
RESULT 707
ID ADU80865 standard; protein; 1097 AA.
DE Human NRSF protein finger 5 variant F5v3.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 7.1e+02;
RESULT 708
ID ABG32157 standard; protein; 1281 AA.
DE N-methyl D-aspartate (NMDA) receptor related protein #1.
PN WO200264772-A1.
PD 22-AUG-2002.
PA (SHIO) SHIONOGI & CO LTD.
Query Match 45.2%; Score 42; DB 5; Length 1281;
Best Local Similarity 46.7%; Pred. No. 8.5e+02;
RESULT 709
ID AAU02944 standard; protein; 1350 AA.
DE Angiotensin converting enzyme (ACEV) splice variant protein #44.
PN WO200136632-A2.
PD 25-MAY-2001.
PA (COMP-) COMPUGEN LTD.
Query Match 45.2%; Score 42; DB 4; Length 1350;
Best Local Similarity 46.7%; Pred. No. 9e+02;
RESULT 710
ID AAR66039 standard; protein; 1464 AA.
DE Human N-methyl-D-aspartate receptor subunit 2A protein.
PN WO9424284-A1.
PD 27-OCT-1994.
PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
Query Match 45.2%; Score 42; DB 2; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.9e+02;
RESULT 711
ID AAR55529 standard; protein; 1464 AA.
DE Human NMDA R2A receptor subunit.
PN WO9411501-A1.
PD 26-MAY-1994.
PA (MERI) MERCK SHARP & DOHME LTD.
Query Match 45.2%; Score 42; DB 2; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.9e+02;
RESULT 712
ID AAR80970 standard; protein; 1464 AA.
DE Human excitatory amino acid receptor modulatory protein NR2A-1.
PN EP674003-A2.
PD 27-SEP-1995.
PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
Query Match 45.2%; Score 42; DB 2; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.9e+02;
RESULT 713
ID AAW85576 standard; protein; 1464 AA.
DE Human N-methyl-D-aspartate receptor subunit NMDAR2A.
PN US5849895-A.
PD 15-DEC-1998.
PA (SIBI-) SIBIA NEUROSCIENCES INC.
Query Match 45.2%; Score 42; DB 2; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.9e+02;
RESULT 714
ID AAY56113 standard; protein; 1464 AA.
DE Human NMDAR2A subunit protein sequence SEQ ID NO:11.
PN US5985586-A.
PD 16-NOV-1999.
PA (SIBI-) SIBIA NEUROSCIENCES INC.
Query Match 45.2%; Score 42; DB 3; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.9e+02;
RESULT 715
ID AAB26215 standard; protein; 1464 AA.
DE Human N-methyl-D-aspartate receptor subunit NMDAR2A.
PN US6111091-A.
PD 29-AUG-2000.
PA (MERI) MERCK & CO INC.
Query Match 45.2%; Score 42; DB 3; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.9e+02;
RESULT 716
ID ABB56507 standard; protein; 1464 AA.
DE Human NMDAR2A SEQ ID NO 11.
PN US6316611-B1.
PD 13-NOV-2001.

PA (MERI) MERCK & CO INC.
Query Match 45.2%; Score 42; DB 5; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.9e+02;
RESULT 717
ID AAO18063 standard; protein; 1464 AA.
DE Human NMDAR2A SEQ ID NO: 11.
PN US6376660-B1.
PD 23-APR-2002.
PA (MERI) MERCK & CO INC.
Query Match 45.2%; Score 42; DB 5; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.9e+02;
RESULT 718
ID ABG32158 standard; protein; 1464 AA.
DE N-methyl D-aspartate (NMDA) receptor related protein #2.
PN WO200264772-A1.
PD 22-AUG-2002.
PA (SHIO) SHIONOGI & CO LTD.
Query Match 45.2%; Score 42; DB 5; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.9e+02;
RESULT 719
ID ABU65878 standard; protein; 1464 AA.
DE Human N-methyl D-aspartate receptor subunit associated protein #1.
PN US2002161215-A1.
PD 31-OCT-2002.
PA (DAGG/) DAGGETT L P.
PA (ELLI/) ELLIS S B.
PA (LIAW/) LIAW C W.
PA (LUCC/) LU C.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.9e+02;
RESULT 720
ID ABU61423 standard; protein; 1464 AA.
DE Human N-methyl-D-aspartate (NMDA) receptor subunit #5.
PN US2002161193-A1.
PD 31-OCT-2002.
PA (DAGG/) DAGGETT L P.
PA (LUCC/) LU C.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.9e+02;
RESULT 721
ID ABU03575 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #241.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.9e+02;
RESULT 722
ID ABU03578 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #244.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.9e+02;
RESULT 723
ID ABU03574 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #240.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.9e+02;
RESULT 724
ID ABU03577 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #243.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.9e+02;
RESULT 725
ID ABU03572 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #238.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.9e+02;
RESULT 726
ID ABU03579 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #245.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.9e+02;
RESULT 727
ID ABU03571 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #237.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.9e+02;
RESULT 728
ID ABU03576 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #242.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.9e+02;
RESULT 729
ID ABU03580 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #246.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.9e+02;
RESULT 730
ID ABU03570 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #236.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.9e+02;
RESULT 731
ID ABU57660 standard; protein; 1464 AA.
DE Human N-methyl-D-aspartate (NMDA) receptor sub-unit #3.
PN US6469142-B1.
PD 22-OCT-2002.
PA (MERI) MERCK & CO INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.9e+02;
RESULT 732
ID ABO43070 standard; protein; 1464 AA.
DE Human NMDA receptor subunit NMDAR2A.
PN US2003013866-A1.
PD 16-JAN-2003.
PA (MERI) MERCK & CO INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.9e+02;
RESULT 733
ID AAE39234 standard; protein; 1464 AA.
DE Human NMDA receptor subunit, NMDAR2A protein.
PN US6521413-B1.
PD 18-FEB-2003.
PA (MERI) MERCK & CO INC.
Query Match 45.2%; Score 42; DB 7; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.9e+02;
RESULT 734
ID AEF64363 standard; protein; 1464 AA.
DE Human N-methyl-D-aspartate (NMDA) receptor NR2A subunit.

PN US2006029546-A1.
PD 09-FEB-2006.
PA (DECO-) DECODE GENETICS INC.
Query Match 45.2%; Score 42; DB 10; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.9e+02;
RESULT 735
ID ABU16324 standard; protein; 355 AA.
DE Protein encoded by Prokaryotic essential gene #1851.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 44.6%; Score 41.5; DB 6; Length 355;
Best Local Similarity 34.6%; Pred. No. 2.4e+02;
RESULT 736
ID ADW94654 standard; protein; 355 AA.
DE Proliferation-required gene SAV0920 protein, SEQ ID 594.
PN US2005026189-A1.
PD 03-FEB-2005.
PA (WANG/) WANG L.
PA (ZAMU/) ZAMUDIO C.
Query Match 44.6%; Score 41.5; DB 9; Length 355;
Best Local Similarity 34.6%; Pred. No. 2.4e+02;
RESULT 737
ID AAW48794 standard; protein; 117 AA.
DE Homo sapiens sprouty 1 cysteine rich protein.
PN WO9820032-A1.
PD 14-MAY-1998.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 44.1%; Score 41; DB 2; Length 117;
Best Local Similarity 58.3%; Pred. No. 84;
RESULT 738
ID AAB41184 standard; protein; 139 AA.
DE Human ORFX ORF948 polypeptide sequence SEQ ID NO:1896.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 44.1%; Score 41; DB 3; Length 139;
Best Local Similarity 58.3%; Pred. No. 1e+02;
RESULT 739
ID ADE83550 standard; protein; 139 AA.
DE Human Protein O43609, SEQ ID NO 11168.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 44.1%; Score 41; DB 7; Length 139;
Best Local Similarity 58.3%; Pred. No. 1e+02;
RESULT 740
ID ADE58772 standard; protein; 139 AA.
DE Human Protein O43609, SEQ ID NO 4658.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 44.1%; Score 41; DB 7; Length 139;
Best Local Similarity 58.3%; Pred. No. 1e+02;
RESULT 741
ID ADN95257 standard; protein; 139 AA.
DE Human BEC/LEC-related protein sequence SeqID179.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 44.1%; Score 41; DB 7; Length 139;
Best Local Similarity 58.3%; Pred. No. 1e+02;
RESULT 742
ID ADG47835 standard; protein; 139 AA.
DE Human sprouty-1 protein.
PN US6485920-B1.
PD 26-NOV-2002.
PA (HYSE-) HYSEQ INC.
Query Match 44.1%; Score 41; DB 8; Length 139;
Best Local Similarity 58.3%; Pred. No. 1e+02;
RESULT 743
ID ADJ95402 standard; protein; 139 AA.
DE Human sprouty-1 polypeptide.
PN US6706871-B1.
PD 16-MAR-2004.
PA (NUVE-) NUVELO INC.
Query Match 44.1%; Score 41; DB 8; Length 139;
Best Local Similarity 58.3%; Pred. No. 1e+02;
RESULT 744
ID AAW48793 standard; protein; 140 AA.
DE Homo sapiens sprouty 1 protein.
PN WO9820032-A1.
PD 14-MAY-1998.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 44.1%; Score 41; DB 2; Length 140;
Best Local Similarity 58.3%; Pred. No. 1e+02;
RESULT 745
ID AAY87596 standard; protein; 156 AA.
DE Human SPROUTY protein short consensus sequence.
PN WO200015781-A1.
PD 23-MAR-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 44.1%; Score 41; DB 3; Length 156;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
RESULT 746
ID AAY87595 standard; protein; 167 AA.
DE Human SPROUTY-1 protein, SEQ ID NO:9.
PN WO200015781-A1.
PD 23-MAR-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 44.1%; Score 41; DB 3; Length 167;
Best Local Similarity 58.3%; Pred. No. 1.3e+02;
RESULT 747
ID ADP29852 standard; protein; 188 AA.
DE Human secreted protein SEQ ID #1850.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 44.1%; Score 41; DB 8; Length 188;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
RESULT 748
ID AAY87597 standard; protein; 288 AA.
DE Human SPROUTY protein long consensus sequence.
PN WO200015781-A1.
PD 23-MAR-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 44.1%; Score 41; DB 3; Length 288;
Best Local Similarity 58.3%; Pred. No. 2.3e+02;
RESULT 749
ID AAY87592 standard; protein; 294 AA.
DE Human SPROUTY-1 protein, SEQ ID NO:3.
PN WO200015781-A1.
PD 23-MAR-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 44.1%; Score 41; DB 3; Length 294;
Best Local Similarity 58.3%; Pred. No. 2.4e+02;
RESULT 750
ID AAY87593 standard; protein; 295 AA.
DE Human SPROUTY-1 protein, SEQ ID NO:5.
PN WO200015781-A1.
PD 23-MAR-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 44.1%; Score 41; DB 3; Length 295;
Best Local Similarity 58.3%; Pred. No. 2.4e+02;
RESULT 751
ID AAU69508 standard; protein; 315 AA.
DE Human purified secretory polypeptide #77.
PN WO200162918-A2.
PD 30-AUG-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 44.1%; Score 41; DB 4; Length 315;
Best Local Similarity 40.0%; Pred. No. 2.6e+02;
RESULT 752

ID AEB51826 standard; protein; 318 AA.
DE Human Sprouty-1 protein.
PN WO2005065686-A1.
PD 21-JUL-2005.
PA (UYQU) UNIV QUEENSLAND.
PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
Query Match 44.1%; Score 41; DB 9; Length 318;
Best Local Similarity 58.3%; Pred. No. 2.6e+02;
RESULT 753
ID AAY87591 standard; protein; 319 AA.
DE Human SPROUTY-1 protein, SEQ ID NO:24.
PN WO200015781-A1.
PD 23-MAR-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 44.1%; Score 41; DB 3; Length 319;
Best Local Similarity 58.3%; Pred. No. 2.6e+02;
RESULT 754
ID AAB64377 standard; protein; 319 AA.
DE Amino acid sequence of human intracellular signalling molecule INTRA9.
PN WO200077040-A2.
PD 21-DEC-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 44.1%; Score 41; DB 4; Length 319;
Best Local Similarity 58.3%; Pred. No. 2.6e+02;
RESULT 755
ID AAM38688 standard; protein; 319 AA.
DE Human polypeptide SEQ ID NO 1833.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 44.1%; Score 41; DB 4; Length 319;
Best Local Similarity 58.3%; Pred. No. 2.6e+02;
RESULT 756
ID ADY16807 standard; protein; 319 AA.
DE PRO polypeptide SEQ ID NO 2613.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 44.1%; Score 41; DB 9; Length 319;
Best Local Similarity 58.3%; Pred. No. 2.6e+02;
RESULT 757
ID AAM40474 standard; protein; 326 AA.
DE Human polypeptide SEQ ID NO 5405.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 44.1%; Score 41; DB 4; Length 326;
Best Local Similarity 58.3%; Pred. No. 2.7e+02;
RESULT 758
ID ABB84246 standard; protein; 335 AA.
DE Human germinal protein 36.85.
PN CN1339486-A.
PD 13-MAR-2002.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 44.1%; Score 41; DB 5; Length 335;
Best Local Similarity 58.3%; Pred. No. 2.8e+02;
RESULT 759
ID ADE08605 standard; protein; 336 AA.
DE Novel protein (useful for identifying genetic disorders) #760.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 44.1%; Score 41; DB 7; Length 336;
Best Local Similarity 40.0%; Pred. No. 2.8e+02;
RESULT 760
ID AAY87594 standard; protein; 338 AA.
DE Human SPROUTY-1 protein, SEQ ID NO:7.
PN WO200015781-A1.
PD 23-MAR-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 44.1%; Score 41; DB 3; Length 338;
Best Local Similarity 58.3%; Pred. No. 2.8e+02;
RESULT 761
ID AAG30407 standard; protein; 449 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36346.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 44.1%; Score 41; DB 3; Length 449;
Best Local Similarity 42.9%; Pred. No. 3.8e+02;
RESULT 762
ID ABB92109 standard; protein; 449 AA.
DE Herbicidally active polypeptide SEQ ID NO 1320.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 44.1%; Score 41; DB 5; Length 449;
Best Local Similarity 42.9%; Pred. No. 3.8e+02;
RESULT 763
ID AED61015 standard; protein; 449 AA.
DE Thale cress protein #58.
PN US2005246785-A1.
PD 03-NOV-2005.
PA (CERE-) CERES INC.
Query Match 44.1%; Score 41; DB 9; Length 449;
Best Local Similarity 42.9%; Pred. No. 3.8e+02;
RESULT 764
ID AEF26507 standard; protein; 449 AA.
DE A. thaliana putative glucosyl transferase SEQ ID NO: 26.
PN US2006015970-A1.
PD 19-JAN-2006.
PA (CERS-) CERS INC.
Query Match 44.1%; Score 41; DB 10; Length 449;
Best Local Similarity 42.9%; Pred. No. 3.8e+02;
RESULT 765
ID AAG30406 standard; protein; 466 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36345.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 44.1%; Score 41; DB 3; Length 466;
Best Local Similarity 42.9%; Pred. No. 4e+02;
RESULT 766
ID AAG41728 standard; protein; 474 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51953.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 44.1%; Score 41; DB 3; Length 474;
Best Local Similarity 50.0%; Pred. No. 4.1e+02;
RESULT 767
ID AEA18817 standard; protein; 496 AA.
DE Amino acid sequence of E3 ubiquitin ligase murine Cb1-3.
PN WO2005044840-A2.
PD 19-MAY-2005.
PA (CBRB-) CBR INST BIOMEDICAL RES INC.
Query Match 44.1%; Score 41; DB 9; Length 496;
Best Local Similarity 66.7%; Pred. No. 4.3e+02;
RESULT 768
ID AAG41727 standard; protein; 497 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51952.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 44.1%; Score 41; DB 3; Length 497;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
RESULT 769
ID AAG41726 standard; protein; 512 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51951.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 44.1%; Score 41; DB 3; Length 512;
Best Local Similarity 50.0%; Pred. No. 4.5e+02;
RESULT 770
ID ADN20612 standard; protein; 597 AA.
DE Bacterial polypeptide #3265.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 44.1%; Score 41; DB 8; Length 597;
Best Local Similarity 88.9%; Pred. No. 5.3e+02;
RESULT 771
ID ADU80837 standard; protein; 1068 AA.
DE Rat NRSF protein.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 44.1%; Score 41; DB 8; Length 1068;
Best Local Similarity 58.3%; Pred. No. 1e+03;
RESULT 772
ID ABU26822 standard; protein; 792 AA.
DE Protein encoded by Prokaryotic essential gene #12349.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 43.5%; Score 40.5; DB 6; Length 792;
Best Local Similarity 37.5%; Pred. No. 8.9e+02;
RESULT 773
ID AAY35218 standard; protein; 797 AA.
DE C. pneumoniae protein involved in metabolism of amino acids.
PN WO9927105-A2.
PD 03-JUN-1999.
PA (GEST) GENSET.
Query Match 43.5%; Score 40.5; DB 2; Length 797;
Best Local Similarity 37.5%; Pred. No. 9e+02;
RESULT 774
ID ADB65067 standard; protein; 158 AA.
DE Human protein encoded by clone SMINT20049920.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 43.0%; Score 40; DB 7; Length 158;
Best Local Similarity 46.7%; Pred. No. 1.7e+02;
RESULT 775
ID AAU23341 standard; protein; 204 AA.
DE Novel human enzyme polypeptide #427.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 43.0%; Score 40; DB 4; Length 204;
Best Local Similarity 44.4%; Pred. No. 2.3e+02;
RESULT 776
ID ADO24768 standard; protein; 281 AA.
DE Cat TRAIL protein.
PN WO2004039307-A2.
PD 13-MAY-2004.
PA (PFIZ) PFIZER PROD INC.
Query Match 43.0%; Score 40; DB 8; Length 281;
Best Local Similarity 50.0%; Pred. No. 3.3e+02;
RESULT 777
ID ADO24766 standard; protein; 281 AA.
DE Dog TRAIL protein.
PN WO2004039307-A2.
PD 13-MAY-2004.
PA (PFIZ) PFIZER PROD INC.
Query Match 43.0%; Score 40; DB 8; Length 281;
Best Local Similarity 50.0%; Pred. No. 3.3e+02;
RESULT 778
ID ADY11675 standard; protein; 358 AA.
DE Plant full length insert polypeptide seqid 67490.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 43.0%; Score 40; DB 8; Length 358;
Best Local Similarity 66.7%; Pred. No. 4.4e+02;
RESULT 779
ID ABU11564 standard; protein; 420 AA.
DE Human MDDT polypeptide SEQ ID 511.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 43.0%; Score 40; DB 6; Length 420;
Best Local Similarity 44.4%; Pred. No. 5.3e+02;
RESULT 780
ID ABU11734 standard; protein; 420 AA.
DE Human MDDT polypeptide SEQ ID 681.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 43.0%; Score 40; DB 6; Length 420;
Best Local Similarity 44.4%; Pred. No. 5.3e+02;
RESULT 781
ID ADO20208 standard; protein; 421 AA.
DE Human PRO polypeptide #557.
PN WO2004043361-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 43.0%; Score 40; DB 8; Length 421;
Best Local Similarity 44.4%; Pred. No. 5.3e+02;
RESULT 782
ID ABP99229 standard; protein; 430 AA.
DE Orthosomycin biosynthetic polypeptide SEQ ID NO 45.
PN WO200279505-A2.
PD 10-OCT-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 43.0%; Score 40; DB 6; Length 430;
Best Local Similarity 58.3%; Pred. No. 5.4e+02;
RESULT 783
ID ABP76709 standard; protein; 430 AA.
DE Streptomyces viridochromogenes AviGT1.
PN WO200268436-A1.
PD 06-SEP-2002.
PA (COMB-) COMBINATURE BIOPHARM AG.
Query Match 43.0%; Score 40; DB 6; Length 430;
Best Local Similarity 58.3%; Pred. No. 5.4e+02;
RESULT 784
ID ABR39814 standard; protein; 600 AA.
DE Human SCAP polypeptide-Incyte Id. 3363254CD1.
PN WO2003008625-A2.
PD 30-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 43.0%; Score 40; DB 6; Length 600;
Best Local Similarity 44.4%; Pred. No. 7.9e+02;
RESULT 785
ID ADR58983 standard; protein; 600 AA.
DE Human Elk1 phosphorylation/Elk1 kinase activation protein - SEQ ID 86.
PN WO2004072277-A2.
PD 26-AUG-2004.
PA (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match 43.0%; Score 40; DB 8; Length 600;
Best Local Similarity 44.4%; Pred. No. 7.9e+02;
RESULT 786
ID ABG20261 standard; protein; 633 AA.
DE Novel human diagnostic protein #20252.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 43.0%; Score 40; DB 4; Length 633;
Best Local Similarity 58.3%; Pred. No. 8.4e+02;
RESULT 787
ID ABG72972 standard; protein; 735 AA.
DE Lactococcus raffinolactis alpha-galactosidase.
PN WO200281674-A1.
PD 17-OCT-2002.
PA (UYLA-) UNIV LAVAL.
Query Match 43.0%; Score 40; DB 6; Length 735;

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  Best Local Similarity   66.7%;  Pred. No. 1e+03;
RESULT 788
ID   ADH22524 standard; protein; 971 AA.
DE   Human transporter & ion channel (TRICH) protein SeqID22.
PN   WO2003093444-A2.
PD   13-NOV-2003.
PA   (INCY-) INCYTE CORP.
  Query Match           43.0%;  Score 40;  DB 8;  Length 971;
  Best Local Similarity   58.8%;  Pred. No. 1.4e+03;
RESULT 789
ID   ADZ80808 standard; protein; 1500 AA.
DE   Amino acid sequence of human homologue of Drosophila gene CG1886.
PN   WO2005039635-A2.
PD   06-MAY-2005.
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS PHARMA GMBH.
  Query Match           43.0%;  Score 40;  DB 9;  Length 1500;
  Best Local Similarity   58.8%;  Pred. No. 2.2e+03;
RESULT 790
ID   AEB28167 standard; protein; 1500 AA.
DE   Human MNK protein.
PN   WO2005062055-A2.
PD   07-JUL-2005.
PA   (CANC-) CANCER RES TECHNOLOGY LTD.
  Query Match           43.0%;  Score 40;  DB 9;  Length 1500;
  Best Local Similarity   58.8%;  Pred. No. 2.2e+03;
RESULT 791
ID   AEB86597 standard; protein; 1581 AA.
DE   Human copper transporting ATPase ATP7A.
PN   WO2005075632-A2.
PD   18-AUG-2005.
PA   (CELL-) CELLZOME AG.
  Query Match           43.0%;  Score 40;  DB 9;  Length 1581;
  Best Local Similarity   58.8%;  Pred. No. 2.4e+03;
RESULT 792
ID   AAY27134 standard; protein; 1591 AA.
DE   Human munc13 (Hmunc13) polypeptide.
PN   WO9931134-A1.
PD   24-JUN-1999.
PA   (SILV/) SILVERMAN M.
PA   (SONG/) SONG Y.
  Query Match           43.0%;  Score 40;  DB 2;  Length 1591;
  Best Local Similarity   50.0%;  Pred. No. 2.4e+03;
RESULT 793
ID   AAE14921 standard; protein; 1591 AA.
DE   Human ubiquitous Munc13-2 protein mutant (W376R).
PN   WO2003039441-A2.
PD   15-MAY-2003.
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
  Query Match           43.0%;  Score 40;  DB 6;  Length 1591;
  Best Local Similarity   50.0%;  Pred. No. 2.4e+03;
RESULT 794
ID   AAE14911 standard; protein; 1591 AA.
DE   Mouse ubiquitous Munc13-2 protein.
PN   WO2003039441-A2.
PD   15-MAY-2003.
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
  Query Match           43.0%;  Score 40;  DB 6;  Length 1591;
  Best Local Similarity   50.0%;  Pred. No. 2.4e+03;
RESULT 795
ID   AAE14912 standard; protein; 1591 AA.
DE   Human ubiquitous Munc13-2 protein.
PN   WO2003039441-A2.
PD   15-MAY-2003.
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
  Query Match           43.0%;  Score 40;  DB 6;  Length 1591;
  Best Local Similarity   50.0%;  Pred. No. 2.4e+03;
RESULT 796
ID   ADJ68886 standard; protein; 1591 AA.
DE   Human heat mitochondrial protein as a therapeutic target SeqID692.
PN   WO2003087768-A2.
PD   23-OCT-2003.
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
  Query Match           43.0%;  Score 40;  DB 7;  Length 1591;
  Best Local Similarity   50.0%;  Pred. No. 2.4e+03;
RESULT 797
ID   AAE14913 standard; protein; 1622 AA.
DE   Rat ubiquitous Munc13-2 protein.
PN   WO2003039441-A2.
PD   15-MAY-2003.
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
  Query Match           43.0%;  Score 40;  DB 6;  Length 1622;
  Best Local Similarity   50.0%;  Pred. No. 2.4e+03;
RESULT 798
ID   AAE14922 standard; protein; 1622 AA.
DE   Rat ubiquitous Munc13-2 protein mutant (W387R).
PN   WO2003039441-A2.
PD   15-MAY-2003.
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
  Query Match           43.0%;  Score 40;  DB 6;  Length 1622;
  Best Local Similarity   50.0%;  Pred. No. 2.4e+03;
RESULT 799
ID   AAE14914 standard; protein; 1985 AA.
DE   Rat brain-specific Munc13-2 protein.
PN   WO2003039441-A2.
PD   15-MAY-2003.
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
  Query Match           43.0%;  Score 40;  DB 6;  Length 1985;
  Best Local Similarity   50.0%;  Pred. No. 3.1e+03;
RESULT 800
ID   ABP76679 standard; protein; 19938 AA.
DE   Streptomyces viridochromogenes Avi gene cluster polypeptide frame 3.
PN   WO200268436-A1.
PD   06-SEP-2002.
PA   (COMB-) COMBINATURE BIOPHARM AG.
  Query Match           43.0%;  Score 40;  DB 6;  Length 19938;
  Best Local Similarity   58.3%;  Pred. No. 4.2e+04;
RESULT 801
ID   AAU61252 standard; protein; 87 AA.
DE   Propionibacterium acnes immunogenic protein #22148.
PN   WO200181581-A2.
PD   01-NOV-2001.
PA   (CORI-) CORIXA CORP.
  Query Match           41.9%;  Score 39;  DB 4;  Length 87;
  Best Local Similarity   43.8%;  Pred. No. 1.3e+02;
RESULT 802
ID   ABM57771 standard; protein; 87 AA.
DE   Propionibacterium acnes predicted ORF-encoded polypeptide #22447.
PN   WO2003033515-A1.
PD   24-APR-2003.
PA   (CORI-) CORIXA CORP.
  Query Match           41.9%;  Score 39;  DB 6;  Length 87;
  Best Local Similarity   43.8%;  Pred. No. 1.3e+02;
RESULT 803
ID   ADT58157 standard; protein; 114 AA.
DE   Plant polypeptide, SEQ ID 8234.
PN   US2004216190-A1.
PD   28-OCT-2004.
PA   (KOVA/) KOVALIC D K.
  Query Match           41.9%;  Score 39;  DB 8;  Length 114;
  Best Local Similarity   50.0%;  Pred. No. 1.8e+02;
RESULT 804
ID   ABB58677 standard; protein; 152 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 2823.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
  Query Match           41.9%;  Score 39;  DB 4;  Length 152;
  Best Local Similarity   41.2%;  Pred. No. 2.5e+02;
RESULT 805
ID   ABU00656 standard; protein; 165 AA.
DE   S. pneumoniae type 4 strain protein from coding region #223.
PN   WO200277021-A2.
PD   03-OCT-2002.
PA   (CHIR-) CHIRON SPA.
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PA (GENO-) INST GENOMIC RES.
Query Match 41.9%; Score 39; DB 6; Length 165;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
RESULT 806
ID ABU44451 standard; protein; 198 AA.
DE Protein encoded by Prokaryotic essential gene #29978.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 41.9%; Score 39; DB 6; Length 198;
Best Local Similarity 61.5%; Pred. No. 3.3e+02;
RESULT 807
ID AAU36069 standard; protein; 215 AA.
DE Klebsiella pneumoniae cellular proliferation protein #57.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 41.9%; Score 39; DB 4; Length 215;
Best Local Similarity 43.8%; Pred. No. 3.7e+02;
RESULT 808
ID AAW38623 standard; protein; 238 AA.
DE S. pneumoniae BSCELABCD NCBI gi: 895746.
PN WO9743303-A1.
PD 20-NOV-1997.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 41.9%; Score 39; DB 2; Length 238;
Best Local Similarity 50.0%; Pred. No. 4.1e+02;
RESULT 809
ID ABU31150 standard; protein; 266 AA.
DE Protein encoded by Prokaryotic essential gene #16677.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 41.9%; Score 39; DB 6; Length 266;
Best Local Similarity 43.8%; Pred. No. 4.7e+02;
RESULT 810
ID AAY93593 standard; protein; 268 AA.
DE Amino acid sequence of a human phosphodiesterase enzyme.
PN EP1018559-A1.
PD 12-JUL-2000.
PA (PFIZ) PFIZER LTD.
PA (PFIZ) PFIZER INC.
Query Match 41.9%; Score 39; DB 3; Length 268;
Best Local Similarity 63.6%; Pred. No. 4.7e+02;
RESULT 811
ID ABU45046 standard; protein; 271 AA.
DE Protein encoded by Prokaryotic essential gene #30573.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 41.9%; Score 39; DB 6; Length 271;
Best Local Similarity 43.8%; Pred. No. 4.8e+02;
RESULT 812
ID AEB06770 standard; protein; 277 AA.
DE E. coli xanthosine phosphorolysis enzyme SEQ ID NO:10.
PN JP2005151962-A.
PD 16-JUN-2005.
PA (KOKU-) KOKURITSU DAIGAKU HOJIN NARA SENTAN KAGA.
Query Match 41.9%; Score 39; DB 9; Length 277;
Best Local Similarity 54.5%; Pred. No. 4.9e+02;
RESULT 813
ID AAY93568 standard; protein; 288 AA.
DE Amino acid sequence of a human phosphodiesterase enzyme.
PN EP1018559-A1.
PD 12-JUL-2000.
PA (PFIZ) PFIZER LTD.
PA (PFIZ) PFIZER INC.
Query Match 41.9%; Score 39; DB 3; Length 288;
Best Local Similarity 63.6%; Pred. No. 5.1e+02;
RESULT 814
ID ABG25942 standard; protein; 300 AA.
DE Novel human diagnostic protein #25933.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 41.9%; Score 39; DB 4; Length 300;
Best Local Similarity 54.5%; Pred. No. 5.4e+02;
RESULT 815
ID AAB36504 standard; protein; 320 AA.
DE Human short phosphodiesterase protein SEQ ID NO:3.
PN US6146876-A.
PD 14-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 41.9%; Score 39; DB 4; Length 320;
Best Local Similarity 63.6%; Pred. No. 5.8e+02;
RESULT 816
ID ADJ58906 standard; protein; 320 AA.
DE Human cyclic nucleotide phosphodiesterase protein #2.
PN US2004006016-A1.
PD 08-JAN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 41.9%; Score 39; DB 8; Length 320;
Best Local Similarity 63.6%; Pred. No. 5.8e+02;
RESULT 817
ID AEF09959 standard; protein; 320 AA.
DE Human phosphodiasterase, 22025 short protein.
PN US2006009632-A1.
PD 12-JAN-2006.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 41.9%; Score 39; DB 10; Length 320;
Best Local Similarity 63.6%; Pred. No. 5.8e+02;
RESULT 818
ID ABB67466 standard; protein; 328 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 29190.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 41.9%; Score 39; DB 4; Length 328;
Best Local Similarity 57.1%; Pred. No. 5.9e+02;
RESULT 819
ID ADY50214 standard; protein; 335 AA.
DE Human PDE7B phosphodiesterase domain SEQ ID NO:23.
PN US2005048573-A1.
PD 03-MAR-2005.
PA (PLEX-) PLEXXIKON INC.
Query Match 41.9%; Score 39; DB 9; Length 335;
Best Local Similarity 63.6%; Pred. No. 6.1e+02;
RESULT 820
ID ADZ46770 standard; protein; 335 AA.
DE Human PDE7B phosphodiesterase domain, SEQ ID NO: 23.
PN US2005079548-A1.
PD 14-APR-2005.
PA (PLEX-) PLEXXIKON INC.
Query Match 41.9%; Score 39; DB 9; Length 335;
Best Local Similarity 63.6%; Pred. No. 6.1e+02;
RESULT 821
ID AAY86040 standard; protein; 341 AA.
DE S. pneumoniae derived protein #249.
PN WO9806734-A1.
PD 19-FEB-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 41.9%; Score 39; DB 2; Length 341;
Best Local Similarity 50.0%; Pred. No. 6.2e+02;
RESULT 822
ID AAU08676 standard; protein; 391 AA.
DE Human phosphodiesterase type 7B #2.
PN WO200162940-A2.
PD 30-AUG-2001.
PA (MERE) MERCK PATENT GMBH.
Query Match 41.9%; Score 39; DB 4; Length 391;
Best Local Similarity 63.6%; Pred. No. 7.2e+02;
RESULT 823
ID AAY93569 standard; protein; 450 AA.
DE Amino acid sequence of a human phosphodiesterase enzyme.
PN EP1018559-A1.

PD 12-JUL-2000.
PA (PFIZ) PFIZER LTD.
PA (PFIZ) PFIZER INC.
Query Match 41.9%; Score 39; DB 3; Length 450;
Best Local Similarity 63.6%; Pred. No. 8.5e+02;
RESULT 824
ID AAU08675 standard; protein; 450 AA.
DE Human phosphodiesterase type 7B #1.
PN WO200162940-A2.
PD 30-AUG-2001.
PA (MERE) MERCK PATENT GMBH.
Query Match 41.9%; Score 39; DB 4; Length 450;
Best Local Similarity 63.6%; Pred. No. 8.5e+02;
RESULT 825
ID AAG78915 standard; protein; 450 AA.
DE Human type 7B phosphodiesterase, PDE7B.
PN JP2001238680-A.
PD 04-SEP-2001.
PA (TANA) TANABE SEIYAKU CO.
Query Match 41.9%; Score 39; DB 4; Length 450;
Best Local Similarity 63.6%; Pred. No. 8.5e+02;
RESULT 826
ID ADP79549 standard; protein; 450 AA.
DE Human phosphodiesterase 7B nucleotide sequence.
PN WO2004044196-A1.
PD 27-MAY-2004.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 41.9%; Score 39; DB 8; Length 450;
Best Local Similarity 63.6%; Pred. No. 8.5e+02;
RESULT 827
ID AAB36503 standard; protein; 502 AA.
DE Human long phosphodiesterase protein SEQ ID NO:1.
PN US6146876-A.
PD 14-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 41.9%; Score 39; DB 4; Length 502;
Best Local Similarity 63.6%; Pred. No. 9.6e+02;
RESULT 828
ID ABB09005 standard; protein; 502 AA.
DE Human phosphodiesterase-1.
PN WO200198471-A2.
PD 27-DEC-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 41.9%; Score 39; DB 5; Length 502;
Best Local Similarity 63.6%; Pred. No. 9.6e+02;
RESULT 829
ID ADJ58904 standard; protein; 502 AA.
DE Human cyclic nucleotide phosphodiesterase protein #1.
PN US2004006016-A1.
PD 08-JAN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 41.9%; Score 39; DB 8; Length 502;
Best Local Similarity 63.6%; Pred. No. 9.6e+02;
RESULT 830
ID AEF09957 standard; protein; 502 AA.
DE Human phosphodiasterase, 22025 long protein.
PN US2006009632-A1.
PD 12-JAN-2006.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 41.9%; Score 39; DB 10; Length 502;
Best Local Similarity 63.6%; Pred. No. 9.6e+02;
RESULT 831
ID ADX65729 standard; protein; 518 AA.
DE Plant full length insert polypeptide seqid 36572.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 41.9%; Score 39; DB 8; Length 518;
Best Local Similarity 52.9%; Pred. No. 9.9e+02;
RESULT 832
ID ADS42354 standard; protein; 524 AA.
DE Bacterial polypeptide #20784.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 41.9%; Score 39; DB 8; Length 524;
Best Local Similarity 54.5%; Pred. No. 1e+03;
RESULT 833
ID ADS21971 standard; protein; 576 AA.
DE Bacterial polypeptide #11004.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 41.9%; Score 39; DB 8; Length 576;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
RESULT 834
ID ADK47528 standard; protein; 659 AA.
DE Streptococcus pneumoniae protein, Seq ID No 4043.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 41.9%; Score 39; DB 8; Length 659;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
RESULT 835
ID ADR95065 standard; protein; 661 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 3700.
PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 41.9%; Score 39; DB 8; Length 661;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
RESULT 836
ID AEA58935 standard; protein; 661 AA.
DE Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:3700.
PN US2005136404-A1.
PD 23-JUN-2005.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 41.9%; Score 39; DB 9; Length 661;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
RESULT 837
ID ADX87416 standard; protein; 739 AA.
DE Plant full length insert polypeptide seqid 50080.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 41.9%; Score 39; DB 8; Length 739;
Best Local Similarity 37.5%; Pred. No. 1.5e+03;
RESULT 838
ID ABM84355 standard; protein; 810 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4604.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 41.9%; Score 39; DB 8; Length 810;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
RESULT 839
ID ABM84354 standard; protein; 810 AA.

DE Human diagnostic and therapeutic pprotein SEQ ID NO:4603.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 41.9%; Score 39; DB 8; Length 810;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
RESULT 840
ID ADT56766 standard; protein; 999 AA.
DE Plant polypeptide, SEQ ID 6843.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 41.9%; Score 39; DB 8; Length 999;
Best Local Similarity 52.9%; Pred. No. 2.1e+03;
RESULT 841
ID AAY58717 standard; protein; 1001 AA.
DE Arabidopsis ran1-1 mutant protein.
PN WO200004760-A1.
PD 03-FEB-2000.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 41.9%; Score 39; DB 3; Length 1001;
Best Local Similarity 52.9%; Pred. No. 2.1e+03;
RESULT 842
ID AAY58677 standard; protein; 1001 AA.
DE Arabidopsis RAN1 copper transporter.
PN WO200004760-A1.
PD 03-FEB-2000.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 41.9%; Score 39; DB 3; Length 1001;
Best Local Similarity 52.9%; Pred. No. 2.1e+03;
RESULT 843
ID AAY58718 standard; protein; 1001 AA.
DE Arabidopsis ran1-2 mutant protein.
PN WO200004760-A1.
PD 03-FEB-2000.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 41.9%; Score 39; DB 3; Length 1001;
Best Local Similarity 52.9%; Pred. No. 2.1e+03;
RESULT 844
ID ABP99398 standard; protein; 1001 AA.
DE Arabidopsis thaliana polypeptide SEQ ID NO 81.
PN WO200266660-A2.
PD 29-AUG-2002.
PA (META-) METANOMICS GMBH & CO KGAA.
Query Match 41.9%; Score 39; DB 5; Length 1001;
Best Local Similarity 52.9%; Pred. No. 2.1e+03;
RESULT 845
ID ADJ70318 standard; protein; 1328 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2124.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 41.9%; Score 39; DB 7; Length 1328;
Best Local Similarity 64.3%; Pred. No. 2.9e+03;
RESULT 846
ID ABP27518 standard; protein; 1368 AA.
DE Streptococcus polypeptide SEQ ID NO 4212.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 41.9%; Score 39; DB 5; Length 1368;
Best Local Similarity 33.3%; Pred. No. 3e+03;
RESULT 847
ID AAR72343 standard; protein; 1411 AA.
DE Wilson disease protein ATP7B.
PN WO9508641-A1.
PD 30-MAR-1995.
PA (HSCR-) HSC RES & DEV LP.
Query Match 41.9%; Score 39; DB 2; Length 1411;
Best Local Similarity 64.3%; Pred. No. 3.1e+03;
RESULT 848
ID AAR70419 standard; protein; 1456 AA.
DE Rat homologue of human Wilson disease gene ATP7B.
PN WO9508641-A1.
PD 30-MAR-1995.
PA (HSCR-) HSC RES & DEV LP.
Query Match 41.9%; Score 39; DB 2; Length 1456;
Best Local Similarity 64.3%; Pred. No. 3.2e+03;
RESULT 849
ID AEB86598 standard; protein; 1464 AA.
DE Human copper transporting ATPase ATP7B.
PN WO2005075632-A2.
PD 18-AUG-2005.
PA (CELL-) CELLZOME AG.
Query Match 41.9%; Score 39; DB 9; Length 1464;
Best Local Similarity 64.3%; Pred. No. 3.2e+03;
RESULT 850
ID AAU71957 standard; protein; 1513 AA.
DE Human bone marrow tissue polypeptide #35.
PN WO200179447-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 41.9%; Score 39; DB 4; Length 1513;
Best Local Similarity 64.3%; Pred. No. 3.4e+03;
RESULT 851
ID ABB65616 standard; protein; 2271 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23640.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 41.9%; Score 39; DB 4; Length 2271;
Best Local Similarity 63.6%; Pred. No. 5.3e+03;
RESULT 852
ID AAU75351 standard; protein; 2291 AA.
DE Drosophila Rotkehlchen, ROT, protein.
PN WO200200864-A2.
PD 03-JAN-2002.
PA (AVET) AVENTIS CROPSCIENCE GMBH.
Query Match 41.9%; Score 39; DB 5; Length 2291;
Best Local Similarity 63.6%; Pred. No. 5.4e+03;
RESULT 853
ID AAU33909 standard; protein; 346 AA.
DE Staphylococcus aureus cellular proliferation protein #185.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 41.4%; Score 38.5; DB 4; Length 346;
Best Local Similarity 34.6%; Pred. No. 7.7e+02;
RESULT 854
ID ADG48173 standard; protein; 355 AA.
DE Staphylococcus aureus COL fabK protein.
PN US6613553-B1.
PD 02-SEP-2003.
PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
Query Match 41.4%; Score 38.5; DB 7; Length 355;
Best Local Similarity 34.6%; Pred. No. 7.9e+02;
RESULT 855
ID ADG48213 standard; protein; 355 AA.
DE Staphylococcus aureus fabK protein.
PN US6613553-B1.
PD 02-SEP-2003.
PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
Query Match 41.4%; Score 38.5; DB 7; Length 355;
Best Local Similarity 34.6%; Pred. No. 7.9e+02;
RESULT 856
ID AEC55863 standard; protein; 355 AA.
DE Staphylococcus aureus subsp. aureus COL enoyl reductase, SEQ ID NO: 8.
PN US2005196758-A1.
PD 08-SEP-2005.
PA (ROCK/) ROCK C O.
PA (HEAT/) HEATH R J.
Query Match 41.4%; Score 38.5; DB 9; Length 355;
Best Local Similarity 34.6%; Pred. No. 7.9e+02;
RESULT 857

ID AEC55903 standard; protein; 355 AA.
DE Staphylococcus aureus enoyl reductase, SEQ ID NO: 48.
PN US2005196758-A1.
PD 08-SEP-2005.
PA (ROCK/) ROCK C O.
PA (HEAT/) HEATH R J.
Query Match 41.4%; Score 38.5; DB 9; Length 355;
Best Local Similarity 34.6%; Pred. No. 7.9e+02;
RESULT 858
ID AAU36919 standard; protein; 388 AA.
DE Staphylococcus aureus cellular proliferation protein #1089.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 41.4%; Score 38.5; DB 4; Length 388;
Best Local Similarity 34.6%; Pred. No. 8.7e+02;
RESULT 859
ID ABM72178 standard; protein; 390 AA.
DE Staphylococcus aureus protein #1418.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 41.4%; Score 38.5; DB 6; Length 390;
Best Local Similarity 34.6%; Pred. No. 8.8e+02;
RESULT 860
ID AAW89800 standard; protein; 393 AA.
DE Staphylococcus aureus protein SEQ ID #5248.
PN EP786519-A2.
PD 30-JUL-1997.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.4%; Score 38.5; DB 2; Length 393;
Best Local Similarity 34.6%; Pred. No. 8.9e+02;
RESULT 861
ID ABB65474 standard; protein; 438 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23214.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 41.4%; Score 38.5; DB 4; Length 438;
Best Local Similarity 55.6%; Pred. No. 1e+03;
RESULT 862
ID AAU12171 standard; peptide; 15 AA.
DE Human NPAT protein 12 N-terminal sequence.
PN WO200194402-A1.
PD 13-DEC-2001.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 40.9%; Score 38; DB 5; Length 15;
Best Local Similarity 75.0%; Pred. No. 27;
RESULT 863
ID AEF33716 standard; protein; 69 AA.
DE Human coronavirus HKU1 amino acid sequence SEQ ID NO:2302.
PN US2006018923-A1.
PD 26-JAN-2006.
PA (YUEN/) YUEN K Y.
PA (WOOC/) WOO C Y P.
PA (LAUK/) LAU K P S.
PA (CHAN/) CHAN K H.
PA (POON/) POON L M.
PA (PEIR/) PEIRIS J S M.
PA (GUAN/) GUAN Y.
Query Match 40.9%; Score 38; DB 10; Length 69;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
RESULT 864
ID AAY59902 standard; protein; 70 AA.
DE Human normal pancreas tissue derived protein 10.
PN DE19818598-A1.
PD 21-OCT-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 40.9%; Score 38; DB 2; Length 70;
Best Local Similarity 41.7%; Pred. No. 1.5e+02;
RESULT 865
ID AAY59907 standard; protein; 70 AA.
DE Human normal pancreas tissue derived protein 15.
PN DE19818598-A1.
PD 21-OCT-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 40.9%; Score 38; DB 2; Length 70;
Best Local Similarity 41.7%; Pred. No. 1.5e+02;
RESULT 866
ID AAY59914 standard; protein; 70 AA.
DE Human normal pancreas tissue derived protein 22.
PN DE19818598-A1.
PD 21-OCT-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 40.9%; Score 38; DB 2; Length 70;
Best Local Similarity 41.7%; Pred. No. 1.5e+02;
RESULT 867
ID ADP07825 standard; protein; 84 AA.
DE Human secreted protein, seq id 308.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 40.9%; Score 38; DB 8; Length 84;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
RESULT 868
ID AAY11056 standard; protein; 100 AA.
DE H. pylori ORF hp2e10911_24804577_c3_104 cellular protein.
PN WO9824475-A1.
PD 11-JUN-1998.
PA (ASTR) ASTRA AB.
Query Match 40.9%; Score 38; DB 2; Length 100;
Best Local Similarity 31.2%; Pred. No. 2.3e+02;
RESULT 869
ID AAU74692 standard; protein; 110 AA.
DE Human NPAT protein 12.
PN WO200194402-A1.
PD 13-DEC-2001.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 40.9%; Score 38; DB 5; Length 110;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
RESULT 870
ID ADC24809 standard; protein; 140 AA.
DE Human breast specific polypeptide (BSP) DEX0238_130, SEQ ID NO:130.
PN WO2003020900-A2.
PD 13-MAR-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 40.9%; Score 38; DB 7; Length 140;
Best Local Similarity 54.5%; Pred. No. 3.3e+02;
RESULT 871
ID ADQ65969 standard; protein; 140 AA.
DE Novel human protein sequence #942.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 40.9%; Score 38; DB 8; Length 140;
Best Local Similarity 63.6%; Pred. No. 3.3e+02;
RESULT 872
ID ADR99381 standard; protein; 142 AA.
DE Chlamydia pneumoniae protein #13 for treating Chlamydia infections.
PN WO2004074318-A2.
PD 02-SEP-2004.
PA (INSP) INST PASTEUR.
PA (CNRS) CENT NAT RECH SCI.
Query Match 40.9%; Score 38; DB 8; Length 142;
Best Local Similarity 47.1%; Pred. No. 3.4e+02;
RESULT 873
ID ADQ08608 standard; protein; 173 AA.
DE Ciona intestinalis nervous system associated protein SeqID10.
PN JP2004057127-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 40.9%; Score 38; DB 8; Length 173;
Best Local Similarity 40.0%; Pred. No. 4.3e+02;
RESULT 874
ID ADJ48525 standard; protein; 178 AA.
DE Oil-associated gene related protein #25.

PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 40.9%; Score 38; DB 8; Length 178;
Best Local Similarity 46.7%; Pred. No. 4.4e+02;
RESULT 875
ID AAG19526 standard; protein; 215 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 21361.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 40.9%; Score 38; DB 3; Length 215;
Best Local Similarity 61.5%; Pred. No. 5.4e+02;
RESULT 876
ID AAU43540 standard; protein; 217 AA.
DE Propionibacterium acnes immunogenic protein #4436.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 40.9%; Score 38; DB 4; Length 217;
Best Local Similarity 33.3%; Pred. No. 5.5e+02;
RESULT 877
ID ABM40059 standard; protein; 217 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #4735.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 40.9%; Score 38; DB 6; Length 217;
Best Local Similarity 33.3%; Pred. No. 5.5e+02;
RESULT 878
ID ADH61297 standard; protein; 270 AA.
DE INTSIG protein 7519192CD1, SEQ ID 14.
PN WO2004001005-A2.
PD 31-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 40.9%; Score 38; DB 8; Length 270;
Best Local Similarity 54.5%; Pred. No. 7e+02;
RESULT 879
ID AAY35206 standard; protein; 291 AA.
DE Chlamydia pneumoniae transmembrane protein sequence.
PN WO9927105-A2.
PD 03-JUN-1999.
PA (GEST) GENSET.
Query Match 40.9%; Score 38; DB 2; Length 291;
Best Local Similarity 47.1%; Pred. No. 7.7e+02;
RESULT 880
ID AAG54677 standard; protein; 296 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 69755.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 40.9%; Score 38; DB 3; Length 296;
Best Local Similarity 58.3%; Pred. No. 7.8e+02;
RESULT 881
ID ABU17283 standard; protein; 302 AA.
DE Protein encoded by Prokaryotic essential gene #2810.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 40.9%; Score 38; DB 6; Length 302;
Best Local Similarity 77.8%; Pred. No. 8e+02;
RESULT 882
ID ABG18959 standard; protein; 325 AA.
DE Novel human diagnostic protein #18950.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 40.9%; Score 38; DB 4; Length 325;
Best Local Similarity 41.2%; Pred. No. 8.7e+02;
RESULT 883
ID ADY50213 standard; protein; 334 AA.
DE Human PDE7A phosphodiesterase domain SEQ ID NO:22.
PN US2005048573-A1.
PD 03-MAR-2005.
PA (PLEX-) PLEXXIKON INC.
Query Match 40.9%; Score 38; DB 9; Length 334;
Best Local Similarity 54.5%; Pred. No. 9e+02;
RESULT 884
ID ADZ46769 standard; protein; 334 AA.
DE Human PDE7A phosphodiesterase domain, SEQ ID NO: 22.
PN US2005079548-A1.
PD 14-APR-2005.
PA (PLEX-) PLEXXIKON INC.
Query Match 40.9%; Score 38; DB 9; Length 334;
Best Local Similarity 54.5%; Pred. No. 9e+02;
RESULT 885
ID ABB07912 standard; protein; 336 AA.
DE Human PDE7a3 splice variant polypeptide.
PN WO200183772-A1.
PD 08-NOV-2001.
PA (MERE) MERCK PATENT GMBH.
Query Match 40.9%; Score 38; DB 5; Length 336;
Best Local Similarity 54.5%; Pred. No. 9e+02;
RESULT 886
ID AAR54070 standard; protein; 339 AA.
DE Prod. of gene participating in homologous recombination.
PN JP06141863-A.
PD 24-MAY-1994.
PA (MORI/) MORITA T.
PA (MATS/) MATSUSHIRO A.
Query Match 40.9%; Score 38; DB 2; Length 339;
Best Local Similarity 53.3%; Pred. No. 9.1e+02;
RESULT 887
ID AAR78183 standard; protein; 339 AA.
DE Human RAD51 protein, involved in DNA repair.
PN JP07143890-A.
PD 06-JUN-1995.
PA (TOYM) TOYOBO KK.
Query Match 40.9%; Score 38; DB 2; Length 339;
Best Local Similarity 53.3%; Pred. No. 9.1e+02;
RESULT 888
ID AAR78181 standard; protein; 339 AA.
DE Mouse RAD51 protein, involved in DNA repair and recombination.
PN JP07143890-A.
PD 06-JUN-1995.
PA (TOYM) TOYOBO KK.
Query Match 40.9%; Score 38; DB 2; Length 339;
Best Local Similarity 53.3%; Pred. No. 9.1e+02;
RESULT 889
ID AAW62523 standard; peptide; 339 AA.
DE Sequence of the specification.
PN WO9820030-A2.
PD 14-MAY-1998.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 40.9%; Score 38; DB 2; Length 339;
Best Local Similarity 53.3%; Pred. No. 9.1e+02;
RESULT 890
ID AAW62522 standard; peptide; 339 AA.
DE Sequence of the specification.
PN WO9820030-A2.
PD 14-MAY-1998.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 40.9%; Score 38; DB 2; Length 339;
Best Local Similarity 53.3%; Pred. No. 9.1e+02;
RESULT 891
ID AAY87918 standard; protein; 339 AA.
DE Human Rad51 protein.
PN US6057104-A.
PD 02-MAY-2000.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 40.9%; Score 38; DB 3; Length 339;
Best Local Similarity 53.3%; Pred. No. 9.1e+02;
RESULT 892
ID AAY87917 standard; protein; 339 AA.

DE Mammalian Rad51 protein.
PN US6057104-A.
PD 02-MAY-2000.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 40.9%; Score 38; DB 3; Length 339;
Best Local Similarity 53.3%; Pred. No. 9.1e+02;
RESULT 893
ID ABB07642 standard; protein; 339 AA.
DE Human RAD51 protein sequence.
PN WO200208432-A2.
PD 31-JAN-2002.
PA (RHOB-) RHOBIO.
Query Match 40.9%; Score 38; DB 5; Length 339;
Best Local Similarity 53.3%; Pred. No. 9.1e+02;
RESULT 894
ID ADK67821 standard; protein; 339 AA.
DE Human RAD51 polypeptide.
PN WO2004012755-A1.
PD 12-FEB-2004.
PA (WIST-) WISTAR INST.
Query Match 40.9%; Score 38; DB 8; Length 339;
Best Local Similarity 53.3%; Pred. No. 9.1e+02;
RESULT 895
ID ADQ07009 standard; protein; 339 AA.
DE Mouse Rad51 protein SEQ ID NO:2.
PN JP2004173512-A.
PD 24-JUN-2004.
PA (MORI/) MORITA T.
Query Match 40.9%; Score 38; DB 8; Length 339;
Best Local Similarity 53.3%; Pred. No. 9.1e+02;
RESULT 896
ID ADQ07011 standard; protein; 339 AA.
DE Human Rad51 protein SEQ ID NO:4.
PN JP2004173512-A.
PD 24-JUN-2004.
PA (MORI/) MORITA T.
Query Match 40.9%; Score 38; DB 8; Length 339;
Best Local Similarity 53.3%; Pred. No. 9.1e+02;
RESULT 897
ID ADY15466 standard; protein; 339 AA.
DE PRO polypeptide SEQ ID NO 1272.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 40.9%; Score 38; DB 9; Length 339;
Best Local Similarity 53.3%; Pred. No. 9.1e+02;
RESULT 898
ID ADZ09769 standard; protein; 339 AA.
DE Human breast cancer marker RAD51 protein.
PN EP1522594-A2.
PD 13-APR-2005.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 40.9%; Score 38; DB 9; Length 339;
Best Local Similarity 53.3%; Pred. No. 9.1e+02;
RESULT 899
ID AED22820 standard; protein; 339 AA.
DE Human RAD51 homolog protein.
PN WO2005097189-A1.
PD 20-OCT-2005.
PA (GENE-) GENECARE RES INST CO LTD.
Query Match 40.9%; Score 38; DB 9; Length 339;
Best Local Similarity 53.3%; Pred. No. 9.1e+02;
RESULT 900
ID ADQ67649 standard; protein; 340 AA.
DE Novel human protein sequence #2315.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 40.9%; Score 38; DB 8; Length 340;
Best Local Similarity 53.3%; Pred. No. 9.1e+02;
RESULT 901
ID ADR46211 standard; protein; 354 AA.
DE Human phosphodiesterase 7A truncation polypeptide 2.
PN WO2004069989-A2.
PD 19-AUG-2004.
PA (AFFI-) AFFINIUM PHARM INC.
Query Match 40.9%; Score 38; DB 8; Length 354;
Best Local Similarity 54.5%; Pred. No. 9.6e+02;
RESULT 902
ID ADR46209 standard; protein; 359 AA.
DE Human phosphodiesterase 7A truncation polypeptide 1.
PN WO2004069989-A2.
PD 19-AUG-2004.
PA (AFFI-) AFFINIUM PHARM INC.
Query Match 40.9%; Score 38; DB 8; Length 359;
Best Local Similarity 54.5%; Pred. No. 9.7e+02;
RESULT 903
ID ABU01155 standard; protein; 361 AA.
DE S. pneumoniae type 4 strain protein from coding region #728.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 40.9%; Score 38; DB 6; Length 361;
Best Local Similarity 50.0%; Pred. No. 9.8e+02;
RESULT 904
ID AAG19525 standard; protein; 363 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 21360.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 40.9%; Score 38; DB 3; Length 363;
Best Local Similarity 61.5%; Pred. No. 9.9e+02;
RESULT 905
ID ADX88971 standard; protein; 365 AA.
DE Plant full length insert polypeptide seqid 51635.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 40.9%; Score 38; DB 8; Length 365;
Best Local Similarity 52.9%; Pred. No. 9.9e+02;
RESULT 906
ID ADR66273 standard; protein; 368 AA.
DE Human prostatic carcinoma derived protein SEQ ID 127 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 40.9%; Score 38; DB 8; Length 368;
Best Local Similarity 70.0%; Pred. No. 1e+03;
RESULT 907
ID ADR66834 standard; protein; 368 AA.
DE Human prostatic carcinoma derived DNA SEQ ID 127 #4.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 40.9%; Score 38; DB 8; Length 368;
Best Local Similarity 70.0%; Pred. No. 1e+03;
RESULT 908
ID ADK16327 standard; protein; 369 AA.
DE Nanoarchaeum equitans cancer-associated (CA) protein #139.
PN WO2003093434-A2.
PD 13-NOV-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 40.9%; Score 38; DB 8; Length 369;

Best Local Similarity 63.6%; Pred. No. 1e+03;
RESULT 909
ID ADN42042 standard; protein; 369 AA.
DE Amino acid sequence of human polypeptide #8.
PN WO2004033686-A1.
PD 22-APR-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 40.9%; Score 38; DB 8; Length 369;
Best Local Similarity 63.6%; Pred. No. 1e+03;
RESULT 910
ID ADN42014 standard; protein; 370 AA.
DE Amino acid sequence of human polypeptide #1.
PN WO2004033686-A1.
PD 22-APR-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 40.9%; Score 38; DB 8; Length 370;
Best Local Similarity 63.6%; Pred. No. 1e+03;
RESULT 911
ID AAG19524 standard; protein; 378 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 21359.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 40.9%; Score 38; DB 3; Length 378;
Best Local Similarity 61.5%; Pred. No. 1e+03;
RESULT 912
ID ADN42040 standard; protein; 380 AA.
DE Amino acid sequence of human polypeptide #7.
PN WO2004033686-A1.
PD 22-APR-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 40.9%; Score 38; DB 8; Length 380;
Best Local Similarity 63.6%; Pred. No. 1e+03;
RESULT 913
ID ADN42029 standard; protein; 381 AA.
DE Amino acid sequence of human polypeptide #2.
PN WO2004033686-A1.
PD 22-APR-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 40.9%; Score 38; DB 8; Length 381;
Best Local Similarity 63.6%; Pred. No. 1e+03;
RESULT 914
ID ADN42038 standard; protein; 381 AA.
DE Amino acid sequence of human polypeptide #6.
PN WO2004033686-A1.
PD 22-APR-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 40.9%; Score 38; DB 8; Length 381;
Best Local Similarity 63.6%; Pred. No. 1e+03;
RESULT 915
ID ADN42030 standard; protein; 382 AA.
DE Amino acid sequence of human polypeptide #3.
PN WO2004033686-A1.
PD 22-APR-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 40.9%; Score 38; DB 8; Length 382;
Best Local Similarity 63.6%; Pred. No. 1e+03;
RESULT 916
ID ADN42036 standard; protein; 383 AA.
DE Amino acid sequence of human polypeptide #5.
PN WO2004033686-A1.
PD 22-APR-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 40.9%; Score 38; DB 8; Length 383;
Best Local Similarity 63.6%; Pred. No. 1e+03;
RESULT 917
ID ADN42031 standard; protein; 384 AA.
DE Amino acid sequence of human polypeptide #4.
PN WO2004033686-A1.
PD 22-APR-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 40.9%; Score 38; DB 8; Length 384;
Best Local Similarity 63.6%; Pred. No. 1.1e+03;
RESULT 918
ID AAR88225 standard; protein; 395 AA.
DE Transcription factor BTF2 complex p44 subunit.
PN WO9529245-A2.
PD 02-NOV-1995.
PA (ASRE-) ASSOC DEV RECH EN GENETIQUE MOLECULAIRE.
Query Match 40.9%; Score 38; DB 2; Length 395;
Best Local Similarity 70.0%; Pred. No. 1.1e+03;
RESULT 919
ID ADN05016 standard; protein; 395 AA.
DE Antipsoriatic protein sequence #688.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 40.9%; Score 38; DB 8; Length 395;
Best Local Similarity 70.0%; Pred. No. 1.1e+03;
RESULT 920
ID ADQ19648 standard; protein; 395 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2467.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 40.9%; Score 38; DB 8; Length 395;
Best Local Similarity 70.0%; Pred. No. 1.1e+03;
RESULT 921
ID ADP55553 standard; protein; 395 AA.
DE Human PRO protein sequence SEQ ID NO:1529.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 40.9%; Score 38; DB 8; Length 395;
Best Local Similarity 70.0%; Pred. No. 1.1e+03;
RESULT 922
ID ADY18147 standard; protein; 395 AA.
DE PRO polypeptide SEQ ID NO 3953.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 40.9%; Score 38; DB 9; Length 395;
Best Local Similarity 70.0%; Pred. No. 1.1e+03;
RESULT 923
ID ADC94935 standard; protein; 400 AA.
DE E. faecium protein sequence SEQ ID 4562.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 40.9%; Score 38; DB 7; Length 400;
Best Local Similarity 58.3%; Pred. No. 1.1e+03;
RESULT 924
ID AAU79713 standard; protein; 424 AA.
DE Human phosphodiesterase, PDE7A3 splice variant.
PN WO200222661-A2.
PD 21-MAR-2002.
PA (BEAV/) BEAVO J A.
PA (SEEB/) SEEBECK T.
PA (SODE/) SODERLING S H.
PA (RASC/) RASCON A.
PA (ZORA/) ZORAGHI R.
PA (KUNZ/) KUNZ S.
PA (GONG/) GONG K.
PA (GLAV/) GLAVAS N.
Query Match 40.9%; Score 38; DB 5; Length 424;
Best Local Similarity 54.5%; Pred. No. 1.2e+03;
RESULT 925
ID AAU79727 standard; protein; 424 AA.
DE Human cyclic nucleotide phosphodiesterase, PDE8A variant #3.
PN WO200222661-A2.
PD 21-MAR-2002.
PA (BEAV/) BEAVO J A.
PA (SEEB/) SEEBECK T.
PA (SODE/) SODERLING S H.
PA (RASC/) RASCON A.
PA (ZORA/) ZORAGHI R.
PA (KUNZ/) KUNZ S.

PA (GONG/) GONG K.
PA (GLAV/) GLAVAS N.
Query Match 40.9%; Score 38; DB 5; Length 424;
Best Local Similarity 54.5%; Pred. No. 1.2e+03;
RESULT 926
ID ABM83119 standard; protein; 425 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3368.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 40.9%; Score 38; DB 8; Length 425;
Best Local Similarity 54.5%; Pred. No. 1.2e+03;
RESULT 927
ID AAE24528 standard; protein; 426 AA.
DE Mouse PDE7 protein.
PN WO200226954-A2.
PD 04-APR-2002.
PA (WARN) WARNER LAMBERT CO.
Query Match 40.9%; Score 38; DB 5; Length 426;
Best Local Similarity 54.5%; Pred. No. 1.2e+03;
RESULT 928
ID AAE24527 standard; protein; 426 AA.
DE Human PDE7 protein.
PN WO200226954-A2.
PD 04-APR-2002.
PA (WARN) WARNER LAMBERT CO.
Query Match 40.9%; Score 38; DB 5; Length 426;
Best Local Similarity 54.5%; Pred. No. 1.2e+03;
RESULT 929
ID AAE24529 standard; protein; 426 AA.
DE Rat PDE7 protein.
PN WO200226954-A2.
PD 04-APR-2002.
PA (WARN) WARNER LAMBERT CO.
Query Match 40.9%; Score 38; DB 5; Length 426;
Best Local Similarity 54.5%; Pred. No. 1.2e+03;
RESULT 930
ID AAE24533 standard; protein; 428 AA.
DE Rat PDE7a protein.
PN WO200226954-A2.
PD 04-APR-2002.
PA (WARN) WARNER LAMBERT CO.
Query Match 40.9%; Score 38; DB 5; Length 428;
Best Local Similarity 54.5%; Pred. No. 1.2e+03;
RESULT 931
ID AAU16967 standard; protein; 432 AA.
DE Human novel secreted protein, SEQ ID 208.
PN WO200155441-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 40.9%; Score 38; DB 4; Length 432;
Best Local Similarity 54.5%; Pred. No. 1.2e+03;
RESULT 932
ID ABM83118 standard; protein; 437 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3367.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 40.9%; Score 38; DB 8; Length 437;
Best Local Similarity 54.5%; Pred. No. 1.2e+03;
RESULT 933
ID ABM83121 standard; protein; 441 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3370.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 40.9%; Score 38; DB 8; Length 441;
Best Local Similarity 54.5%; Pred. No. 1.2e+03;
RESULT 934
ID ABR40577 standard; protein; 445 AA.
DE Human secreted protein #SEQ ID 327.
PN WO200268628-A1.
PD 06-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 40.9%; Score 38; DB 5; Length 445;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
RESULT 935
ID AAE24532 standard; protein; 446 AA.
DE Human PDE7A2 protein.
PN WO200226954-A2.
PD 04-APR-2002.
PA (WARN) WARNER LAMBERT CO.
Query Match 40.9%; Score 38; DB 5; Length 446;
Best Local Similarity 54.5%; Pred. No. 1.2e+03;
RESULT 936
ID AAR97669 standard; protein; 448 AA.
DE Chicken Yes proto-oncogene associated protein YAP65.
PN WO9617061-A1.
PD 06-JUN-1996.
PA (UYRQ) UNIV ROCKEFELLER.
PA (DELB-) DELBRUECK CENT MOLECULAR MEDICINE MAX.
Query Match 40.9%; Score 38; DB 2; Length 448;
Best Local Similarity 58.3%; Pred. No. 1.3e+03;
RESULT 937
ID AAE24530 standard; protein; 456 AA.
DE Mouse PDE7A2 protein.
PN WO200226954-A2.
PD 04-APR-2002.
PA (WARN) WARNER LAMBERT CO.
Query Match 40.9%; Score 38; DB 5; Length 456;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
RESULT 938
ID ADO21910 standard; protein; 456 AA.
DE Human cAMP phosphodiesterase PDE7a2 protein.
PN WO2004044229-A2.
PD 27-MAY-2004.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 40.9%; Score 38; DB 8; Length 456;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
RESULT 939
ID ADY18172 standard; protein; 456 AA.
DE PRO polypeptide SEQ ID NO 3978.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 40.9%; Score 38; DB 9; Length 456;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
RESULT 940
ID ABM83120 standard; protein; 468 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3369.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 40.9%; Score 38; DB 8; Length 468;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
RESULT 941
ID ABR40523 standard; protein; 477 AA.
DE Human secreted protein #SEQ ID 273.
PN WO200268628-A1.
PD 06-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 40.9%; Score 38; DB 5; Length 477;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
RESULT 942
ID AAE24531 standard; protein; 482 AA.
DE Human PDE7A1 protein.
PN WO200226954-A2.
PD 04-APR-2002.
PA (WARN) WARNER LAMBERT CO.
Query Match 40.9%; Score 38; DB 5; Length 482;
Best Local Similarity 54.5%; Pred. No. 1.4e+03;
RESULT 943
ID ADO40842 standard; protein; 482 AA.
DE Human phosphodiesterase 7a1, PDE7a1.
PN WO2004044235-A1.
PD 27-MAY-2004.

PA (FARB) BAYER HEALTHCARE AG.
Query Match 40.9%; Score 38; DB 8; Length 482;
Best Local Similarity 54.5%; Pred. No. 1.4e+03;
RESULT 944
ID ADR46207 standard; protein; 482 AA.
DE Human phosphodiesterase 7A.
PN WO2004069989-A2.
PD 19-AUG-2004.
PA (AFFI-) AFFINIUM PHARM INC.
Query Match 40.9%; Score 38; DB 8; Length 482;
Best Local Similarity 54.5%; Pred. No. 1.4e+03;
RESULT 945
ID ADY18092 standard; protein; 482 AA.
DE PRO polypeptide SEQ ID NO 3898.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 40.9%; Score 38; DB 9; Length 482;
Best Local Similarity 54.5%; Pred. No. 1.4e+03;
RESULT 946
ID AAW00094 standard; protein; 498 AA.
DE cAMP phosphodiesterase encoded by plasmid pTM22 (ATCC 68601).
PN US5527896-A.
PD 18-JUN-1996.
PA (COLD-) COLD SPRING HARBOR LAB.
Query Match 40.9%; Score 38; DB 2; Length 498;
Best Local Similarity 54.5%; Pred. No. 1.4e+03;
RESULT 947
ID AAY49808 standard; protein; 498 AA.
DE Human glioblastoma cell cAMP phosphodiesterase pTM22 protein.
PN US5977305-A.
PD 02-NOV-1999.
PA (COLD-) COLD SPRING HARBOR LAB.
Query Match 40.9%; Score 38; DB 2; Length 498;
Best Local Similarity 54.5%; Pred. No. 1.4e+03;
RESULT 948
ID AAB20619 standard; protein; 498 AA.
DE pTM22 human glioblastoma cell insert protein sequence SEQ ID NO:20.
PN US6100025-A.
PD 08-AUG-2000.
PA (COLD-) COLD SPRING HARBOR LAB.
Query Match 40.9%; Score 38; DB 3; Length 498;
Best Local Similarity 54.5%; Pred. No. 1.4e+03;
RESULT 949
ID ADR66097 standard; protein; 498 AA.
DE Human prostatic carcinoma derived protein SEQ ID 293 #1.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 40.9%; Score 38; DB 8; Length 498;
Best Local Similarity 54.5%; Pred. No. 1.4e+03;
RESULT 950
ID ADR66439 standard; protein; 498 AA.
DE Human prostatic carcinoma derived protein SEQ ID 293 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 40.9%; Score 38; DB 8; Length 498;
Best Local Similarity 54.5%; Pred. No. 1.4e+03;
RESULT 951
ID ADY25040 standard; protein; 507 AA.
DE Plant full length insert polypeptide seqid 72824.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 40.9%; Score 38; DB 8; Length 507;
Best Local Similarity 47.1%; Pred. No. 1.4e+03;
RESULT 952
ID ABM88992 standard; protein; 525 AA.
DE Rice abiotic stress responsive polypeptide SEQ ID NO:7238.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 40.9%; Score 38; DB 7; Length 525;
Best Local Similarity 63.6%; Pred. No. 1.5e+03;
RESULT 953
ID AAB42693 standard; protein; 529 AA.
DE Human ORFX ORF2457 polypeptide sequence SEQ ID NO:4914.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 40.9%; Score 38; DB 3; Length 529;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
RESULT 954
ID ADU80839 standard; protein; 529 AA.
DE Xenopus NRSF protein.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 40.9%; Score 38; DB 8; Length 529;
Best Local Similarity 46.7%; Pred. No. 1.5e+03;
RESULT 955
ID ADY70504 standard; protein; 529 AA.
DE Human beta-amyloid precursor protein, MGC4022.
PN WO2005023858-A1.
PD 17-MAR-2005.
PA (CELL-) CELLZOME AG.
Query Match 40.9%; Score 38; DB 9; Length 529;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
RESULT 956
ID ABU29965 standard; protein; 548 AA.
DE Protein encoded by Prokaryotic essential gene #15492.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 40.9%; Score 38; DB 6; Length 548;
Best Local Similarity 58.3%; Pred. No. 1.6e+03;
RESULT 957
ID ADJ50318 standard; protein; 558 AA.
DE Oil-associated gene related protein #1818.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 40.9%; Score 38; DB 8; Length 558;
Best Local Similarity 58.3%; Pred. No. 1.6e+03;
RESULT 958
ID ADN72631 standard; protein; 558 AA.
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 526.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Query Match 40.9%; Score 38; DB 8; Length 558;
Best Local Similarity 58.3%; Pred. No. 1.6e+03;
RESULT 959
ID ABR40445 standard; protein; 591 AA.
DE Human secreted protein #SEQ ID 195.
PN WO200268628-A1.
PD 06-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.

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  Query Match             40.9%;  Score 38;  DB 5;  Length 591;
  Best Local Similarity   60.0%;  Pred. No. 1.7e+03;
RESULT 960
ID   ADY80077 standard; protein; 607 AA.
DE   Amino acid sequence of murine pannexin 2.
PN   WO2005026170-A2.
PD   24-MAR-2005.
PA   (INSP ) INST PASTEUR.
  Query Match             40.9%;  Score 38;  DB 9;  Length 607;
  Best Local Similarity   41.2%;  Pred. No. 1.8e+03;
RESULT 961
ID   ADY80065 standard; protein; 633 AA.
DE   Amino acid sequence of human pannexin 2.
PN   WO2005026170-A2.
PD   24-MAR-2005.
PA   (INSP ) INST PASTEUR.
  Query Match             40.9%;  Score 38;  DB 9;  Length 633;
  Best Local Similarity   41.2%;  Pred. No. 1.9e+03;
RESULT 962
ID   ABR42418 standard; protein; 653 AA.
DE   Human potassium channel Kv1.4.
PN   WO2003035690-A2.
PD   01-MAY-2003.
PA   (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
  Query Match             40.9%;  Score 38;  DB 6;  Length 653;
  Best Local Similarity   50.0%;  Pred. No. 1.9e+03;
RESULT 963
ID   ADA83742 standard; protein; 653 AA.
DE   Human KCNA4 protein.
PN   WO2002103028-A2.
PD   27-DEC-2002.
PA   (BIOM-) BIOMEDICAL CENT.
  Query Match             40.9%;  Score 38;  DB 6;  Length 653;
  Best Local Similarity   50.0%;  Pred. No. 1.9e+03;
RESULT 964
ID   ADE57786 standard; protein; 653 AA.
DE   Human Protein P22459, SEQ ID NO 3651.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
  Query Match             40.9%;  Score 38;  DB 7;  Length 653;
  Best Local Similarity   50.0%;  Pred. No. 1.9e+03;
RESULT 965
ID   ADE63497 standard; protein; 653 AA.
DE   Human Protein P22459, SEQ ID NO 9441.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
  Query Match             40.9%;  Score 38;  DB 7;  Length 653;
  Best Local Similarity   50.0%;  Pred. No. 1.9e+03;
RESULT 966
ID   ABO59441 standard; protein; 653 AA.
DE   Human genome derived single exon protein #5675.
PN   US2003194704-A1.
PD   16-OCT-2003.
PA   (PENN/) PENN S G.
PA   (RANK/) RANK D R.
PA   (HANZ/) HANZEL D K.
  Query Match             40.9%;  Score 38;  DB 8;  Length 653;
  Best Local Similarity   50.0%;  Pred. No. 1.9e+03;
RESULT 967
ID   ADE63495 standard; protein; 655 AA.
DE   Rat Protein CAA34133, SEQ ID NO 9439.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
  Query Match             40.9%;  Score 38;  DB 7;  Length 655;
  Best Local Similarity   50.0%;  Pred. No. 1.9e+03;
RESULT 968
ID   ADE57784 standard; protein; 655 AA.
DE   Rat Protein P15385, SEQ ID NO 3649.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
  Query Match             40.9%;  Score 38;  DB 7;  Length 655;
  Best Local Similarity   50.0%;  Pred. No. 1.9e+03;
RESULT 969
ID   ADY80071 standard; protein; 664 AA.
DE   Amino acid sequence of rat pannexin 2.
PN   WO2005026170-A2.
PD   24-MAR-2005.
PA   (INSP ) INST PASTEUR.
  Query Match             40.9%;  Score 38;  DB 9;  Length 664;
  Best Local Similarity   41.2%;  Pred. No. 2e+03;
RESULT 970
ID   ADM04783 standard; protein; 667 AA.
DE   Human protein of the invention SEQ ID NO:3468.
PN   EP1347046-A1.
PD   24-SEP-2003.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
  Query Match             40.9%;  Score 38;  DB 7;  Length 667;
  Best Local Similarity   41.2%;  Pred. No. 2e+03;
RESULT 971
ID   AEC87713 standard; protein; 667 AA.
DE   Human cDNA clone protein KIDNE20021910, SEQ ID 3468.
PN   EP1580263-A1.
PD   28-SEP-2005.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
  Query Match             40.9%;  Score 38;  DB 9;  Length 667;
  Best Local Similarity   41.2%;  Pred. No. 2e+03;
RESULT 972
ID   ADJ38278 standard; protein; 670 AA.
DE   Plastid division-related Arc5 orthlogue protein 60.
PN   WO2004001003-A2.
PD   31-DEC-2003.
PA   (UNMS ) UNIV MICHIGAN STATE.
  Query Match             40.9%;  Score 38;  DB 8;  Length 670;
  Best Local Similarity   50.0%;  Pred. No. 2e+03;
RESULT 973
ID   ABO75000 standard; protein; 700 AA.
DE   Pseudomonas aeruginosa polypeptide #7175.
PN   US6551795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match             40.9%;  Score 38;  DB 7;  Length 700;
  Best Local Similarity   43.8%;  Pred. No. 2.1e+03;
RESULT 974
ID   ADS23975 standard; protein; 712 AA.
DE   Bacterial polypeptide #13008.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
  Query Match             40.9%;  Score 38;  DB 8;  Length 712;
  Best Local Similarity   38.5%;  Pred. No. 2.1e+03;
RESULT 975
ID   ADS43873 standard; protein; 757 AA.
DE   Bacterial polypeptide #22303.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
  Query Match             40.9%;  Score 38;  DB 8;  Length 757;
  Best Local Similarity   50.0%;  Pred. No. 2.3e+03;
RESULT 976
ID   AAE03804 standard; protein; 772 AA.
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DE Schizosaccharomyces pombe RAD 15 protein.
PN WO200142434-A1.
PD 14-JUN-2001.
PA (MERI) MERCK & CO INC.
Query Match 40.9%; Score 38; DB 4; Length 772;
Best Local Similarity 60.0%; Pred. No. 2.3e+03;
RESULT 977
ID ADN19422 standard; protein; 772 AA.
DE Bacterial polypeptide #2075.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 40.9%; Score 38; DB 8; Length 772;
Best Local Similarity 60.0%; Pred. No. 2.3e+03;
RESULT 978
ID ABM84550 standard; protein; 793 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4799.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 40.9%; Score 38; DB 8; Length 793;
Best Local Similarity 40.0%; Pred. No. 2.4e+03;
RESULT 979
ID ADT55566 standard; protein; 811 AA.
DE Plant polypeptide, SEQ ID 5643.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 40.9%; Score 38; DB 8; Length 811;
Best Local Similarity 46.2%; Pred. No. 2.5e+03;
RESULT 980
ID ADS24019 standard; protein; 822 AA.
DE Bacterial polypeptide #13052.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 40.9%; Score 38; DB 8; Length 822;
Best Local Similarity 60.0%; Pred. No. 2.5e+03;
RESULT 981
ID ABB58526 standard; protein; 882 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 2370.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 40.9%; Score 38; DB 4; Length 882;
Best Local Similarity 38.9%; Pred. No. 2.7e+03;
RESULT 982
ID ADN19659 standard; protein; 886 AA.
DE Bacterial polypeptide #2312.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 40.9%; Score 38; DB 8; Length 886;
Best Local Similarity 40.0%; Pred. No. 2.7e+03;
RESULT 983
ID ABO75893 standard; protein; 940 AA.
DE Pseudomonas aeruginosa polypeptide #8068.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 40.9%; Score 38; DB 7; Length 940;
Best Local Similarity 63.6%; Pred. No. 2.9e+03;
RESULT 984
ID ABM90649 standard; protein; 981 AA.
DE M. xanthus protein sequence, seq id 9848.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 40.9%; Score 38; DB 9; Length 981;
Best Local Similarity 42.9%; Pred. No. 3e+03;
RESULT 985
ID ADX05670 standard; protein; 998 AA.
DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 235.
PN WO2005012875-A2.
PD 10-FEB-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 40.9%; Score 38; DB 9; Length 998;
Best Local Similarity 60.0%; Pred. No. 3.1e+03;
RESULT 986
ID AAR43341 standard; protein; 1068 AA.
DE p110.
PN WO9321328-A1.
PD 28-OCT-1993.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 40.9%; Score 38; DB 2; Length 1068;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
RESULT 987
ID AAR43342 standard; protein; 1068 AA.
DE Human p110.
PN WO9321328-A1.
PD 28-OCT-1993.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 40.9%; Score 38; DB 2; Length 1068;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
RESULT 988
ID AAR46294 standard; protein; 1068 AA.
DE PtdIns 3-kinase 110 kD catalytic subnit.
PN WO9403609-A1.
PD 17-FEB-1994.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
Query Match 40.9%; Score 38; DB 2; Length 1068;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
RESULT 989
ID AAU09687 standard; protein; 1068 AA.
DE Human p110alpha isoform of PI3-kinase.
PN WO200185986-A2.
PD 15-NOV-2001.
PA (ICOS-) ICOS CORP.
Query Match 40.9%; Score 38; DB 5; Length 1068;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
RESULT 990
ID ADH68169 standard; protein; 1068 AA.
DE PI3K-alpha protein.
PN US2003182669-A1.
PD 25-SEP-2003.
PA (ROCK/) ROCKMAN H A.
PA (PRAS/) NAGA PRASAD S V.
PA (LAPO/) LAPORTE S A.
PA (BARA/) BARAK L S.
PA (CARO/) CARON M G.
Query Match 40.9%; Score 38; DB 8; Length 1068;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
RESULT 991
ID ADU06422 standard; protein; 1068 AA.
DE Novel bronchial cancer-associated human protein SeqID646.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 40.9%; Score 38; DB 8; Length 1068;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
RESULT 992
ID ADZ00491 standard; protein; 1068 AA.

DE p110-beta.
PN WO2005031341-A2.
PD 07-APR-2005.
PA (PFIZ) PFIZER HEALTH AB.
Query Match 40.9%; Score 38; DB 9; Length 1068;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
RESULT 993
ID AED31619 standard; protein; 1068 AA.
DE Human phosphatidylinositol 3-kinase (PIK3CA).
PN WO2005091849-A2.
PD 06-OCT-2005.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 40.9%; Score 38; DB 9; Length 1068;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
RESULT 994
ID AEF64786 standard; protein; 1068 AA.
DE Human phosphoinositide 3-kinase (PI3K) alpha protein.
PN US2006026702-A1.
PD 02-FEB-2006.
PA (UYDU-) UNIV DUKE.
Query Match 40.9%; Score 38; DB 10; Length 1068;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
RESULT 995
ID AAG70814 standard; protein; 1276 AA.
DE S cerevisiae apoptosis associated protein YPL090C.
PN WO200102550-A2.
PD 11-JAN-2001.
PA (JANC) JANSSEN PHARM NV.
Query Match 40.9%; Score 38; DB 4; Length 1276;
Best Local Similarity 70.0%; Pred. No. 4.1e+03;
RESULT 996
ID AAR11465 standard; peptide; 15 AA.
DE Lepidoptera allostatin polypeptide analogue.
PN EP421935-A.
PD 10-APR-1991.
PA (SANO) SANDOZ LTD.
PA (KRAM/) KRAMER S J.
PA (NOVS) NOVARTIS AG.
Query Match 40.3%; Score 37.5; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 32;
RESULT 997
ID ABP72616 standard; peptide; 15 AA.
DE Manduca sexta allatostatin.
PN WO2003014150-A2.
PD 20-FEB-2003.
PA (UYDU-) UNIV DURHAM.
PA (ENVI-) DEPT ENVIRONMENT FOOD & RURAL AFFAIRS.
Query Match 40.3%; Score 37.5; DB 6; Length 15;
Best Local Similarity 60.0%; Pred. No. 32;
RESULT 998
ID ADE14702 standard; peptide; 15 AA.
DE DmGPCR binding ligand #150.
PN US2003180297-A1.
PD 25-SEP-2003.
PA (LOWE/) LOWERY D E.
PA (SMIT/) SMITH V G.
PA (KUBI/) KUBIAK T M.
PA (LARS/) LARSEN M J.
Query Match 40.3%; Score 37.5; DB 7; Length 15;
Best Local Similarity 60.0%; Pred. No. 32;
RESULT 999
ID ADL83598 standard; peptide; 15 AA.
DE Manducta sexta allatostatin-C peptide.
PN US2003162223-A1.
PD 28-AUG-2003.
PA (LOWE/) LOWERY D E.
PA (SMIT/) SMITH V G.
PA (KUBI/) KUBIAK T M.
PA (LARS/) LARSEN M J.
Query Match 40.3%; Score 37.5; DB 7; Length 15;
Best Local Similarity 60.0%; Pred. No. 32;
RESULT 1000
ID ADY80079 standard; protein; 392 AA.
DE Amino acid sequence of murine pannexin 3.
PN WO2005026170-A2.
PD 24-MAR-2005.
PA (INSP) INST PASTEUR.
Query Match 40.3%; Score 37.5; DB 9; Length 392;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
RESULT 1001
ID ADY80073 standard; protein; 392 AA.
DE Amino acid sequence of rat pannexin 3.
PN WO2005026170-A2.
PD 24-MAR-2005.
PA (INSP) INST PASTEUR.
Query Match 40.3%; Score 37.5; DB 9; Length 392;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
RESULT 1002
ID ADY80067 standard; protein; 392 AA.
DE Amino acid sequence of human pannexin 3.
PN WO2005026170-A2.
PD 24-MAR-2005.
PA (INSP) INST PASTEUR.
Query Match 40.3%; Score 37.5; DB 9; Length 392;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
RESULT 1003
ID ABM70582 standard; protein; 806 AA.
DE Photorhabdus luminescens protein sequence #3679.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 40.3%; Score 37.5; DB 6; Length 806;
Best Local Similarity 36.4%; Pred. No. 3e+03;
RESULT 1004
ID ABB91321 standard; protein; 838 AA.
DE Herbicidally active polypeptide SEQ ID NO 532.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 40.3%; Score 37.5; DB 5; Length 838;
Best Local Similarity 56.2%; Pred. No. 3.1e+03;
RESULT 1005
ID ABG22709 standard; protein; 29 AA.
DE Novel human diagnostic protein #22700.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 4; Length 29;
Best Local Similarity 42.9%; Pred. No. 83;
RESULT 1006
ID AAM16024 standard; protein; 42 AA.
DE Peptide #2458 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 42;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
RESULT 1007
ID ABB35016 standard; peptide; 42 AA.
DE Peptide #2522 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 42;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
RESULT 1008
ID AAM28525 standard; protein; 42 AA.
DE Peptide #2562 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 42;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
RESULT 1009
ID AAM68206 standard; protein; 42 AA.

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 28512.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 42;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
RESULT 1010
ID AAM55833 standard; protein; 42 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 27938.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 42;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
RESULT 1011
ID ABG49853 standard; peptide; 42 AA.
DE Human liver peptide, SEQ ID No 28501.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 42;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
RESULT 1012
ID AAM03755 standard; protein; 42 AA.
DE Peptide #2437 encoded by probe for measuring breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 42;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
RESULT 1013
ID ADZ40090 standard; peptide; 48 AA.
DE HIV-1 gp41 ectodomain peptide variant, Seq 2.
PN WO2005034842-A2.
PD 21-APR-2005.
PA (PROG-) PROGENICS PHARM INC.
Query Match 39.8%; Score 37; DB 9; Length 48;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
RESULT 1014
ID ADU80332 standard; peptide; 50 AA.
DE HIV transmembrane envelope glycoprotein GP41-based peptide, SEQ ID 2.
PN WO2004103312-A2.
PD 02-DEC-2004.
PA (PROG-) PROGENICS PHARM INC.
Query Match 39.8%; Score 37; DB 8; Length 50;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
RESULT 1015
ID AAY12353 standard; protein; 55 AA.
DE Human 5' EST secreted protein SEQ ID NO:384.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 39.8%; Score 37; DB 2; Length 55;
Best Local Similarity 46.2%; Pred. No. 1.7e+02;
RESULT 1016
ID ABP43919 standard; protein; 64 AA.
DE FLJ20040 fis clone COL00417.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 5; Length 64;
Best Local Similarity 46.7%; Pred. No. 2e+02;
RESULT 1017
ID ADH32550 standard; protein; 70 AA.
DE Yeast smORF338-encoded polypeptide, SEQ ID NO:1008.
PN WO200268693-A2.
PD 06-SEP-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 39.8%; Score 37; DB 5; Length 70;
Best Local Similarity 41.7%; Pred. No. 2.3e+02;
RESULT 1018
ID AAM85399 standard; protein; 74 AA.
DE Human immune/haematopoietic antigen SEQ ID NO:12992.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 4; Length 74;
Best Local Similarity 53.8%; Pred. No. 2.4e+02;
RESULT 1019
ID AAB45011 standard; protein; 83 AA.
DE Human secreted protein encoded by gene 37 homologue.
PN WO200055200-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 3; Length 83;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
RESULT 1020
ID AAB45012 standard; protein; 83 AA.
DE Human secreted protein encoded by gene 37 homologue.
PN WO200055200-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 3; Length 83;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
RESULT 1021
ID ABP07339 standard; protein; 85 AA.
DE Human ORFX protein sequence SEQ ID NO:14660.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 39.8%; Score 37; DB 5; Length 85;
Best Local Similarity 27.8%; Pred. No. 2.8e+02;
RESULT 1022
ID ADI67220 standard; protein; 104 AA.
DE Lactobacillus rhamnosus polypeptide sequence #94.
PN US20040009490-A1.
PD 15-JAN-2004.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 39.8%; Score 37; DB 8; Length 104;
Best Local Similarity 41.2%; Pred. No. 3.5e+02;
RESULT 1023
ID ABB97814 standard; protein; 107 AA.
DE Human secretory polypeptide (SPTM) 66.
PN WO200220756-A2.
PD 14-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 39.8%; Score 37; DB 5; Length 107;
Best Local Similarity 46.2%; Pred. No. 3.7e+02;
RESULT 1024
ID ADY22702 standard; protein; 120 AA.
DE Plant full length insert polypeptide seqid 70486.
PN US20040034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 39.8%; Score 37; DB 8; Length 120;
Best Local Similarity 53.8%; Pred. No. 4.2e+02;
RESULT 1025
ID AAG05261 standard; protein; 149 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1600.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 149;
Best Local Similarity 47.1%; Pred. No. 5.3e+02;
RESULT 1026
ID ABG06103 standard; protein; 163 AA.
DE Novel human diagnostic protein #6094.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 4; Length 163;
Best Local Similarity 41.2%; Pred. No. 5.9e+02;

RESULT 1027
ID AAG59595 standard; protein; 166 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77099.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 166;
Best Local Similarity 47.1%; Pred. No. 6e+02;
RESULT 1028
ID AAG07269 standard; protein; 166 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4358.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 166;
Best Local Similarity 47.1%; Pred. No. 6e+02;
RESULT 1029
ID AAR57031 standard; protein; 178 AA.
DE Serotonin receptor encoded by human PCR S10 clone.
PN WO9414957-A2.
PD 07-JUL-1994.
PA (SYNA-) SYNAPTIC PHARM CORP.
Query Match 39.8%; Score 37; DB 2; Length 178;
Best Local Similarity 26.7%; Pred. No. 6.5e+02;
RESULT 1030
ID AAG10820 standard; protein; 181 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9294.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 181;
Best Local Similarity 53.8%; Pred. No. 6.6e+02;
RESULT 1031
ID AAG06866 standard; protein; 181 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 3798.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 181;
Best Local Similarity 53.8%; Pred. No. 6.6e+02;
RESULT 1032
ID AAG54822 standard; protein; 185 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 70045.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 185;
Best Local Similarity 53.8%; Pred. No. 6.8e+02;
RESULT 1033
ID AAG06865 standard; protein; 193 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 3797.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 193;
Best Local Similarity 53.8%; Pred. No. 7.1e+02;
RESULT 1034
ID AAG10819 standard; protein; 193 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9293.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 193;
Best Local Similarity 53.8%; Pred. No. 7.1e+02;
RESULT 1035
ID AAG05260 standard; protein; 194 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1599.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 194;
Best Local Similarity 47.1%; Pred. No. 7.2e+02;
RESULT 1036
ID AAG05259 standard; protein; 204 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1598.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 204;
Best Local Similarity 47.1%; Pred. No. 7.6e+02;
RESULT 1037
ID AAG10818 standard; protein; 205 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9292.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 205;
Best Local Similarity 53.8%; Pred. No. 7.6e+02;
RESULT 1038
ID AAG06864 standard; protein; 205 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 3796.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 205;
Best Local Similarity 53.8%; Pred. No. 7.6e+02;
RESULT 1039
ID AAG59594 standard; protein; 206 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77098.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 206;
Best Local Similarity 47.1%; Pred. No. 7.7e+02;
RESULT 1040
ID AAG07268 standard; protein; 206 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4357.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 206;
Best Local Similarity 47.1%; Pred. No. 7.7e+02;
RESULT 1041
ID ABG03816 standard; protein; 209 AA.
DE Novel human diagnostic protein #3807.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 4; Length 209;
Best Local Similarity 41.2%; Pred. No. 7.8e+02;
RESULT 1042
ID AAG59593 standard; protein; 215 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77097.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 215;
Best Local Similarity 47.1%; Pred. No. 8.1e+02;
RESULT 1043
ID AAG07267 standard; protein; 215 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4356.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 215;
Best Local Similarity 47.1%; Pred. No. 8.1e+02;
RESULT 1044
ID ABG12667 standard; protein; 225 AA.
DE Novel human diagnostic protein #12658.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 4; Length 225;
Best Local Similarity 40.0%; Pred. No. 8.5e+02;
RESULT 1045
ID AAY74526 standard; protein; 243 AA.
DE Neisseria meningitidis ORF 136 protein sequence SEQ ID NO:526.
PN WO9957280-A2.
PD 11-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match 39.8%; Score 37; DB 3; Length 243;
Best Local Similarity 60.0%; Pred. No. 9.3e+02;
RESULT 1046
ID ABU24490 standard; protein; 265 AA.
DE Protein encoded by Prokaryotic essential gene #10017.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 39.8%; Score 37; DB 6; Length 265;
Best Local Similarity 58.3%; Pred. No. 1e+03;

RESULT 1047
ID AAB96515 standard; protein; 271 AA.
DE Putative P. abyssi Fe-S oxidoreductase #7.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Query Match 39.8%; Score 37; DB 4; Length 271;
Best Local Similarity 53.8%; Pred. No. 1e+03;
RESULT 1048
ID AAM17915 standard; protein; 276 AA.
DE Peptide #4349 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 276;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
RESULT 1049
ID ABB36945 standard; peptide; 276 AA.
DE Peptide #4451 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 276;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
RESULT 1050
ID AAM30426 standard; protein; 276 AA.
DE Peptide #4463 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 276;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
RESULT 1051
ID ABB31724 standard; peptide; 276 AA.
DE Peptide #4375 encoded by breast cell single exon nucleic acid probe.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 276;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
RESULT 1052
ID AAM70088 standard; protein; 276 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30394.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 276;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
RESULT 1053
ID ABG51785 standard; peptide; 276 AA.
DE Human liver peptide, SEQ ID No 30433.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 276;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
RESULT 1054
ID AAM05567 standard; protein; 276 AA.
DE Peptide #4249 encoded by probe for measuring breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 276;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
RESULT 1055
ID ABG39722 standard; peptide; 276 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 29387.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 5; Length 276;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
RESULT 1056
ID ADA36649 standard; protein; 277 AA.
DE Acinetobacter baumannii protein #3810.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 39.8%; Score 37; DB 6; Length 277;
Best Local Similarity 44.4%; Pred. No. 1.1e+03;
RESULT 1057
ID AAY74527 standard; protein; 278 AA.
DE Neisseria meningitidis ORF 136 protein sequence SEQ ID NO:528.
PN WO9957280-A2.
PD 11-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match 39.8%; Score 37; DB 3; Length 278;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
RESULT 1058
ID ADD30040 standard; protein; 292 AA.
DE Plant yield-related protein from clone G1453.
PN WO2003013227-A2.
PD 20-FEB-2003.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 39.8%; Score 37; DB 7; Length 292;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
RESULT 1059
ID ADI44161 standard; protein; 292 AA.
DE Plant transcription factor related polypeptide #1669.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAAK/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
Query Match 39.8%; Score 37; DB 8; Length 292;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
RESULT 1060
ID AAU20366 standard; protein; 301 AA.
DE Human secreted protein, Seq ID No 358.
PN WO200155326-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 4; Length 301;
Best Local Similarity 40.0%; Pred. No. 1.2e+03;
RESULT 1061
ID ADX92357 standard; protein; 306 AA.
DE Plant full length insert polypeptide seqid 55021.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 39.8%; Score 37; DB 8; Length 306;
Best Local Similarity 77.8%; Pred. No. 1.2e+03;
RESULT 1062
ID ABB51278 standard; protein; 307 AA.
DE Human secreted protein encoded by gene 30 SEQ ID NO:1235.
PN WO200162891-A2.
PD 30-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 4; Length 307;
Best Local Similarity 46.2%; Pred. No. 1.2e+03;
RESULT 1063
ID ABB51275 standard; protein; 307 AA.
DE Human secreted protein encoded by gene 30 SEQ ID NO:1232.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 4; Length 307;
Best Local Similarity 46.2%; Pred. No. 1.2e+03;
RESULT 1064
ID ADX94522 standard; protein; 314 AA.
DE Plant full length insert polypeptide seqid 57186.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 39.8%; Score 37; DB 8; Length 314;
Best Local Similarity 58.8%; Pred. No. 1.2e+03;
RESULT 1065
ID AAW48792 standard; protein; 315 AA.
DE Homo sapiens sprouty 2 protein.
PN WO9820032-A1.
PD 14-MAY-1998.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 39.8%; Score 37; DB 2; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1066
ID ABO07185 standard; protein; 315 AA.
DE Human p53 modifying protein, SEQ ID 145.
PN WO200299122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 39.8%; Score 37; DB 6; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1067
ID ADE61338 standard; protein; 315 AA.
DE Human Protein O43597, SEQ ID NO 7256.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 39.8%; Score 37; DB 7; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1068
ID ADG14302 standard; protein; 315 AA.
DE Human Sprouty 2 (SPRY2), SEQ ID 4.
PN WO2003074007-A2.
PD 12-SEP-2003.
PA (RIGE-) RIGEL PHARM INC.
Query Match 39.8%; Score 37; DB 7; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1069
ID ADG47834 standard; protein; 315 AA.
DE Human sprouty-2 protein.
PN US6485920-B1.
PD 26-NOV-2002.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 8; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1070
ID ADG47837 standard; protein; 315 AA.
DE Mouse sprouty-2 protein.
PN US6485920-B1.
PD 26-NOV-2002.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 8; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1071
ID ADJ95401 standard; protein; 315 AA.
DE Human sprouty-2 polypeptide.
PN US6706871-B1.
PD 16-MAR-2004.
PA (NUVE-) NUVELO INC.
Query Match 39.8%; Score 37; DB 8; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1072
ID ADJ95404 standard; protein; 315 AA.
DE Mouse sprouty-2 polypeptide.
PN US6706871-B1.
PD 16-MAR-2004.
PA (NUVE-) NUVELO INC.
Query Match 39.8%; Score 37; DB 8; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1073
ID ADN11324 standard; protein; 315 AA.
DE Human Sprouty2, marker for breast cancer.
PN WO2004029295-A1.
PD 08-APR-2004.
PA (SCTE-) AGENCY SCI TECHNOLOGY & RES.
Query Match 39.8%; Score 37; DB 8; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1074
ID ADQ21111 standard; protein; 315 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3931.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 39.8%; Score 37; DB 8; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1075
ID ADP23634 standard; protein; 315 AA.
DE PRO polypeptide SEQ ID NO:812.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 39.8%; Score 37; DB 8; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1076
ID ADS15841 standard; protein; 315 AA.
DE Human sprouty-2 SEQ ID 4.
PN WO2004082704-A1.
PD 30-SEP-2004.
PA (DNAV-) DNAVEC RES INC.
Query Match 39.8%; Score 37; DB 8; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1077
ID ADY19896 standard; protein; 315 AA.
DE PRO polypeptide SEQ ID NO 5702.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 39.8%; Score 37; DB 9; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1078
ID ADY15230 standard; protein; 315 AA.
DE PRO polypeptide SEQ ID NO 1036.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 39.8%; Score 37; DB 9; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1079
ID ADM25514 standard; protein; 316 AA.
DE Hyperthermophile Methanopyrus kandleri protein #120.
PN WO2003076575-A2.
PD 18-SEP-2003.
PA (FIDE-) FIDELITY SYSTEMS INC.
PA (MALY/) MALYKH A.
Query Match 39.8%; Score 37; DB 7; Length 316;
Best Local Similarity 42.9%; Pred. No. 1.2e+03;

RESULT 1080
ID ABB51277 standard; protein; 321 AA.
DE Human secreted protein encoded by gene 30 SEQ ID NO:1234.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 4; Length 321;
Best Local Similarity 46.2%; Pred. No. 1.3e+03;
RESULT 1081
ID ABU29258 standard; protein; 324 AA.
DE Protein encoded by Prokaryotic essential gene #14785.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 39.8%; Score 37; DB 6; Length 324;
Best Local Similarity 33.3%; Pred. No. 1.3e+03;
RESULT 1082
ID AAB19393 standard; protein; 325 AA.
DE Amino acid sequence of a human secreted protein.
PN WO200061755-A2.
PD 19-OCT-2000.
PA (CHIR) CHIRON CORP.
Query Match 39.8%; Score 37; DB 3; Length 325;
Best Local Similarity 46.2%; Pred. No. 1.3e+03;
RESULT 1083
ID AAB23045 standard; protein; 326 AA.
DE Human peroxisome associated protein splice variant, SECX 3884846-1.
PN WO200053742-A2.
PD 14-SEP-2000.
PA (CURA-) CURAGEN CORP.
Query Match 39.8%; Score 37; DB 3; Length 326;
Best Local Similarity 46.2%; Pred. No. 1.3e+03;
RESULT 1084
ID ADA23352 standard; protein; 326 AA.
DE Human SECX polypeptide, SEC7 #2.
PN US2003054514-A1.
PD 20-MAR-2003.
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
Query Match 39.8%; Score 37; DB 6; Length 326;
Best Local Similarity 46.2%; Pred. No. 1.3e+03;
RESULT 1085
ID ADH87324 standard; protein; 339 AA.
DE Enterococcus faecalis polypeptide #1804.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 39.8%; Score 37; DB 7; Length 339;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
RESULT 1086
ID AAR22463 standard; protein; 343 AA.
DE Acetylpolyamine amidohydrolase.
PN JP04071489-A.
PD 06-MAR-1992.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 39.8%; Score 37; DB 2; Length 343;
Best Local Similarity 58.3%; Pred. No. 1.4e+03;
RESULT 1087
ID ADO57333 standard; protein; 351 AA.
DE Kidney development associated protein seqid 100.
PN US2004068763-A1.
PD 08-APR-2004.
PA (HOPK/) HOPKINS N.
PA (GOLL/) GOLLING G.
PA (AMST/) AMSTERDAM A.
PA (SUNZ/) SUN Z.
Query Match 39.8%; Score 37; DB 8; Length 351;
Best Local Similarity 40.0%; Pred. No. 1.4e+03;
RESULT 1088
ID ADP29942 standard; protein; 351 AA.
DE Human secreted protein SEQ ID #1940.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 39.8%; Score 37; DB 8; Length 351;
Best Local Similarity 38.5%; Pred. No. 1.4e+03;
RESULT 1089
ID ADA57263 standard; protein; 362 AA.
DE Human secreted protein #546.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 6; Length 362;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1090
ID ADA57577 standard; protein; 362 AA.
DE Human secreted protein #546.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 6; Length 362;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1091
ID ADA41146 standard; protein; 362 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 6; Length 362;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1092
ID ADA41471 standard; protein; 362 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 6; Length 362;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1093
ID ADC74585 standard; protein; 362 AA.
DE Human secreted protein - SEQ ID 1218.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 7; Length 362;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1094
ID ADC74351 standard; protein; 362 AA.
DE Human secreted protein - SEQ ID 984.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 7; Length 362;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1095
ID ADD38093 standard; protein; 362 AA.
DE Human secreted protein #276.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 7; Length 362;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1096
ID ADD37992 standard; protein; 362 AA.
DE Human secreted protein #175.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 7; Length 362;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1097
ID AAW88563 standard; protein; 363 AA.
DE Secreted protein encoded by gene 30 clone HTPBW79.
PN WO9854963-A2.
PD 10-DEC-1998.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 2; Length 363;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1098
ID AAY36333 standard; protein; 363 AA.
DE Human secreted protein encoded by gene 110.
PN WO9931117-A1.
PD 24-JUN-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 2; Length 363;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1099
ID ABB50330 standard; protein; 363 AA.
DE Human secreted protein encoded by gene 30 SEQ ID NO:278.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 4; Length 363;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1100
ID ABB51276 standard; protein; 363 AA.
DE Human secreted protein encoded by gene 30 SEQ ID NO:1233.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 4; Length 363;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1101
ID ABO44587 standard; protein; 363 AA.
DE Novel human secreted protein #30.
PN US2003065160-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 6; Length 363;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1102
ID ABO26067 standard; protein; 363 AA.
DE Human protein from novel secreted protein gene 30.
PN US6525174-B1.
PD 25-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 7; Length 363;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1103
ID ABB53913 standard; protein; 365 AA.
DE Lactococcus lactis protein serC.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 39.8%; Score 37; DB 5; Length 365;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
RESULT 1104
ID ADS29312 standard; protein; 365 AA.
DE Bacterial polypeptide #18345.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 39.8%; Score 37; DB 8; Length 365;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
RESULT 1105
ID AAW88777 standard; protein; 370 AA.
DE Polypeptide fragment encoded by gene 30.
PN WO9854963-A2.
PD 10-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 2; Length 370;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1106
ID ABB50610 standard; protein; 370 AA.
DE Human secreted protein encoded by gene 30 SEQ ID NO:558.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 4; Length 370;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1107
ID ABO44867 standard; protein; 370 AA.
DE Novel human secreted protein #30 fragment #1.
PN US2003065160-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 6; Length 370;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1108
ID ABO26347 standard; protein; 370 AA.
DE Protein associated with novel secreted protein gene 30 #1.
PN US6525174-B1.
PD 25-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 7; Length 370;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1109
ID AAY36194 standard; protein; 393 AA.
DE Human secreted protein #66.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST) GENSET.
Query Match 39.8%; Score 37; DB 2; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1110
ID AAY94883 standard; protein; 393 AA.
DE Human protein clone HP10530.
PN WO200005367-A2.
PD 03-FEB-2000.
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
Query Match 39.8%; Score 37; DB 3; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1111
ID AAB61136 standard; protein; 393 AA.
DE Human NOV6 protein.
PN WO200075321-A2.
PD 14-DEC-2000.
PA (CURA-) CURAGEN CORP.
Query Match 39.8%; Score 37; DB 4; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1112
ID AAM79115 standard; protein; 393 AA.
DE Human protein SEQ ID NO 1777.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 4; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1113
ID AAB93277 standard; protein; 393 AA.
DE Human protein sequence SEQ ID NO:12320.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 39.8%; Score 37; DB 4; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1114
ID ABO23238 standard; protein; 393 AA.
DE Human breast tumour associated protein 47-like polypeptide NOV6.
PN US2003027158-A1.
PD 06-FEB-2003.
PA (CURA-) CURAGEN CORP.
Query Match 39.8%; Score 37; DB 6; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1115
ID ADJ46046 standard; protein; 393 AA.

DE Novel human secreted protein-related protein sequence SeqID199.
PN US2003144490-A1.
PD 31-JUL-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 39.8%; Score 37; DB 7; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1116
ID ADM56375 standard; protein; 393 AA.
DE Human cell adhesion molecule NOV6.
PN US2003082554-A1.
PD 01-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 39.8%; Score 37; DB 7; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1117
ID ADF66739 standard; protein; 393 AA.
DE Novel human protein NOV6.
PN US2003199103-A1.
PD 23-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 39.8%; Score 37; DB 8; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1118
ID ADI19776 standard; protein; 393 AA.
DE Human NOV6 protein.
PN US2004002134-A1.
PD 01-JAN-2004.
PA (CURA-) CURAGEN CORP.
Query Match 39.8%; Score 37; DB 8; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1119
ID ADO58690 standard; protein; 393 AA.
DE Human regulatory molecule HRM-11.
PN US2002058264-A1.
PD 16-MAY-2002.
PA (INCY-) INCYTE PHARM INC.
Query Match 39.8%; Score 37; DB 8; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1120
ID ADO60249 standard; protein; 393 AA.
DE Human NOV6 protein.
PN US2003134430-A1.
PD 17-JUL-2003.
PA (CURA-) CURAGEN CORP.
Query Match 39.8%; Score 37; DB 8; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1121
ID ADP19455 standard; protein; 393 AA.
DE Human secreted polypeptide #306.
PN US2004110939-A1.
PD 10-JUN-2004.
PA (GEST) GENSET SA.
Query Match 39.8%; Score 37; DB 8; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1122
ID ADQ65337 standard; protein; 393 AA.
DE Novel human protein sequence #310.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 39.8%; Score 37; DB 8; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1123
ID AEE72675 standard; protein; 393 AA.
DE Human endometriosis-associated antigen ME-2, SEQ:6.
PN EP1614692-A2.
PD 11-JAN-2006.
PA (DIAG-) DIAGNOSTIC PROD CORP.
Query Match 39.8%; Score 37; DB 10; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1124
ID ADA57578 standard; protein; 415 AA.
DE Human secreted protein #546.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 6; Length 415;
Best Local Similarity 46.2%; Pred. No. 1.7e+03;
RESULT 1125
ID ADA41472 standard; protein; 415 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 6; Length 415;
Best Local Similarity 46.2%; Pred. No. 1.7e+03;
RESULT 1126
ID ADC74586 standard; protein; 415 AA.
DE Human secreted protein - SEQ ID 1219.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 7; Length 415;
Best Local Similarity 46.2%; Pred. No. 1.7e+03;
RESULT 1127
ID ADD38094 standard; protein; 415 AA.
DE Human secreted protein #277.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 7; Length 415;
Best Local Similarity 46.2%; Pred. No. 1.7e+03;
RESULT 1128
ID AAW88745 standard; protein; 416 AA.
DE Secreted protein encoded by gene 30 clone HTSEV09.
PN WO9854963-A2.
PD 10-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 2; Length 416;
Best Local Similarity 46.2%; Pred. No. 1.7e+03;
RESULT 1129
ID ABB50513 standard; protein; 416 AA.
DE Human secreted protein encoded by gene 30 SEQ ID NO:461.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 4; Length 416;
Best Local Similarity 46.2%; Pred. No. 1.7e+03;
RESULT 1130
ID AAM25861 standard; protein; 416 AA.
DE Human protein sequence SEQ ID NO:1376.
PN WO200153455-A2.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 4; Length 416;
Best Local Similarity 46.2%; Pred. No. 1.7e+03;
RESULT 1131
ID ABO44770 standard; protein; 416 AA.
DE Novel human secreted protein #213.
PN US2003065160-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 6; Length 416;
Best Local Similarity 46.2%; Pred. No. 1.7e+03;
RESULT 1132
ID ABO26250 standard; protein; 416 AA.
DE Human protein from novel secreted protein gene 30 #2.
PN US6525174-B1.
PD 25-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 7; Length 416;
Best Local Similarity 46.2%; Pred. No. 1.7e+03;
RESULT 1133
ID ABB11390 standard; peptide; 435 AA.

DE Human secreted protein homologue, SEQ ID NO:1760.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 4; Length 435;
Best Local Similarity 46.2%; Pred. No. 1.8e+03;
RESULT 1134
ID AAM80099 standard; protein; 435 AA.
DE Human protein SEQ ID NO 3745.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 4; Length 435;
Best Local Similarity 46.2%; Pred. No. 1.8e+03;
RESULT 1135
ID ADS28270 standard; protein; 445 AA.
DE Bacterial polypeptide #17303.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J..
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 39.8%; Score 37; DB 8; Length 445;
Best Local Similarity 75.0%; Pred. No. 1.8e+03;
RESULT 1136
ID ADF60384 standard; protein; 469 AA.
DE Human contig polypeptide sequence SEQ ID NO:2751.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 7; Length 469;
Best Local Similarity 38.5%; Pred. No. 2e+03;
RESULT 1137
ID AAB69271 standard; protein; 494 AA.
DE HIV-1 non-subtype B clone 92RW009-6 gag protein.
PN WO200026416-A1.
PD 11-MAY-2000.
PA (UABR-) UAB RES FOUND.
Query Match 39.8%; Score 37; DB 3; Length 494;
Best Local Similarity 47.1%; Pred. No. 2.1e+03;
RESULT 1138
ID ADX39491 standard; protein; 494 AA.
DE HIV Gag protein #67.
PN WO2005012502-A2.
PD 10-FEB-2005.
PA (EPIM-) EPIMMUNE INC.
Query Match 39.8%; Score 37; DB 9; Length 494;
Best Local Similarity 47.1%; Pred. No. 2.1e+03;
RESULT 1139
ID ADT57574 standard; protein; 496 AA.
DE Plant polypeptide, SEQ ID 7651.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 39.8%; Score 37; DB 8; Length 496;
Best Local Similarity 58.3%; Pred. No. 2.1e+03;
RESULT 1140
ID ADN17531 standard; protein; 497 AA.
DE Bacterial polypeptide #184.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 39.8%; Score 37; DB 8; Length 497;
Best Local Similarity 60.0%; Pred. No. 2.1e+03;
RESULT 1141
ID ADY09236 standard; protein; 508 AA.
DE Plant full length insert polypeptide seqid 65051.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 39.8%; Score 37; DB 8; Length 508;
Best Local Similarity 58.3%; Pred. No. 2.1e+03;
RESULT 1142
ID ADX80031 standard; protein; 533 AA.
DE Plant full length insert polypeptide seqid 49397.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 39.8%; Score 37; DB 8; Length 533;
Best Local Similarity 52.9%; Pred. No. 2.3e+03;
RESULT 1143
ID ABU29646 standard; protein; 547 AA.
DE Protein encoded by Prokaryotic essential gene #15173.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 39.8%; Score 37; DB 6; Length 547;
Best Local Similarity 36.4%; Pred. No. 2.3e+03;
RESULT 1144
ID ADC97213 standard; protein; 549 AA.
DE E. faecium protein sequence SEQ ID 6840.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 39.8%; Score 37; DB 7; Length 549;
Best Local Similarity 36.4%; Pred. No. 2.3e+03;
RESULT 1145
ID ADP29943 standard; protein; 561 AA.
DE Human secreted protein SEQ ID #1941.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 39.8%; Score 37; DB 8; Length 561;
Best Local Similarity 38.5%; Pred. No. 2.4e+03;
RESULT 1146
ID ABP73959 standard; protein; 569 AA.
DE Candida albicans essential protein SEQ ID NO 7796.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 39.8%; Score 37; DB 5; Length 569;
Best Local Similarity 50.0%; Pred. No. 2.4e+03;
RESULT 1147
ID ABG12666 standard; protein; 570 AA.
DE Novel human diagnostic protein #12657.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 4; Length 570;
Best Local Similarity 40.0%; Pred. No. 2.4e+03;
RESULT 1148
ID AAW83428 standard; protein; 611 AA.
DE Munc13-1-interacting domain of Doc2-alpha.
PN JP10313866-A.
PD 02-DEC-1998.
PA (SHIO) SHIONOGI & CO LTD.
Query Match 39.8%; Score 37; DB 2; Length 611;
Best Local Similarity 53.8%; Pred. No. 2.6e+03;
RESULT 1149
ID ADY23680 standard; protein; 616 AA.

DE Plant full length insert polypeptide seqid 71464.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 39.8%; Score 37; DB 8; Length 616;
Best Local Similarity 66.7%; Pred. No. 2.7e+03;
RESULT 1150
ID ADK64436 standard; protein; 647 AA.
DE Disease treating protein complex-derived protein #1157.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 39.8%; Score 37; DB 7; Length 647;
Best Local Similarity 46.2%; Pred. No. 2.8e+03;
RESULT 1151
ID ADA55125 standard; protein; 707 AA.
DE Human protein, SEQ ID 2693.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 39.8%; Score 37; DB 6; Length 707;
Best Local Similarity 38.5%; Pred. No. 3.1e+03;
RESULT 1152
ID ABP54927 standard; protein; 731 AA.
DE Mouse gelsolin.
PN WO200274982-A1.
PD 26-SEP-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 39.8%; Score 37; DB 5; Length 731;
Best Local Similarity 47.6%; Pred. No. 3.2e+03;
RESULT 1153
ID ABM04819 standard; protein; 731 AA.
DE Murine gelsolin.
PN EP1284298-A2.
PD 19-FEB-2003.
PA (WARN) WARNER LAMBERT CO.
Query Match 39.8%; Score 37; DB 6; Length 731;
Best Local Similarity 47.6%; Pred. No. 3.2e+03;
RESULT 1154
ID ADF72344 standard; protein; 731 AA.
DE Mouse gelsolin protein SEQ ID NO:40.
PN WO2003103595-A2.
PD 18-DEC-2003.
PA (UYRP) UNIV ROCHESTER.
Query Match 39.8%; Score 37; DB 8; Length 731;
Best Local Similarity 47.6%; Pred. No. 3.2e+03;
RESULT 1155
ID AAM93424 standard; protein; 733 AA.
DE Human polypeptide, SEQ ID NO: 3048.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 39.8%; Score 37; DB 4; Length 733;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
RESULT 1156
ID AAM93852 standard; protein; 733 AA.
DE Human polypeptide, SEQ ID NO: 3939.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 39.8%; Score 37; DB 4; Length 733;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
RESULT 1157
ID AAE29757 standard; protein; 733 AA.
DE Human nucleic acid-associated protein (NAAP-4).
PN WO200277231-A2.
PD 03-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 39.8%; Score 37; DB 6; Length 733;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
RESULT 1158
ID ADL31015 standard; protein; 733 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3048.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 39.8%; Score 37; DB 8; Length 733;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
RESULT 1159
ID ADL31906 standard; protein; 733 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3939.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 39.8%; Score 37; DB 8; Length 733;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
RESULT 1160
ID ABJ25779 standard; protein; 794 AA.
DE Aspergillus fumigatus essential gene protein #437.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 39.8%; Score 37; DB 6; Length 794;
Best Local Similarity 60.0%; Pred. No. 3.6e+03;
RESULT 1161
ID ABJ26379 standard; protein; 794 AA.
DE Aspergillus fumigatus essential gene protein #1037.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 39.8%; Score 37; DB 6; Length 794;
Best Local Similarity 60.0%; Pred. No. 3.6e+03;
RESULT 1162
ID ABB65490 standard; protein; 799 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23262.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 39.8%; Score 37; DB 4; Length 799;
Best Local Similarity 46.2%; Pred. No. 3.6e+03;
RESULT 1163
ID ABB07508 standard; protein; 802 AA.
DE Human aminoacyl tRNA synthetase (ATRS) polypeptide (ID: 7474756CD1).
PN WO200204611-A2.
PD 17-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 39.8%; Score 37; DB 5; Length 802;
Best Local Similarity 38.5%; Pred. No. 3.6e+03;
RESULT 1164
ID ADR08945 standard; protein; 922 AA.
DE Human protein useful for treating neurological disease Seq 2451.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 39.8%; Score 37; DB 8; Length 922;
Best Local Similarity 53.8%; Pred. No. 4.2e+03;
RESULT 1165
ID ABB90849 standard; protein; 1055 AA.
DE Herbicidally active polypeptide SEQ ID NO 60.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 39.8%; Score 37; DB 5; Length 1055;
Best Local Similarity 63.6%; Pred. No. 4.9e+03;
RESULT 1166
ID ABP57716 standard; protein; 1073 AA.
DE Novel human protein #3.
PN WO200277257-A1.
PD 03-OCT-2002.
PA (HYSE-) HYSEQ INC.

Query Match 39.8%; Score 37; DB 6; Length 1073;
Best Local Similarity 53.8%; Pred. No. 5e+03;
RESULT 1167
ID ABU43426 standard; protein; 1096 AA.
DE Protein encoded by Prokaryotic essential gene #28953.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 39.8%; Score 37; DB 6; Length 1096;
Best Local Similarity 41.2%; Pred. No. 5.1e+03;
RESULT 1168
ID ADB70293 standard; protein; 1116 AA.
DE C. neoformans amino acid sequence SEQ ID NO:3337.
PN WO2003052076-A2.
PD 26-JUN-2003.
PA (ELIT-) ELITRA PHARM INC.
Query Match 39.8%; Score 37; DB 7; Length 1116;
Best Local Similarity 50.0%; Pred. No. 5.2e+03;
RESULT 1169
ID AAR13309 standard; protein; 1180 AA.
DE Modified thermostable protoxin.
PN EP440581-A.
PD 07-AUG-1991.
PA (CIBA) CIBA GEIGY AG.
Query Match 39.8%; Score 37; DB 2; Length 1180;
Best Local Similarity 46.2%; Pred. No. 5.6e+03;
RESULT 1170
ID ABU54638 standard; protein; 1713 AA.
DE Human NOVX polypeptide #97.
PN WO200281498-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 39.8%; Score 37; DB 6; Length 1713;
Best Local Similarity 53.8%; Pred. No. 8.5e+03;
RESULT 1171
ID AAE14920 standard; protein; 1735 AA.
DE Rat Munc13-1 protein mutant (W464R).
PN WO2003039441-A2.
PD 15-MAY-2003.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 39.8%; Score 37; DB 6; Length 1735;
Best Local Similarity 53.8%; Pred. No. 8.6e+03;
RESULT 1172
ID AAE14910 standard; protein; 1735 AA.
DE Rat Munc13-1 protein.
PN WO2003039441-A2.
PD 15-MAY-2003.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 39.8%; Score 37; DB 6; Length 1735;
Best Local Similarity 53.8%; Pred. No. 8.6e+03;
RESULT 1173
ID AAW83431 standard; protein; 1763 AA.
DE Rat Munc13-1.
PN JP10313866-A.
PD 02-DEC-1998.
PA (SHIO) SHIONOGI & CO LTD.
Query Match 39.8%; Score 37; DB 2; Length 1763;
Best Local Similarity 53.8%; Pred. No. 8.8e+03;
RESULT 1174
ID ADN24058 standard; protein; 238 AA.
DE Bacterial polypeptide #6711.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 39.2%; Score 36.5; DB 8; Length 238;
Best Local Similarity 53.3%; Pred. No. 1.1e+03;
RESULT 1175
ID ABP41601 standard; protein; 261 AA.
DE Human ovarian antigen HOCPO73, SEQ ID NO:2733.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.2%; Score 36.5; DB 5; Length 261;
Best Local Similarity 46.2%; Pred. No. 1.2e+03;
RESULT 1176
ID ABO61655 standard; protein; 291 AA.
DE Klebsiella pneumoniae polypeptide seqid 8172.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 39.2%; Score 36.5; DB 7; Length 291;
Best Local Similarity 35.3%; Pred. No. 1.4e+03;
RESULT 1177
ID ABB70793 standard; protein; 308 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39171.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 39.2%; Score 36.5; DB 4; Length 308;
Best Local Similarity 52.9%; Pred. No. 1.5e+03;
RESULT 1178
ID AAY72889 standard; protein; 644 AA.
DE Human pCMVN5 mutant with deleted alpha helix 4 region.
PN WO200116168-A2.
PD 08-MAR-2001.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 39.2%; Score 36.5; DB 4; Length 644;
Best Local Similarity 46.2%; Pred. No. 3.4e+03;
RESULT 1179
ID AAY72887 standard; protein; 657 AA.
DE Human pCMVN5-PP mutant (L617P/W620P).
PN WO200116168-A2.
PD 08-MAR-2001.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 39.2%; Score 36.5; DB 4; Length 657;
Best Local Similarity 46.2%; Pred. No. 3.5e+03;
RESULT 1180
ID AAY72888 standard; protein; 657 AA.
DE Human pCMVN5-R mutant (W620R).
PN WO200116168-A2.
PD 08-MAR-2001.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 39.2%; Score 36.5; DB 4; Length 657;
Best Local Similarity 46.2%; Pred. No. 3.5e+03;
RESULT 1181
ID AAY72883 standard; protein; 657 AA.
DE Human p84N5 protein involved in cancer therapy.
PN WO200116168-A2.
PD 08-MAR-2001.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 39.2%; Score 36.5; DB 4; Length 657;
Best Local Similarity 46.2%; Pred. No. 3.5e+03;
RESULT 1182
ID ABP70646 standard; protein; 657 AA.
DE Amino acid sequence of p84N5, an expression product of the N5 gene.
PN WO2003002067-A2.
PD 09-JAN-2003.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 39.2%; Score 36.5; DB 6; Length 657;
Best Local Similarity 46.2%; Pred. No. 3.5e+03;
RESULT 1183
ID ABO52983 standard; protein; 657 AA.
DE Human putative spliceosome associated protein (SAP) #12.
PN US2003068803-A1.
PD 10-APR-2003.
PA (REED/) REED R.
PA (ZHOU/) ZHOU Z.
Query Match 39.2%; Score 36.5; DB 6; Length 657;
Best Local Similarity 46.2%; Pred. No. 3.5e+03;
RESULT 1184
ID ABO53063 standard; protein; 657 AA.
DE Human putative spliceosome associated protein (SAP) #40.

PN US2003068803-A1.
PD 10-APR-2003.
PA (REED/) REED R.
PA (ZHOU/) ZHOU Z.
Query Match 39.2%; Score 36.5; DB 6; Length 657;
Best Local Similarity 46.2%; Pred. No. 3.5e+03;
RESULT 1185
ID AED11077 standard; protein; 657 AA.
DE Human nuclear matrix protein p84, SEQ ID NO: 11 #1.
PN US2005208054-A1.
PD 22-SEP-2005.
PA (UYMA-) UNIV MASSACHUSETTS.
Query Match 39.2%; Score 36.5; DB 9; Length 657;
Best Local Similarity 46.2%; Pred. No. 3.5e+03;
RESULT 1186
ID AED11098 standard; protein; 657 AA.
DE Human nuclear matrix protein p84, SEQ ID NO: 11 #2.
PN US2005208054-A1.
PD 22-SEP-2005.
PA (UYMA-) UNIV MASSACHUSETTS.
Query Match 39.2%; Score 36.5; DB 9; Length 657;
Best Local Similarity 46.2%; Pred. No. 3.5e+03;
RESULT 1187
ID ABG06945 standard; protein; 673 AA.
DE Novel human diagnostic protein #6936.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 39.2%; Score 36.5; DB 4; Length 673;
Best Local Similarity 46.2%; Pred. No. 3.6e+03;
RESULT 1188
ID AAU38327 standard; protein; 804 AA.
DE Salmonella typhi cellular proliferation protein #218.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 39.2%; Score 36.5; DB 4; Length 804;
Best Local Similarity 38.1%; Pred. No. 4.4e+03;
RESULT 1189
ID ABU48260 standard; protein; 804 AA.
DE Protein encoded by Prokaryotic essential gene #33787.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 39.2%; Score 36.5; DB 6; Length 804;
Best Local Similarity 38.1%; Pred. No. 4.4e+03;
RESULT 1190
ID AAW40059 standard; protein; 813 AA.
DE Mouse P300/CBP-associated transcriptional cofactor P/CAF.
PN WO9803652-A2.
PD 29-JAN-1998.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 39.2%; Score 36.5; DB 2; Length 813;
Best Local Similarity 53.3%; Pred. No. 4.4e+03;
RESULT 1191
ID AAW40052 standard; protein; 832 AA.
DE Human P300/CBP-associated transcriptional cofactor P/CAF.
PN WO9803652-A2.
PD 29-JAN-1998.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 39.2%; Score 36.5; DB 2; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.6e+03;
RESULT 1192
ID ADN06247 standard; protein; 832 AA.
DE Human p300/CBP-associated factor (P/CAF) protein.
PN US2004043378-A1.
PD 04-MAR-2004.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match 39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.6e+03;
RESULT 1193
ID ADN06310 standard; protein; 832 AA.
DE Human p300/CBP-associated factor (P/CAF) mutant protein, Y802A.
PN US2004043378-A1.
PD 04-MAR-2004.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match 39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.6e+03;
RESULT 1194
ID ADN06311 standard; protein; 832 AA.
DE Human p300/CBP-associated factor (P/CAF) mutant protein, Y760A.
PN US2004043378-A1.
PD 04-MAR-2004.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match 39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.6e+03;
RESULT 1195
ID ADN06309 standard; protein; 832 AA.
DE Human p300/CBP-associated factor (P/CAF) mutant protein, Y809A.
PN US2004043378-A1.
PD 04-MAR-2004.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match 39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.6e+03;
RESULT 1196
ID ADN06312 standard; protein; 832 AA.
DE Human p300/CBP-associated factor (P/CAF) mutant protein, V752A.
PN US2004043378-A1.
PD 04-MAR-2004.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match 39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.6e+03;
RESULT 1197
ID ADO40043 standard; protein; 832 AA.
DE Human p300/CBP-associated factor (P/CAF) mutant protein, Y809A.
PN US2004009613-A1.
PD 15-JAN-2004.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match 39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.6e+03;
RESULT 1198
ID ADO40046 standard; protein; 832 AA.
DE Human p300/CBP-associated factor (P/CAF) mutant protein, V752A.
PN US2004009613-A1.
PD 15-JAN-2004.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match 39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.6e+03;
RESULT 1199
ID ADO40045 standard; protein; 832 AA.
DE Human p300/CBP-associated factor (P/CAF) mutant protein, Y760A.
PN US2004009613-A1.
PD 15-JAN-2004.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.

PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match 39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.6e+03;
RESULT 1200
ID ADO40044 standard; protein; 832 AA.
DE Human p300/CBP-associated factor (P/CAF) mutant protein, Y802A.
PN US2004009613-A1.
PD 15-JAN-2004.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match 39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.6e+03;
RESULT 1201
ID ADO39984 standard; protein; 832 AA.
DE Human p300/CBP-associated factor (P/CAF) protein.
PN US2004009613-A1.
PD 15-JAN-2004.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match 39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.6e+03;
RESULT 1202
ID ADZ70677 standard; protein; 832 AA.
DE Human protein from lung cancer marker gene PCAF.
PN WO2005032495-A2.
PD 14-APR-2005.
PA (FARB) BAYER PHARM CORP.
Query Match 39.2%; Score 36.5; DB 9; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.6e+03;
RESULT 1203
ID AEF31200 standard; protein; 832 AA.
DE PCAF protein.
PN WO2006007411-A2.
PD 19-JAN-2006.
PA (HARD) HARVARD COLLEGE.
Query Match 39.2%; Score 36.5; DB 10; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.6e+03;
RESULT 1204
ID ADE14747 standard; peptide; 14 AA.
DE Fruit fly allostatin #4.
PN US2003180297-A1.
PD 25-SEP-2003.
PA (LOWE/) LOWERY D E.
PA (SMIT/) SMITH V G.
PA (KUBI/) KUBIAK T M.
PA (LARS/) LARSEN M J.
Query Match 38.7%; Score 36; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 54;
RESULT 1205
ID ADE14700 standard; peptide; 14 AA.
DE DmGPCR binding ligand #148.
PN US2003180297-A1.
PD 25-SEP-2003.
PA (LOWE/) LOWERY D E.
PA (SMIT/) SMITH V G.
PA (KUBI/) KUBIAK T M.
PA (LARS/) LARSEN M J.
Query Match 38.7%; Score 36; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 54;
RESULT 1206
ID ADE14701 standard; peptide; 14 AA.
DE DmGPCR binding ligand #149.
PN US2003180297-A1.
PD 25-SEP-2003.
PA (LOWE/) LOWERY D E.
PA (SMIT/) SMITH V G.
PA (KUBI/) KUBIAK T M.
PA (LARS/) LARSEN M J.
Query Match 38.7%; Score 36; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 54;
RESULT 1207
ID ADL83600 standard; peptide; 14 AA.
DE Drosophila allatostatin-C peptide.
PN US2003162223-A1.
PD 28-AUG-2003.
PA (LOWE/) LOWERY D E.
PA (SMIT/) SMITH V G.
PA (KUBI/) KUBIAK T M.
PA (LARS/) LARSEN M J.
Query Match 38.7%; Score 36; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 54;
RESULT 1208
ID ADE14703 standard; peptide; 15 AA.
DE DmGPCR binding ligand #151.
PN US2003180297-A1.
PD 25-SEP-2003.
PA (LOWE/) LOWERY D E.
PA (SMIT/) SMITH V G.
PA (KUBI/) KUBIAK T M.
PA (LARS/) LARSEN M J.
Query Match 38.7%; Score 36; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
RESULT 1209
ID ADL83599 standard; peptide; 15 AA.
DE Manducta sexta drostatin-C peptide.
PN US2003162223-A1.
PD 28-AUG-2003.
PA (LOWE/) LOWERY D E.
PA (SMIT/) SMITH V G.
PA (KUBI/) KUBIAK T M.
PA (LARS/) LARSEN M J.
Query Match 38.7%; Score 36; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
RESULT 1210
ID ADH52754 standard; peptide; 29 AA.
DE Porphyromonas gulae B43 OprF peptide 2.
PN WO2003054755-A2.
PD 03-JUL-2003.
PA (PFIZ) PFIZER PROD INC.
Query Match 38.7%; Score 36; DB 7; Length 29;
Best Local Similarity 42.9%; Pred. No. 1.2e+02;
RESULT 1211
ID AEE47269 standard; peptide; 29 AA.
DE P. gulae oprF fragment SEQ ID NO 133.
PN WO2005112993-A1.
PD 01-DEC-2005.
PA (PFIZ) PFIZER PROD INC.
Query Match 38.7%; Score 36; DB 10; Length 29;
Best Local Similarity 42.9%; Pred. No. 1.2e+02;
RESULT 1212
ID ADX88003 standard; protein; 61 AA.
DE Plant full length insert polypeptide seqid 50667.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 38.7%; Score 36; DB 8; Length 61;
Best Local Similarity 54.5%; Pred. No. 2.9e+02;
RESULT 1213
ID AAG02548 standard; protein; 70 AA.
DE Human secreted protein, SEQ ID NO: 6629.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 38.7%; Score 36; DB 3; Length 70;
Best Local Similarity 42.9%; Pred. No. 3.4e+02;
RESULT 1214

ID ABP06392 standard; protein; 79 AA.
DE Human ORFX protein sequence SEQ ID NO:12766.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 5; Length 79;
Best Local Similarity 54.5%; Pred. No. 3.8e+02;
RESULT 1215
ID ABU70954 standard; protein; 85 AA.
DE Human adipocyte Selected Interacting domain, SID, #585.
PN WO200286122-A2.
PD 31-OCT-2002.
PA (HYBR-) HYBRIGENICS.
Query Match 38.7%; Score 36; DB 6; Length 85;
Best Local Similarity 50.0%; Pred. No. 4.2e+02;
RESULT 1216
ID AAU79594 standard; protein; 88 AA.
DE Human TRAIL splice variant 1, TRA-3-T7, protein.
PN US2002061525-A1.
PD 23-MAY-2002.
PA (YELI/) YELIN R.
PA (KHOS/) KHOSRAVI R.
PA (SAVI/) SAVITZKY K.
Query Match 38.7%; Score 36; DB 5; Length 88;
Best Local Similarity 41.7%; Pred. No. 4.3e+02;
RESULT 1217
ID AAG12285 standard; protein; 89 AA.
DE Zea mays protein fragment SEQ ID NO: 11339.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 89;
Best Local Similarity 54.5%; Pred. No. 4.4e+02;
RESULT 1218
ID AAY75956 standard; protein; 90 AA.
DE Rat skin cell protein, SEQ ID 134.
PN WO9955865-A1.
PD 04-NOV-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 38.7%; Score 36; DB 3; Length 90;
Best Local Similarity 46.2%; Pred. No. 4.5e+02;
RESULT 1219
ID AAB55895 standard; protein; 90 AA.
DE Skin cell protein, SEQ ID NO: 134.
PN WO200069884-A2.
PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 38.7%; Score 36; DB 4; Length 90;
Best Local Similarity 46.2%; Pred. No. 4.5e+02;
RESULT 1220
ID ABB72095 standard; protein; 90 AA.
DE Rat protein isolated from skin cells SEQ ID NO: 134.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 38.7%; Score 36; DB 5; Length 90;
Best Local Similarity 46.2%; Pred. No. 4.5e+02;
RESULT 1221
ID AAU79595 standard; protein; 98 AA.
DE Human TRAIL splice variant 2, TRA-31-T7, protein.
PN US2002061525-A1.
PD 23-MAY-2002.
PA (YELI/) YELIN R.
PA (KHOS/) KHOSRAVI R.
PA (SAVI/) SAVITZKY K.
Query Match 38.7%; Score 36; DB 5; Length 98;
Best Local Similarity 41.7%; Pred. No. 4.9e+02;
RESULT 1222
ID ABO84414 standard; protein; 98 AA.
DE Human cancer-associated protein HP7-053.2.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 38.7%; Score 36; DB 8; Length 98;
Best Local Similarity 41.7%; Pred. No. 4.9e+02;
RESULT 1223
ID AAU43074 standard; protein; 100 AA.
DE Propionibacterium acnes immunogenic protein #3970.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 38.7%; Score 36; DB 4; Length 100;
Best Local Similarity 50.0%; Pred. No. 5e+02;
RESULT 1224
ID AAB93388 standard; protein; 100 AA.
DE Human protein sequence SEQ ID NO:12562.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 38.7%; Score 36; DB 4; Length 100;
Best Local Similarity 55.6%; Pred. No. 5e+02;
RESULT 1225
ID ABM39593 standard; protein; 100 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #4269.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 38.7%; Score 36; DB 6; Length 100;
Best Local Similarity 50.0%; Pred. No. 5e+02;
RESULT 1226
ID AAW19790 standard; protein; 101 AA.
DE Human apoptosis inducer cytokine TRAIL deletion variant.
PN WO9701633-A1.
PD 16-JAN-1997.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 2; Length 101;
Best Local Similarity 41.7%; Pred. No. 5.1e+02;
RESULT 1227
ID AAW56761 standard; protein; 101 AA.
DE Human TRAIL deletion variant (huTRAILdv) clone protein sequence.
PN US5763223-A.
PD 09-JUN-1998.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 2; Length 101;
Best Local Similarity 41.7%; Pred. No. 5.1e+02;
RESULT 1228
ID AAY79163 standard; protein; 101 AA.
DE Human endothelial PAS domain protein-1 C-terminal polypeptide.
PN WO200009657-A2.
PD 24-FEB-2000.
PA (HARD) HARVARD COLLEGE.
Query Match 38.7%; Score 36; DB 3; Length 101;
Best Local Similarity 54.5%; Pred. No. 5.1e+02;
RESULT 1229
ID AAE11032 standard; protein; 101 AA.
DE Human TRAIL deletion variant (huTRAILdv).
PN US6284236-B1.
PD 04-SEP-2001.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 4; Length 101;
Best Local Similarity 41.7%; Pred. No. 5.1e+02;
RESULT 1230
ID ABU08559 standard; protein; 101 AA.
DE Human TNF Related Apoptosis Inducing Ligand, TRAIL, deletion variant.
PN US6521228-B1.
PD 18-FEB-2003.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 6; Length 101;
Best Local Similarity 41.7%; Pred. No. 5.1e+02;
RESULT 1231
ID ADK15500 standard; protein; 101 AA.
DE Human TRAIL protein (deletion variant).
PN US20040052788-A1.
PD 18-MAR-2004.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 8; Length 101;
Best Local Similarity 41.7%; Pred. No. 5.1e+02;

RESULT 1232
ID AEB92346 standard; protein; 101 AA.
DE Human TRAIL deletion variant (huTRAILdv), SEQ ID 4.
PN US2005158823-A1.
PD 21-JUL-2005.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 9; Length 101;
Best Local Similarity 41.7%; Pred. No. 5.1e+02;
RESULT 1233
ID AAB43222 standard; protein; 104 AA.
DE Human ORFX ORF2986 polypeptide sequence SEQ ID NO:5972.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 3; Length 104;
Best Local Similarity 54.5%; Pred. No. 5.3e+02;
RESULT 1234
ID AAG22301 standard; protein; 104 AA.
DE Zea mays protein fragment SEQ ID NO: 25176.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 104;
Best Local Similarity 54.5%; Pred. No. 5.3e+02;
RESULT 1235
ID AAG21375 standard; protein; 105 AA.
DE Zea mays protein fragment SEQ ID NO: 23910.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 105;
Best Local Similarity 54.5%; Pred. No. 5.3e+02;
RESULT 1236
ID AAG33020 standard; protein; 105 AA.
DE Zea mays protein fragment SEQ ID NO: 39947.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 105;
Best Local Similarity 54.5%; Pred. No. 5.3e+02;
RESULT 1237
ID ADT87801 standard; protein; 105 AA.
DE Plant homologue of yeast SRP YLR275W #2.
PN WO2004092398-A2.
PD 28-OCT-2004.
PA (BADI) BASF PLANT SCI GMBH.
Query Match 38.7%; Score 36; DB 8; Length 105;
Best Local Similarity 54.5%; Pred. No. 5.3e+02;
RESULT 1238
ID AAU79600 standard; protein; 113 AA.
DE Human TRAIL splice variant 7, TRA-54-f1, protein.
PN US2002061525-A1.
PD 23-MAY-2002.
PA (YELI/) YELIN R.
PA (KHOS/) KHOSRAVI R.
PA (SAVI/) SAVITZKY K.
Query Match 38.7%; Score 36; DB 5; Length 113;
Best Local Similarity 41.7%; Pred. No. 5.8e+02;
RESULT 1239
ID ADL98267 standard; protein; 120 AA.
DE Human TNF-related apoptosis inducing ligand splice variant protein #4.
PN US6720182-B1.
PD 13-APR-2004.
PA (COMP-) COMPUGEN LTD CORP.
Query Match 38.7%; Score 36; DB 8; Length 120;
Best Local Similarity 41.7%; Pred. No. 6.2e+02;
RESULT 1240
ID ADW00623 standard; protein; 120 AA.
DE Human protein encoded by gene splice variant #6.
PN US2004258681-A1.
PD 23-DEC-2004.
PA (COMP-) COMPUGEN LTD CORP.
Query Match 38.7%; Score 36; DB 9; Length 120;
Best Local Similarity 41.7%; Pred. No. 6.2e+02;
RESULT 1241
ID AAG03752 standard; protein; 121 AA.
DE Human secreted protein, SEQ ID NO: 7833.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 38.7%; Score 36; DB 3; Length 121;
Best Local Similarity 41.7%; Pred. No. 6.2e+02;
RESULT 1242
ID ABB69940 standard; protein; 122 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 36612.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 38.7%; Score 36; DB 4; Length 122;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
RESULT 1243
ID ADL98266 standard; protein; 122 AA.
DE Human TNF-related apoptosis inducing ligand splice variant protein #3.
PN US6720182-B1.
PD 13-APR-2004.
PA (COMP-) COMPUGEN LTD CORP.
Query Match 38.7%; Score 36; DB 8; Length 122;
Best Local Similarity 41.7%; Pred. No. 6.3e+02;
RESULT 1244
ID ADW00622 standard; protein; 122 AA.
DE Human protein encoded by gene splice variant #5.
PN US2004258681-A1.
PD 23-DEC-2004.
PA (COMP-) COMPUGEN LTD CORP.
Query Match 38.7%; Score 36; DB 9; Length 122;
Best Local Similarity 41.7%; Pred. No. 6.3e+02;
RESULT 1245
ID AAY35754 standard; protein; 125 AA.
DE Chlamydia pneumoniae protein not found in C. trachomatis.
PN WO9927105-A2.
PD 03-JUN-1999.
PA (GEST) GENSET.
Query Match 38.7%; Score 36; DB 2; Length 125;
Best Local Similarity 66.7%; Pred. No. 6.5e+02;
RESULT 1246
ID ADY30583 standard; protein; 127 AA.
DE Human splice variant protein expressed in ovary cells DEX0487_010.aa.1.
PN WO2005017102-A2.
PD 24-FEB-2005.
PA (DIAD-) DIADEXUS INC.
Query Match 38.7%; Score 36; DB 9; Length 127;
Best Local Similarity 41.7%; Pred. No. 6.6e+02;
RESULT 1247
ID AAU54614 standard; protein; 130 AA.
DE Propionibacterium acnes immunogenic protein #15510.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 38.7%; Score 36; DB 4; Length 130;
Best Local Similarity 38.9%; Pred. No. 6.8e+02;
RESULT 1248
ID ABM51133 standard; protein; 130 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #15809.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 38.7%; Score 36; DB 6; Length 130;
Best Local Similarity 38.9%; Pred. No. 6.8e+02;
RESULT 1249
ID ABP72618 standard; protein; 131 AA.
DE Snowdrop agglutinin-Manduca sexta allatostatin protein fusion.
PN WO2003014150-A2.
PD 20-FEB-2003.
PA (UYDU-) UNIV DURHAM.
PA (ENVI-) DEPT ENVIRONMENT FOOD & RURAL AFFAIRS.
Query Match 38.7%; Score 36; DB 6; Length 131;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
RESULT 1250
ID AAB67715 standard; protein; 133 AA.

DE Protein encoded by cDNA clone with similarity to murine GL50 cDNA.
PN WO200121796-A2.
PD 29-MAR-2001.
PA (GEMY) GENETICS INST INC.
Query Match 38.7%; Score 36; DB 4; Length 133;
Best Local Similarity 42.9%; Pred. No. 6.9e+02;
RESULT 1251
ID ABB70442 standard; protein; 137 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 38118.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 38.7%; Score 36; DB 4; Length 137;
Best Local Similarity 40.0%; Pred. No. 7.2e+02;
RESULT 1252
ID AAU67799 standard; protein; 137 AA.
DE Propionibacterium acnes immunogenic protein #28695.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 38.7%; Score 36; DB 4; Length 137;
Best Local Similarity 38.9%; Pred. No. 7.2e+02;
RESULT 1253
ID ABM64318 standard; protein; 137 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #28994.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 38.7%; Score 36; DB 6; Length 137;
Best Local Similarity 38.9%; Pred. No. 7.2e+02;
RESULT 1254
ID AAG20539 standard; protein; 144 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22770.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 144;
Best Local Similarity 41.2%; Pred. No. 7.6e+02;
RESULT 1255
ID AAG47787 standard; protein; 144 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 60268.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 144;
Best Local Similarity 41.2%; Pred. No. 7.6e+02;
RESULT 1256
ID ADR09299 standard; protein; 151 AA.
DE Human protein useful for treating neurological disease Seq 2805.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 38.7%; Score 36; DB 8; Length 151;
Best Local Similarity 46.2%; Pred. No. 8e+02;
RESULT 1257
ID ADY12886 standard; protein; 151 AA.
DE Plant full length insert polypeptide seqid 68701.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 38.7%; Score 36; DB 8; Length 151;
Best Local Similarity 75.0%; Pred. No. 8e+02;
RESULT 1258
ID AAB58333 standard; protein; 157 AA.
DE Lung cancer associated polypeptide sequence SEQ ID 671.
PN WO200055180-A2.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 38.7%; Score 36; DB 3; Length 157;
Best Local Similarity 54.5%; Pred. No. 8.4e+02;
RESULT 1259
ID AAG33019 standard; protein; 163 AA.
DE Zea mays protein fragment SEQ ID NO: 39946.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 163;
Best Local Similarity 54.5%; Pred. No. 8.7e+02;
RESULT 1260
ID ADL98264 standard; protein; 169 AA.
DE Human TNF-related apoptosis inducing ligand splice variant protein #1.
PN US6720182-B1.
PD 13-APR-2004.
PA (COMP-) COMPUGEN LTD CORP.
Query Match 38.7%; Score 36; DB 8; Length 169;
Best Local Similarity 41.7%; Pred. No. 9.1e+02;
RESULT 1261
ID ADW00620 standard; protein; 169 AA.
DE Human protein encoded by gene splice variant #3.
PN US20042586681-A1.
PD 23-DEC-2004.
PA (COMP-) COMPUGEN LTD CORP.
Query Match 38.7%; Score 36; DB 9; Length 169;
Best Local Similarity 41.7%; Pred. No. 9.1e+02;
RESULT 1262
ID AAG21373 standard; protein; 172 AA.
DE Zea mays protein fragment SEQ ID NO: 23908.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 172;
Best Local Similarity 54.5%; Pred. No. 9.3e+02;
RESULT 1263
ID AAG60079 standard; protein; 174 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77779.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 174;
Best Local Similarity 38.5%; Pred. No. 9.4e+02;
RESULT 1264
ID AAG60078 standard; protein; 176 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77778.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 176;
Best Local Similarity 38.5%; Pred. No. 9.5e+02;
RESULT 1265
ID AAG60077 standard; protein; 179 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77777.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 179;
Best Local Similarity 38.5%; Pred. No. 9.7e+02;
RESULT 1266
ID ADF55456 standard; protein; 179 AA.
DE Human novel polypeptide #20.
PN JP2003245081-A.
PD 02-SEP-2003.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
Query Match 38.7%; Score 36; DB 7; Length 179;
Best Local Similarity 50.0%; Pred. No. 9.7e+02;
RESULT 1267
ID ADB63818 standard; protein; 185 AA.
DE Human protein encoded by clone ADRGL20021910.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 38.7%; Score 36; DB 7; Length 185;
Best Local Similarity 42.9%; Pred. No. 1e+03;
RESULT 1268
ID AAU79599 standard; protein; 188 AA.
DE Human TRAIL splice variant 6, TRA-33-T7, protein.
PN US2002061525-A1.

PD 23-MAY-2002.
PA (YELI/) YELIN R.
PA (KHOS/) KHOSRAVI R.
PA (SAVI/) SAVITZKY K.
Query Match 38.7%; Score 36; DB 5; Length 188;
Best Local Similarity 41.7%; Pred. No. 1e+03;
RESULT 1269
ID ADY11445 standard; protein; 188 AA.
DE Plant full length insert polypeptide seqid 67260.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 38.7%; Score 36; DB 8; Length 188;
Best Local Similarity 54.5%; Pred. No. 1e+03;
RESULT 1270
ID ABG21529 standard; protein; 190 AA.
DE Novel human diagnostic protein #21520.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 38.7%; Score 36; DB 4; Length 190;
Best Local Similarity 50.0%; Pred. No. 1e+03;
RESULT 1271
ID ABG00247 standard; protein; 192 AA.
DE Novel human diagnostic protein #238.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 38.7%; Score 36; DB 4; Length 192;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
RESULT 1272
ID ABB72279 standard; protein; 193 AA.
DE Human protein isolated from skin cells SEQ ID NO: 491.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 38.7%; Score 36; DB 5; Length 193;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
RESULT 1273
ID ADU00112 standard; protein; 203 AA.
DE Amino acid sequence of G-protein coupled receptor GCREC-4.
PN WO2004092350-A2.
PD 28-OCT-2004.
PA (INCY-) INCYTE CORP.
Query Match 38.7%; Score 36; DB 8; Length 203;
Best Local Similarity 46.2%; Pred. No. 1.1e+03;
RESULT 1274
ID AAY09197 standard; protein; 208 AA.
DE Human DNAX interleukin-40 (DIL-40) alternative sequence.
PN WO9919491-A2.
PD 22-APR-1999.
PA (SCHE) SCHERING CORP.
Query Match 38.7%; Score 36; DB 2; Length 208;
Best Local Similarity 53.8%; Pred. No. 1.2e+03;
RESULT 1275
ID AAY09196 standard; protein; 208 AA.
DE Human DNAX interleukin-40 (DIL-40) polypeptide.
PN WO9919491-A2.
PD 22-APR-1999.
PA (SCHE) SCHERING CORP.
Query Match 38.7%; Score 36; DB 2; Length 208;
Best Local Similarity 53.8%; Pred. No. 1.2e+03;
RESULT 1276
ID ADT90843 standard; protein; 208 AA.
DE Human DNAX IL-40.
PN US2004192891-A1.
PD 30-SEP-2004.
PA (SCHE) SCHERING CORP.
Query Match 38.7%; Score 36; DB 8; Length 208;
Best Local Similarity 53.8%; Pred. No. 1.2e+03;
RESULT 1277
ID ADT61031 standard; protein; 208 AA.
DE Human cytokine DNAX IL-40 (DIL-40).
PN US6800460-B1.
PD 05-OCT-2004.
PA (SCHE) SCHERING CORP.
Query Match 38.7%; Score 36; DB 8; Length 208;
Best Local Similarity 53.8%; Pred. No. 1.2e+03;
RESULT 1278
ID ADY57156 standard; protein; 208 AA.
DE Human DNAX IL-40 protein.
PN US2005048625-A1.
PD 03-MAR-2005.
PA (SCHE) SCHERING CORP.
Query Match 38.7%; Score 36; DB 9; Length 208;
Best Local Similarity 53.8%; Pred. No. 1.2e+03;
RESULT 1279
ID AAU99301 standard; protein; 212 AA.
DE Human TRAIL splice variant 8, rp1-6-6, protein.
PN US2002061525-A1.
PD 23-MAY-2002.
PA (YELI/) YELIN R.
PA (KHOS/) KHOSRAVI R.
PA (SAVI/) SAVITZKY K.
Query Match 38.7%; Score 36; DB 5; Length 212;
Best Local Similarity 41.7%; Pred. No. 1.2e+03;
RESULT 1280
ID AEB40635 standard; protein; 212 AA.
DE L. pneumophila protein SEQ ID NO 4967.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 38.7%; Score 36; DB 9; Length 212;
Best Local Similarity 53.8%; Pred. No. 1.2e+03;
RESULT 1281
ID AEB37312 standard; protein; 216 AA.
DE L. pneumophila protein SEQ ID NO 1644.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 38.7%; Score 36; DB 9; Length 216;
Best Local Similarity 53.8%; Pred. No. 1.2e+03;
RESULT 1282
ID AAB94978 standard; protein; 226 AA.
DE Human protein sequence SEQ ID NO:16560.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 38.7%; Score 36; DB 4; Length 226;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
RESULT 1283
ID AAG20538 standard; protein; 227 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22769.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 227;
Best Local Similarity 41.2%; Pred. No. 1.3e+03;
RESULT 1284
ID AAG47786 standard; protein; 227 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 60267.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 227;
Best Local Similarity 41.2%; Pred. No. 1.3e+03;
RESULT 1285

ID ABB92117 standard; protein; 227 AA.
DE Herbicidally active polypeptide SEQ ID NO 1328.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 38.7%; Score 36; DB 5; Length 227;
Best Local Similarity 41.2%; Pred. No. 1.3e+03;
RESULT 1286
ID ABP79680 standard; protein; 233 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 5890.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match 38.7%; Score 36; DB 6; Length 233;
Best Local Similarity 41.2%; Pred. No. 1.3e+03;
RESULT 1287
ID ADD12586 standard; protein; 233 AA.
DE Human ENZM-46 protein SEQ ID NO:46.
PN WO2003072729-A2.
PD 04-SEP-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 38.7%; Score 36; DB 7; Length 233;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
RESULT 1288
ID ADH71888 standard; protein; 235 AA.
DE Human protein of the invention NOV31h SEQ ID NO:784.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 8; Length 235;
Best Local Similarity 42.9%; Pred. No. 1.3e+03;
RESULT 1289
ID AEF83457 standard; protein; 241 AA.
DE Human Apo-2 ligand Apo2L/TRAIL fragment #1.
PN WO2006017531-A2.
PD 16-FEB-2006.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 10; Length 241;
Best Local Similarity 41.7%; Pred. No. 1.4e+03;
RESULT 1290
ID ADM05434 standard; protein; 242 AA.
DE Human protein of the invention SEQ ID NO:4119.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 38.7%; Score 36; DB 7; Length 242;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
RESULT 1291
ID AEC88364 standard; protein; 242 AA.
DE Human cDNA clone protein SPLEN20000640, SEQ ID 4119.
PN EP1580263-A1.
PD 28-SEP-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 38.7%; Score 36; DB 9; Length 242;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
RESULT 1292
ID AEF43692 standard; protein; 243 AA.
DE Human Apo-2 ligand residues 39-281.
PN WO2006009731-A1.
PD 26-JAN-2006.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 10; Length 243;
Best Local Similarity 41.7%; Pred. No. 1.4e+03;
RESULT 1293
ID ADF59116 standard; protein; 244 AA.
DE Human polypeptide sequence SEQ ID NO:1524.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match 38.7%; Score 36; DB 7; Length 244;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
RESULT 1294
ID ABB65303 standard; protein; 245 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 22701.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 38.7%; Score 36; DB 4; Length 245;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
RESULT 1295
ID ABB50023 standard; protein; 246 AA.
DE Listeria monocytogenes protein #2727.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 38.7%; Score 36; DB 5; Length 246;
Best Local Similarity 30.8%; Pred. No. 1.4e+03;
RESULT 1296
ID AAU79598 standard; protein; 246 AA.
DE Human TRAIL splice variant 5, TRA-20-SP6, protein.
PN US2002061525-A1.
PD 23-MAY-2002.
PA (YELI/) YELIN R.
PA (KHOS/) KHOSRAVI R.
PA (SAVI/) SAVITZKY K.
Query Match 38.7%; Score 36; DB 5; Length 246;
Best Local Similarity 41.7%; Pred. No. 1.4e+03;
RESULT 1297
ID ADI17038 standard; protein; 247 AA.
DE Human NOVX protein homologue SeqID 574.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 5; Length 247;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
RESULT 1298
ID ADX72396 standard; protein; 250 AA.
DE Plant full length insert polypeptide seqid 41762.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 38.7%; Score 36; DB 8; Length 250;
Best Local Similarity 35.7%; Pred. No. 1.4e+03;
RESULT 1299
ID ABM94614 standard; protein; 250 AA.
DE M. xanthus protein sequence, seq id 13813.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 38.7%; Score 36; DB 9; Length 250;
Best Local Similarity 42.9%; Pred. No. 1.4e+03;
RESULT 1300
ID AAW84141 standard; peptide; 252 AA.
DE Desaturase enzyme peptide sequence.
PN WO9846763-A1.
PD 22-OCT-1998.
PA (CALJ) CALGENE LLC.
PA (ABBO) ABBOTT LAB.
Query Match 38.7%; Score 36; DB 2; Length 252;
Best Local Similarity 40.0%; Pred. No. 1.4e+03;
RESULT 1301
ID ADY26629 standard; protein; 262 AA.
DE Streptomyces vinaceus VioH protein.
PN US2005042726-A1.
PD 24-FEB-2005.
PA (THOM/) THOMAS M G.
PA (CHAN/) CHAN Y A.
PA (OZAN/) OZANICK S G.
Query Match 38.7%; Score 36; DB 9; Length 262;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
RESULT 1302

ID AAY72935 standard; protein; 266 AA.
DE OmpA signal peptide-human TRAIL fusion protein.
PN WO200125397-A2.
PD 12-APR-2001.
PA (VION-) VION PHARM INC.
Query Match 38.7%; Score 36; DB 4; Length 266;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1303
ID ABU09032 standard; protein; 267 AA.
DE Human tumour wilting extract protein, Apo-2L I_100.
PN CN1367248-A.
PD 04-SEP-2002.
PA (TWOM-) NO 2 MILITARY MEDICAL COLLEGE PLA.
Query Match 38.7%; Score 36; DB 6; Length 267;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1304
ID ABR82204 standard; protein; 270 AA.
DE Chimeric hTNFalpha/hTRAIL protein.
PN WO2003050254-A2.
PD 19-JUN-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 38.7%; Score 36; DB 6; Length 270;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1305
ID ADL98265 standard; protein; 271 AA.
DE Human TNF-related apoptosis inducing ligand splice variant protein #2.
PN US6720182-B1.
PD 13-APR-2004.
PA (COMP-) COMPUGEN LTD CORP.
Query Match 38.7%; Score 36; DB 8; Length 271;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1306
ID ADW00621 standard; protein; 271 AA.
DE Human protein encoded by gene splice variant #4.
PN US2004258681-A1.
PD 23-DEC-2004.
PA (COMP-) COMPUGEN LTD CORP.
Query Match 38.7%; Score 36; DB 9; Length 271;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1307
ID ADF58901 standard; protein; 274 AA.
DE Human polypeptide sequence SEQ ID NO:1309.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match 38.7%; Score 36; DB 7; Length 274;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
RESULT 1308
ID ADT59020 standard; protein; 278 AA.
DE Plant polypeptide, SEQ ID 9097.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 38.7%; Score 36; DB 8; Length 278;
Best Local Similarity 45.5%; Pred. No. 1.6e+03;
RESULT 1309
ID AEF11626 standard; protein; 278 AA.
DE Soybean methionine production associated protein SEQ ID NO: 379.
PN WO2005098015-A2.
PD 20-OCT-2005.
PA (META-) METANOMICS GMBH & CO KGAA.
Query Match 38.7%; Score 36; DB 10; Length 278;
Best Local Similarity 25.0%; Pred. No. 1.6e+03;
RESULT 1310
ID AAW76332 standard; protein; 279 AA.
DE Human TL2 (TRAIL), ligand for TR5.
PN EP867509-A2.
PD 30-SEP-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 38.7%; Score 36; DB 2; Length 279;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1311
ID AAW95032 standard; protein; 279 AA.
DE Tumour necrosis factor receptor (TNF-R) related polypeptide TL2.
PN EP897114-A2.
PD 17-FEB-1999.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 38.7%; Score 36; DB 2; Length 279;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1312
ID ADX71478 standard; protein; 279 AA.
DE Plant full length insert polypeptide seqid 40844.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 38.7%; Score 36; DB 8; Length 279;
Best Local Similarity 25.0%; Pred. No. 1.6e+03;
RESULT 1313
ID ADN95444 standard; protein; 280 AA.
DE Human BEC/LEC-related protein sequence SeqID367.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 38.7%; Score 36; DB 7; Length 280;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1314
ID AAW19777 standard; protein; 281 AA.
DE Novel cytokine Apo-2 ligand.
PN WO9725428-A1.
PD 17-JUL-1997.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 2; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1315
ID AAW27134 standard; protein; 281 AA.
DE Human Apoptosis inducing molecule-I (AIM-I).
PN WO9733899-A1.
PD 18-SEP-1997.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 2; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1316
ID AAW19787 standard; protein; 281 AA.
DE Human apoptosis inducer cytokine TRAIL.
PN WO9701633-A1.
PD 16-JAN-1997.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 2; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1317
ID AAW76829 standard; protein; 281 AA.
DE Human TL2 protein.
PN EP870827-A2.
PD 14-OCT-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 38.7%; Score 36; DB 2; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1318
ID AAW56760 standard; protein; 281 AA.
DE Human TRAIL polypeptide.
PN US5763223-A.
PD 09-JUN-1998.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 2; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1319
ID AAW44354 standard; protein; 281 AA.
DE Human AGP-1.
PN WO9746686-A2.
PD 11-DEC-1997.

PA (AMGE-) AMGEN INC.
Query Match 38.7%; Score 36; DB 2; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1320
ID AAY01517 standard; peptide; 281 AA.
DE Protein associated with neurodegenerative and autoimmune diseases.
PN FR2766713-A1.
PD 05-FEB-1999.
PA (INMR) BIO MERIEUX.
Query Match 38.7%; Score 36; DB 2; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1321
ID AAY01516 standard; peptide; 281 AA.
DE Protein associated with neurodegenerative and autoimmune diseases.
PN FR2766713-A1.
PD 05-FEB-1999.
PA (INMR) BIO MERIEUX.
Query Match 38.7%; Score 36; DB 2; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1322
ID AAY27018 standard; protein; 281 AA.
DE Human Apo-2 ligand (Apo-2L) variant D269A.
PN WO9936535-A1.
PD 22-JUL-1999.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 2; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1323
ID AAY27019 standard; protein; 281 AA.
DE Human Apo-2 ligand (Apo-2L) variant D203A, D218A, D269A.
PN WO9936535-A1.
PD 22-JUL-1999.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 2; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1324
ID AAY27016 standard; protein; 281 AA.
DE Human Apo-2 ligand (Apo-2L) variant D203A.
PN WO9936535-A1.
PD 22-JUL-1999.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 2; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1325
ID AAY27017 standard; protein; 281 AA.
DE Human Apo-2 ligand (Apo-2L) variant D218A.
PN WO9936535-A1.
PD 22-JUL-1999.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 2; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1326
ID AAY27012 standard; protein; 281 AA.
DE Human Apo-2 ligand (Apo-2L) polypeptide.
PN WO9936535-A1.
PD 22-JUL-1999.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 2; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1327
ID AAY81956 standard; protein; 281 AA.
DE Human Apo-2 ligand protein sequence.
PN US6046048-A.
PD 04-APR-2000.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 3; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1328
ID AAB24038 standard; protein; 281 AA.
DE Human PRO1096 protein sequence SEQ ID NO:51.
PN WO200053750-A1.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 3; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1329
ID AAB08545 standard; protein; 281 AA.
DE Amino acid sequence of a human TRAIL polypeptide.
PN WO200048619-A1.
PD 24-AUG-2000.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 38.7%; Score 36; DB 3; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1330
ID AAB28691 standard; protein; 281 AA.
DE Human AGP-1.
PN WO200063253-A1.
PD 26-OCT-2000.
PA (AMGE-) AMGEN INC.
Query Match 38.7%; Score 36; DB 3; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1331
ID AAB50977 standard; protein; 281 AA.
DE Human PRO1096 protein.
PN WO200073348-A2.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 4; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1332
ID AAB67243 standard; protein; 281 AA.
DE Human Apo2 ligand.
PN WO200100832-A1.
PD 04-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 4; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1333
ID AAE11031 standard; protein; 281 AA.
DE Human TNF related apoptosis inducing ligand (TRAIL) protein.
PN US6284236-B1.
PD 04-SEP-2001.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 4; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1334
ID AAB48350 standard; protein; 281 AA.
DE Human TL2 polypeptide.
PN WO200077191-A1.
PD 21-DEC-2000.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 38.7%; Score 36; DB 4; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1335
ID ABB08133 standard; protein; 281 AA.
DE Human TRAIL polypeptide.
PN WO200236141-A2.
PD 10-MAY-2002.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 5; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1336
ID ABG31630 standard; protein; 281 AA.
DE Human TRAIL protein.
PN WO200266044-A2.
PD 29-AUG-2002.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 5; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1337
ID AAU75062 standard; protein; 281 AA.
DE Human TNF related apoptosis inducing ligand (TRAIL) protein.
PN US6329148-B1.
PD 11-DEC-2001.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 38.7%; Score 36; DB 5; Length 281;

Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1338
ID ABG72257 standard; protein; 281 AA.
DE Human tumour related apoptosis inducing ligand (Trail).
PN CN1354183-A.
PD 19-JUN-2002.
PA (TWOM-) NO 2 MILITARY MEDICAL COLLEGE PLA.
Query Match 38.7%; Score 36; DB 5; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1339
ID AAM51077 standard; protein; 281 AA.
DE Human Apo-2 ligand (TRAIL).
PN WO200209755-A2.
PD 07-FEB-2002.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 5; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1340
ID ABP51954 standard; protein; 281 AA.
DE Human Apo-2 ligand protein sequence SEQ ID NO:4.
PN WO200248376-A2.
PD 20-JUN-2002.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 5; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1341
ID AAO19095 standard; protein; 281 AA.
DE C neoformans antigen expressing dendritic cell related protein #4.
PN WO200266053-A2.
PD 29-AUG-2002.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 5; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1342
ID AAU79593 standard; protein; 281 AA.
DE Human TNF-related apoptosis inducing ligand (TRAIL) protein.
PN US2002061525-A1.
PD 23-MAY-2002.
PA (YELI/) YELIN R.
PA (KHOS/) KHOSRAVI R.
PA (SAVI/) SAVITZKY K.
Query Match 38.7%; Score 36; DB 5; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1343
ID ABG73861 standard; protein; 281 AA.
DE Human Apo-2 ligand protein.
PN US6462176-B1.
PD 08-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1344
ID ABU10205 standard; protein; 281 AA.
DE Human Apo-2 ligand.
PN US2003004313-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1345
ID ABU71443 standard; protein; 281 AA.
DE Human neoplasia inhibiting PRO polypeptide PRO1096.
PN US2002192209-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1346
ID ABG72738 standard; protein; 281 AA.
DE Human TNF-related apoptosis inducing ligand (TRAIL) protein.
PN WO200283946-A1.
PD 24-OCT-2002.
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN AGENCY NATION.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1347
ID AAO29543 standard; protein; 281 AA.
DE Human TRAIL protein.
PN WO2003042367-A2.
PD 22-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1348
ID ABU08558 standard; protein; 281 AA.
DE Human TNF Related Apoptosis Inducing Ligand, TRAIL.
PN US6521228-B1.
PD 18-FEB-2003.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1349
ID ABR42313 standard; protein; 281 AA.
DE Human TRAIL protein.
PN WO2003040307-A2.
PD 15-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1350
ID ABG71905 standard; protein; 281 AA.
DE Human TRAIL receptor-associated protein.
PN WO200279377-A2.
PD 10-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1351
ID ABP60546 standard; protein; 281 AA.
DE Human tumour necrosis factor TRAIL.
PN WO200294192-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1352
ID AAE36258 standard; protein; 281 AA.
DE Human TR4 ligand, TRAIL protein.
PN WO200297033-A2.
PD 05-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1353
ID AAO31151 standard; protein; 281 AA.
DE Human TNF-related apoptosis-inducing ligand (TRAIL).
PN WO2003054216-A2.
PD 03-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1354
ID ABO25125 standard; protein; 281 AA.
DE Human TNF-related apoptosis inducing ligand TRAIL Incyte 059509CD1.
PN US2003013099-A1.
PD 16-JAN-2003.
PA (LASE/) LASEK A K W.
PA (JONE/) JONES D A.
PA (KARP/) KARPF A R.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1355
ID ADB61480 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant R115C.
PN WO2003029420-A2.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1356
ID ADB61482 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant N134C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1357
ID ADB61484 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant E144C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1358
ID ADB61495 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant H264C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1359
ID ADB61478 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant S111C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1360
ID ADB61494 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant E263C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1361
ID ADB61481 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant E116C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1362
ID ADB61487 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant R170C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1363
ID ADB61485 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant N152C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1364
ID ADB61490 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant K179C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1365
ID ADB61471 standard; protein; 281 AA.
DE Native human Apo-2 ligand protein.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1366
ID ADB61477 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant S101C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1367
ID ADB61479 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant V114C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1368
ID ADB61491 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant D234C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1369
ID ADB61493 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant R255C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1370
ID ADB61486 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant S153C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1371
ID ADB61488 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant R170K.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1372
ID ADB61483 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant N140C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1373
ID ADB61489 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant R170S.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1374
ID ADB61476 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant S96C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1375
ID ADB61492 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant E249C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1376
ID ADC35202 standard; protein; 281 AA.
DE Human TNF ligand family member #10.
PN US2003100074-A1.
PD 29-MAY-2003.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (NARD/) NARDELLI B.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1377
ID ADD14080 standard; protein; 281 AA.
DE Human src biomarker polypeptide SEQ ID NO:269.
PN WO2003062395-A2.
PD 31-JUL-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1378
ID ADD19010 standard; protein; 281 AA.
DE Human disease related protein SeqID499.
PN WO2003018621-A2.
PD 06-MAR-2003.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1379
ID ABW02276 standard; protein; 281 AA.
DE Human TRAIL protein.
PN US2003198640-A1.
PD 23-OCT-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1380
ID ADE76953 standard; protein; 281 AA.
DE Human protein expressed in a liver disorder #32.
PN US2003108871-A1.
PD 12-JUN-2003.
PA (KASE/) KASER M R.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1381
ID ADK72311 standard; protein; 281 AA.
DE Human Apo-2 ligand with potential substitutions highlighted #4.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1382
ID ADK72306 standard; protein; 281 AA.
DE Human Apo-2 ligand variant #2.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1383
ID ADK72313 standard; protein; 281 AA.
DE Human Apo-2 ligand variant #7.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1384
ID ADK72305 standard; protein; 281 AA.
DE Human Apo-2 ligand variant #1.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1385
ID ADK72309 standard; protein; 281 AA.
DE Human Apo-2 ligand variant #5.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1386
ID ADK72303 standard; protein; 281 AA.
DE Human Apo-2 ligand with potential substitutions highlighted #1.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1387
ID ADK72304 standard; protein; 281 AA.
DE Human Apo-2 ligand with potential substitutions highlighted #2.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1388
ID ADK72308 standard; protein; 281 AA.
DE Human Apo-2 ligand variant #4.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1389
ID ADK72312 standard; protein; 281 AA.
DE Human Apo-2 ligand variant #6.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1390
ID ADK72307 standard; protein; 281 AA.
DE Human Apo-2 ligand variant #3.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1391
ID ADK72296 standard; protein; 281 AA.
DE Human wild-type Apo-2 ligand, seq id 1.
PN WO2004001009-A2.
PD 31-DEC-2003.

PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1392
ID ADK72310 standard; protein; 281 AA.
DE Human Apo-2 ligand with potential substitutions highlighted #3.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1393
ID ADJ63976 standard; protein; 281 AA.
DE Human apoptosis inducing molecule 1, AIM-1.
PN US2004038347-A1.
PD 26-FEB-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1394
ID ADL71816 standard; protein; 281 AA.
DE Human apoptosis inducing molecule-I (AIM-I) protein.
PN US2004047864-A1.
PD 11-MAR-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1395
ID ADK15498 standard; protein; 281 AA.
DE Human TRAIL protein.
PN US2004052788-A1.
PD 18-MAR-2004.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1396
ID ADN07587 standard; protein; 281 AA.
DE Human apoptosis inducing molecule-1 protein.
PN US2004048340-A1.
PD 11-MAR-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1397
ID ADR14209 standard; protein; 281 AA.
DE Human NF-kappaB pathway-associated protein SeqID210.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1398
ID ADK82215 standard; protein; 281 AA.
DE Human TRAIL amino acid sequence SEQ ID NO:66.
PN WO2004016753-A2.
PD 26-FEB-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1399
ID ADS88000 standard; protein; 281 AA.
DE Tumour treatment-related human protein sequence SeqID36.
PN WO2004034995-A2.
PD 29-APR-2004.
PA (UYPI-) UNIV PITTSBURGH.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1400
ID ABO84415 standard; protein; 281 AA.
DE Human cancer-associated protein HP7-053.3.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1401
ID ADP23388 standard; protein; 281 AA.
DE PRO polypeptide SEQ ID NO:566.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1402
ID ADT55244 standard; protein; 281 AA.
DE Amino acid sequence of human TRAIL protein.
PN WO2004087930-A2.
PD 14-OCT-2004.
PA (UYSL-) UNIV SAINT LOUIS.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1403
ID ADU22883 standard; protein; 281 AA.
DE Human apoptosis inducing DR4/DR5 ligand (Apo2L) protein.
PN US2004224389-A1.
PD 11-NOV-2004.
PA (COLS) UNIV COLORADO.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1404
ID ADU22881 standard; protein; 281 AA.
DE Human apoptosis inducing DR4/DR5 ligand (TRAIL) protein.
PN US2004224389-A1.
PD 11-NOV-2004.
PA (COLS) UNIV COLORADO.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1405
ID ADU77157 standard; protein; 281 AA.
DE Human Apo-2 ligand.
PN WO2004101608-A2.
PD 25-NOV-2004.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1406
ID ADW02206 standard; protein; 281 AA.
DE Human membrane bound TRAIL protein.
PN WO2005000220-A2.
PD 06-JAN-2005.
PA (CELL-) CELL GENESYS INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1407
ID ADY34239 standard; protein; 281 AA.
DE Human TRAIL protein.
PN WO2005016236-A2.
PD 24-FEB-2005.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1408
ID ADY14868 standard; protein; 281 AA.
DE PRO polypeptide SEQ ID NO 674.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1409
ID ADY14870 standard; protein; 281 AA.
DE PRO polypeptide SEQ ID NO 676.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 9; Length 281;

Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1410
ID ADY19766 standard; protein; 281 AA.
DE PRO polypeptide SEQ ID NO 5572.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1411
ID ADZ72350 standard; protein; 281 AA.
DE Human Apo-2 ligand protein, SEQ ID NO: 1.
PN US2005089958-A1.
PD 28-APR-2005.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1412
ID AEA21853 standard; protein; 281 AA.
DE Human kininogen D5-TRAIL related protein SEQ ID NO 4.
PN CN1546528-A.
PD 17-NOV-2004.
PA (UYPL-) UNIV PLA SECOND MILITARY MEDICAL.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1413
ID AEA23811 standard; protein; 281 AA.
DE Human PRO polypeptide SEQ ID NO 353.
PN WO2005051988-A2.
PD 09-JUN-2005.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1414
ID AEA23728 standard; protein; 281 AA.
DE Human PRO polypeptide SEQ ID NO 270.
PN WO2005051988-A2.
PD 09-JUN-2005.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1415
ID AEA27598 standard; protein; 281 AA.
DE Human TRAIL protein SEQ ID NO:66.
PN US2005129616-A1.
PD 16-JUN-2005.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1416
ID AEA55214 standard; protein; 281 AA.
DE Human TRAIL protein, SEQ ID NO:66.
PN US2005129699-A1.
PD 16-JUN-2005.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1417
ID AEB16293 standard; protein; 281 AA.
DE Trail cytokine.
PN WO2005056596-A1.
PD 23-JUN-2005.
PA (UYGR-) RIJKSUNIV GRONINGEN.
PA (EUMO-) EURO MOLECULAR BIOLOGY LAB.
PA (UYNA-) UNIV NAT IRELAND.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1418
ID AEA81246 standard; protein; 281 AA.
DE Human tumor necrosis factor superfamily-10 protein.
PN US2005136465-A1.
PD 23-JUN-2005.
PA (CLER/) CLERC R G.
PA (DUCH/) DUCHATEAU-NGUYEN G.
PA (GARD/) GARDES C.
PA (MIZR/) MIZRAHI J.
PA (OSTE/) OSTENSON C.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1419
ID AEB92344 standard; protein; 281 AA.
DE Human TRAIL, SEQ ID 2.
PN US2005158823-A1.
PD 21-JUL-2005.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1420
ID AEC77095 standard; protein; 281 AA.
DE Human splice variant protein #9.
PN WO2005082934-A2.
PD 09-SEP-2005.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1421
ID AED07288 standard; protein; 281 AA.
DE Human TNF-related apoptosis inducing ligand (TRAIL) SEQ ID NO:66.
PN US2005214209-A1.
PD 29-SEP-2005.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1422
ID AED07358 standard; protein; 281 AA.
DE Human TNF-related apoptosis inducing ligand (TRAIL) SEQ ID NO:66.
PN US2005214210-A1.
PD 29-SEP-2005.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1423
ID AEC62664 standard; protein; 281 AA.
DE Human apoptosis-inducing ligand-2 (Apo2L)/TRAIL.
PN WO2005087802-A2.
PD 22-SEP-2005.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1424
ID AED07475 standard; protein; 281 AA.
DE Human TNF-related apoptosis inducing ligand (TRAIL) SEQ ID NO:72.
PN US2005214205-A1.
PD 29-SEP-2005.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1425
ID AEC92274 standard; protein; 281 AA.
DE Human tumor necrosis factor related apoptosis inducing ligand protein.
PN US2005216960-A1.
PD 29-SEP-2005.
PA (REGC) UNIV CALIFORNIA.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1426
ID AED55194 standard; protein; 281 AA.
DE Human TRAIL protein SEQ ID NO:17.
PN US2005227283-A1.
PD 13-OCT-2005.
PA (CARR/) CARROLL P M.
PA (CHEN/) CHEN J.
PA (RAMA/) RAMANATHAN C S.
PA (XIAO/) XIAO H.
PA (GUAN/) GUAN B.
PA (BOWE/) BOWEN M A.

Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1427
ID AED55616 standard; protein; 281 AA.
DE Human apolipoprotein 2 (Apo-2) ligand SEQ ID NO 2.
PN WO2005100399-A2.
PD 27-OCT-2005.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1428
ID AED74460 standard; protein; 281 AA.
DE Human placental protein SEQ ID NO:1288.
PN US2005255114-A1.
PD 17-NOV-2005.
PA (NUVE-) NUVELO INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1429
ID AEG07278 standard; protein; 281 AA.
DE TNF-related apoptosis inducing ligand, TRAIL.
PN CN1609124-A.
PD 27-APR-2005.
PA (SHAN-) SHANGHAI QIAER BIOTECHNOLOGY CO LTD.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1430
ID AEE25411 standard; protein; 281 AA.
DE Wild type TNF-related apoptosis inducing ligand (TRAIL) SEQ ID NO 5.
PN WO2005113598-A2.
PD 01-DEC-2005.
PA (XENC-) XENCOR INC.
Query Match 38.7%; Score 36; DB 10; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1431
ID AEE48551 standard; protein; 281 AA.
DE Human TNF-Related Apoptosis-Inducing Ligand (TRAIL).
PN WO2005114187-A2.
PD 01-DEC-2005.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 38.7%; Score 36; DB 10; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1432
ID AEF43681 standard; protein; 281 AA.
DE Human Apo-2 ligand.
PN WO2006009731-A1.
PD 26-JAN-2006.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 10; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1433
ID AEF83443 standard; protein; 281 AA.
DE Human Apo-2 ligand Apo2L/TRAIL.
PN WO2006017531-A2.
PD 16-FEB-2006.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 10; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1434
ID AEF95125 standard; protein; 281 AA.
DE Human Apo-2 ligand (Apo2L).
PN WO2006017859-A2.
PD 16-FEB-2006.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 10; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
RESULT 1435
ID ABM67549 standard; protein; 283 AA.
DE Photorhabdus luminescens protein sequence #646.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.

Query Match 38.7%; Score 36; DB 6; Length 283;
Best Local Similarity 47.1%; Pred. No. 1.6e+03;
RESULT 1436
ID ADH71894 standard; protein; 284 AA.
DE Human protein of the invention NOV31k SEQ ID NO:790.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 8; Length 284;
Best Local Similarity 42.9%; Pred. No. 1.6e+03;
RESULT 1437
ID AAB08727 standard; protein; 288 AA.
DE Amino acid sequence of a human B7RP1 polypeptide.
PN WO200046240-A2.
PD 10-AUG-2000.
PA (AMGE-) AMGEN INC.
Query Match 38.7%; Score 36; DB 3; Length 288;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1438
ID AAU99785 standard; protein; 288 AA.
DE Human B7 related protein-1 (B7RP1) #1.
PN WO200244364-A2.
PD 06-JUN-2002.
PA (AMGE-) AMGEN INC.
PA (AMGE-) AMGEN CANADA INC.
Query Match 38.7%; Score 36; DB 5; Length 288;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1439
ID ADH71880 standard; protein; 290 AA.
DE Human protein of the invention NOV31d SEQ ID NO:776.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 8; Length 290;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1440
ID AAB08729 standard; protein; 302 AA.
DE Amino acid sequence of a human B7RP1 polypeptide.
PN WO200046240-A2.
PD 10-AUG-2000.
PA (AMGE-) AMGEN INC.
Query Match 38.7%; Score 36; DB 3; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1441
ID AAB87395 standard; protein; 302 AA.
DE Human gene 2 encoded secreted protein HMWDB84, SEQ ID NO:136.
PN WO200118022-A1.
PD 15-MAR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 4; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1442
ID AAG67292 standard; protein; 302 AA.
DE Amino acid sequence of a human hB7-H2 polypeptide.
PN WO200164704-A1.
PD 07-SEP-2001.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 38.7%; Score 36; DB 4; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1443
ID ABG65402 standard; protein; 302 AA.
DE Human albumin fusion protein #2077.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 5; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1444
ID AAU99789 standard; protein; 302 AA.
DE Human B7 related protein-1 (B7RP1) #2.
PN WO200244364-A2.
PD 06-JUN-2002.
PA (AMGE-) AMGEN INC.

PA (AMGE-) AMGEN CANADA INC.
Query Match 38.7%; Score 36; DB 5; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1445
ID ADH47719 standard; protein; 302 AA.
DE NOV3a protein, SEQ ID 16.
PN WO200268647-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 5; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1446
ID ADA41234 standard; protein; 302 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 6; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1447
ID ADC74429 standard; protein; 302 AA.
DE Human secreted protein - SEQ ID 1062.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 7; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1448
ID ADD25558 standard; protein; 302 AA.
DE Binding domain-immunoglobulin fusion protein-associated protein #56.
PN US2003118592-A1.
PD 26-JUN-2003.
PA (GENE-) GENECRAFT INC.
Query Match 38.7%; Score 36; DB 7; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1449
ID ADP68255 standard; protein; 302 AA.
DE Human NOV3a protein, a B7-H2 like protein SeqID 16.
PN WO200281510-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 7; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1450
ID ADH71892 standard; protein; 302 AA.
DE Human protein of the invention NOV31j SEQ ID NO:788.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 8; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1451
ID ADH71886 standard; protein; 302 AA.
DE Human protein of the invention NOV31g SEQ ID NO:782.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 8; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1452
ID ADH71884 standard; protein; 302 AA.
DE Human protein of the invention NOV31f SEQ ID NO:780.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 8; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1453
ID ADH71896 standard; protein; 302 AA.
DE Human protein of the invention NOV311 SEQ ID NO:792.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 8; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1454
ID ADH73010 standard; protein; 302 AA.
DE Human B7-related protein-1, B7RP-1.
PN US2004001831-A1.
PD 01-JAN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
PA (KOCH-) KOCH INST ROBERT.
Query Match 38.7%; Score 36; DB 8; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1455
ID ADL78669 standard; protein; 302 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 2151.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 38.7%; Score 36; DB 8; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1456
ID ADL25602 standard; protein; 302 AA.
DE Human diagnostic protein, NOV3a.
PN US2004005557-A1.
PD 08-JAN-2004.
PA (PADI/) PADIGARU M.
PA (ALSO/) ALSOBROOK J P.
PA (COLM/) COLMAN S D.
PA (SPYT/) SPYTEK K A.
PA (BOLD/) BOLDOG F L.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (SHEN/) SHENOY S G.
PA (CASM/) CASMAN S J.
PA (GUOX/) GUO X.
PA (EDIN/) EDINGER S R.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (PATT/) PATTURAJAN M.
PA (SHIM/) SHIMKETS R A.
PA (PENA/) PENA C E A.
PA (TCHE/) TCHERNEV V T.
PA (ZERH/) ZERHUSEN B D.
PA (MILL/) MILLET I.
PA (MILL/) MILLER C E.
PA (LEPL/) LEPLEY D M.
PA (SMIT/) SMITHSON G.
PA (BAUM/) BAUMGARTNER J C.
PA (HERR/) HERRMANN J L.
PA (PEYM/) PEYMAN J A.
PA (GORM/) GORMAN L.
PA (MEZE/) MEZES P D.
PA (KEKU/) KEKUDA R.
PA (TAUP/) TAUPIER R J.
PA (GERL/) GERLACH V.
PA (GROS/) GROSSE W M.
PA (LIUX/) LIU X.
PA (ELLE/) ELLERMAN K.
PA (ROTH/) ROTHENBERG M.
PA (STON/) STONE D J.
PA (BURG/) BURGESS C E.
Query Match 38.7%; Score 36; DB 8; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1457
ID ADN59025 standard; protein; 302 AA.
DE Human B7H protein #3.
PN US2004102398-A1.
PD 27-MAY-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 38.7%; Score 36; DB 8; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1458
ID ADN59021 standard; protein; 302 AA.

DE Human B7H protein #1.
PN US2004102398-A1.
PD 27-MAY-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 38.7%; Score 36; DB 8; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1459
ID ADR89355 standard; protein; 302 AA.
DE Human ICOS Ligand protein for immunotherapy method.
PN WO2004073732-A1.
PD 02-SEP-2004.
PA (LORA-) LORANTIS LTD.
Query Match 38.7%; Score 36; DB 8; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1460
ID AEA18914 standard; protein; 302 AA.
DE Amino acid sequence of the human B7-like protein.
PN WO2005044999-A2.
PD 19-MAY-2005.
PA (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
Query Match 38.7%; Score 36; DB 9; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1461
ID ADX76510 standard; protein; 303 AA.
DE Plant full length insert polypeptide seqid 45876.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 38.7%; Score 36; DB 8; Length 303;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
RESULT 1462
ID ABG30730 standard; protein; 304 AA.
DE Human B7-H2 transcript 1 (B7-H2 V1) polypeptide.
PN WO200253733-A2.
PD 11-JUL-2002.
PA (FARB) BAYER AG.
Query Match 38.7%; Score 36; DB 5; Length 304;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1463
ID AAB67713 standard; protein; 309 AA.
DE Amino acid sequence of a human GL50 polypeptide.
PN WO200121796-A2.
PD 29-MAR-2001.
PA (GEMY) GENETICS INST INC.
Query Match 38.7%; Score 36; DB 4; Length 309;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1464
ID AAO15802 standard; protein; 309 AA.
DE Human B7RP-1 protein.
PN US2002106730-A1.
PD 08-AUG-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 38.7%; Score 36; DB 5; Length 309;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1465
ID ADH71882 standard; protein; 309 AA.
DE Human protein of the invention NOV31e SEQ ID NO:778.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 8; Length 309;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1466
ID ADN59023 standard; protein; 309 AA.
DE Human B7H protein #2.
PN US2004102398-A1.
PD 27-MAY-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 38.7%; Score 36; DB 8; Length 309;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1467
ID ADQ76299 standard; protein; 309 AA.
DE Human B7RP-1 protein.
PN US2004137577-A1.
PD 15-JUL-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 38.7%; Score 36; DB 8; Length 309;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
RESULT 1468
ID ADN42318 standard; protein; 310 AA.
DE Human novel proteinNOV 54b.
PN US2004033493-A1.
PD 19-FEB-2004.
PA (TCHE/) TCHERNEV V T.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (GANG/) GANGOLLI E A.
PA (PADI/) PADIGARU M.
PA (ANDE/) ANDERSON D W.
PA (RAST/) RASTELLI L.
PA (MILL/) MILLER C E.
PA (GERL/) GERLACH V.
PA (TAUP/) TAUPIER R J.
PA (GUSE/) GUSEV V Y.
PA (COLM/) COLMAN S D.
PA (WOLE/) WOLENC A R.
PA (PENA/) PENA C E A.
PA (FURT/) FURTAK K.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
Query Match 38.7%; Score 36; DB 8; Length 310;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
RESULT 1469
ID AAB93542 standard; protein; 314 AA.
DE Human protein sequence SEQ ID NO:12910.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 38.7%; Score 36; DB 4; Length 314;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
RESULT 1470
ID AAB94208 standard; protein; 314 AA.
DE Human protein sequence SEQ ID NO:14557.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 38.7%; Score 36; DB 4; Length 314;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
RESULT 1471
ID AAB36628 standard; protein; 314 AA.
DE Human FLEXHT-50 protein sequence SEQ ID NO:50.
PN WO200070047-A2.
PD 23-NOV-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 38.7%; Score 36; DB 4; Length 314;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
RESULT 1472
ID AAE14787 standard; protein; 314 AA.
DE Human purple acid phosphatase.
PN WO200240684-A2.
PD 23-MAY-2002.
PA (FARB) BAYER AG.
Query Match 38.7%; Score 36; DB 5; Length 314;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
RESULT 1473

ID ADW07261 standard; protein; 314 AA.
DE Human hepatotoxicity biomarker protein BMS-PTX-062 SeqID13.
PN US2004265889-A1.
PD 30-DEC-2004.
PA (DURH/) DURHAM S K.
PA (DAMB/) DAMBACH D.
PA (HEFT/) HEFTA S.
PA (MOUL/) MOULIN F.
PA (GAOJ/) GAO J.
PA (OPIT/) OPITECK G.
PA (STOR/) STORM S M.
PA (GARU/) GARULACAN L A.
PA (LINJ/) LIN J.
Query Match 38.7%; Score 36; DB 9; Length 314;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
RESULT 1474
ID ADY17085 standard; protein; 321 AA.
DE PRO polypeptide SEQ ID NO 2891.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 9; Length 321;
Best Local Similarity 41.7%; Pred. No. 1.9e+03;
RESULT 1475
ID AAY74886 standard; protein; 327 AA.
DE Neisseria meningitidis ORF 298 protein sequence SEQ ID NO:1246.
PN WO9957280-A2.
PD 11-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match 38.7%; Score 36; DB 3; Length 327;
Best Local Similarity 66.7%; Pred. No. 1.9e+03;
RESULT 1476
ID AAY74884 standard; protein; 327 AA.
DE Neisseria gonorrheae ORF 298 protein sequence SEQ ID NO:1242.
PN WO9957280-A2.
PD 11-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match 38.7%; Score 36; DB 3; Length 327;
Best Local Similarity 66.7%; Pred. No. 1.9e+03;
RESULT 1477
ID AAY74885 standard; protein; 327 AA.
DE Neisseria meningitidis ORF 298 protein sequence SEQ ID NO:1244.
PN WO9957280-A2.
PD 11-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match 38.7%; Score 36; DB 3; Length 327;
Best Local Similarity 66.7%; Pred. No. 1.9e+03;
RESULT 1478
ID ADW17396 standard; protein; 328 AA.
DE Eucalyptus grandis transcription factor protein MYB family Seq 1152.
PN WO2005001050-A2.
PD 06-JAN-2005.
PA (ARBO-) ARBORGEN LLC.
Query Match 38.7%; Score 36; DB 9; Length 328;
Best Local Similarity 58.3%; Pred. No. 1.9e+03;
RESULT 1479
ID ADQ94415 standard; protein; 332 AA.
DE Rat lactate dehydrogenase A.
PN WO2004065552-A2.
PD 05-AUG-2004.
PA (UYDU-) UNIV DUKE.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 38.7%; Score 36; DB 8; Length 332;
Best Local Similarity 46.7%; Pred. No. 2e+03;
RESULT 1480
ID ADR89010 standard; protein; 332 AA.
DE Rat lactate dehydrogenase A (LDH-A) polypeptide.
PN WO2004071405-A2.
PD 26-AUG-2004.
PA (UYDU-) UNIV DUKE.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 38.7%; Score 36; DB 8; Length 332;
Best Local Similarity 46.7%; Pred. No. 2e+03;
RESULT 1481
ID ABP78644 standard; protein; 335 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 3818.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match 38.7%; Score 36; DB 6; Length 335;
Best Local Similarity 66.7%; Pred. No. 2e+03;
RESULT 1482
ID ADB08318 standard; protein; 336 AA.
DE Alloiococcus otitis antigenic protein SEQ ID NO:2258.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 38.7%; Score 36; DB 6; Length 336;
Best Local Similarity 63.6%; Pred. No. 2e+03;
RESULT 1483
ID ABB10322 standard; protein; 343 AA.
DE Human cDNA SEQ ID NO: 630.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 4; Length 343;
Best Local Similarity 42.9%; Pred. No. 2e+03;
RESULT 1484
ID ABP66909 standard; protein; 343 AA.
DE Human polypeptide SEQ ID NO 630.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 38.7%; Score 36; DB 5; Length 343;
Best Local Similarity 42.9%; Pred. No. 2e+03;
RESULT 1485
ID AAU18067 standard; protein; 344 AA.
DE Human immunoglobulin polypeptide SEQ ID No 212.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 4; Length 344;
Best Local Similarity 42.9%; Pred. No. 2e+03;
RESULT 1486
ID ABB10504 standard; protein; 344 AA.
DE Human cDNA SEQ ID NO: 812.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 4; Length 344;
Best Local Similarity 42.9%; Pred. No. 2e+03;
RESULT 1487
ID ABP67091 standard; protein; 344 AA.
DE Human polypeptide SEQ ID NO 812.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 38.7%; Score 36; DB 5; Length 344;
Best Local Similarity 42.9%; Pred. No. 2e+03;
RESULT 1488
ID ADB31691 standard; protein; 344 AA.
DE Human novel protein SEQ ID NO 212.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 7; Length 344;
Best Local Similarity 42.9%; Pred. No. 2e+03;
RESULT 1489
ID AAU18065 standard; protein; 345 AA.

DE Human immunoglobulin polypeptide SEQ ID No 210.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 4; Length 345;
Best Local Similarity 42.9%; Pred. No. 2e+03;
RESULT 1490
ID ABB10502 standard; protein; 345 AA.
DE Human cDNA SEQ ID NO: 810.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 4; Length 345;
Best Local Similarity 42.9%; Pred. No. 2e+03;
RESULT 1491
ID ABP67089 standard; protein; 345 AA.
DE Human polypeptide SEQ ID NO 810.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 38.7%; Score 36; DB 5; Length 345;
Best Local Similarity 42.9%; Pred. No. 2e+03;
RESULT 1492
ID ADB31689 standard; protein; 345 AA.
DE Human novel protein SEQ ID NO 210.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 7; Length 345;
Best Local Similarity 42.9%; Pred. No. 2e+03;
RESULT 1493
ID AAU15973 standard; protein; 351 AA.
DE Human novel secreted protein, Seq ID 926.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 4; Length 351;
Best Local Similarity 38.9%; Pred. No. 2.1e+03;
RESULT 1494
ID ABU55042 standard; protein; 351 AA.
DE Human novel polypeptide #129.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 38.7%; Score 36; DB 6; Length 351;
Best Local Similarity 38.9%; Pred. No. 2.1e+03;
RESULT 1495
ID AAG81561 standard; protein; 352 AA.
DE S. epidermidis open reading frame protein sequence SEQ ID NO:216.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 38.7%; Score 36; DB 4; Length 352;
Best Local Similarity 61.5%; Pred. No. 2.1e+03;
RESULT 1496
ID ADB80938 standard; protein; 359 AA.
DE RING-SH complex related protein, SEQ ID No 12.
PN WO2003033646-A2.
PD 24-APR-2003.
PA (PROT-) PROTEOLOGICS INC.
Query Match 38.7%; Score 36; DB 7; Length 359;
Best Local Similarity 57.1%; Pred. No. 2.1e+03;
RESULT 1497
ID ADE54266 standard; protein; 359 AA.
DE Human Protein O00623, SEQ ID NO 69.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 38.7%; Score 36; DB 7; Length 359;
Best Local Similarity 57.1%; Pred. No. 2.1e+03;
RESULT 1498
ID AAU36115 standard; protein; 361 AA.
DE Klebsiella pneumoniae cellular proliferation protein #103.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 38.7%; Score 36; DB 4; Length 361;
Best Local Similarity 37.5%; Pred. No. 2.2e+03;
RESULT 1499
ID ABU28113 standard; protein; 361 AA.
DE Protein encoded by Prokaryotic essential gene #13640.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 38.7%; Score 36; DB 6; Length 361;
Best Local Similarity 37.5%; Pred. No. 2.2e+03;
RESULT 1500
ID ABU31873 standard; protein; 361 AA.
DE Protein encoded by Prokaryotic essential gene #17400.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 38.7%; Score 36; DB 6; Length 361;
Best Local Similarity 37.5%; Pred. No. 2.2e+03;

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OM protein - protein search, using sw model

Run on: November 21, 2006, 20:09:55 ; Search time 5.2844 Seconds
(without alignments)
298.151 Million cell updates/sec

Title: US-10-063-553-48_COPY_32_49
Perfect score: 93
Sequence: 1 VSLVEEDQFSQNPISCFE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued_Patents_AA:*
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6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	93	100.0	229	2	US-09-991-181-258	Sequence 258, App
2	93	100.0	229	2	US-09-990-444-258	Sequence 258, App
3	93	100.0	229	2	US-09-997-333-258	Sequence 258, App
4	93	100.0	229	2	US-09-992-598-258	Sequence 258, App
5	93	100.0	229	2	US-09-989-735-258	Sequence 258, App
6	93	100.0	229	3	US-09-989-726-258	Sequence 258, App
7	93	100.0	229	3	US-09-997-514-258	Sequence 258, App
8	93	100.0	229	3	US-09-989-728-258	Sequence 258, App
9	93	100.0	229	3	US-09-997-349-258	Sequence 258, App
10	93	100.0	229	3	US-09-997-653-258	Sequence 258, App
11	93	100.0	229	3	US-09-989-293A-258	Sequence 258, App
12	43	46.2	1110	1	US-08-118-441-29	Sequence 29, Appl
13	43	46.2	1110	2	US-08-338-579A-29	Sequence 29, Appl
14	43	46.2	1110	5	PCT-US94-09851-29	Sequence 29, Appl
15	42	45.2	676	1	US-08-398-590A-40	Sequence 40, Appl
16	42	45.2	676	2	US-08-894-997-40	Sequence 40, Appl
17	42	45.2	676	2	US-09-873-155A-40	Sequence 40, Appl
18	42	45.2	976	2	US-08-894-997-50	Sequence 50, Appl
19	42	45.2	976	2	US-09-873-155A-50	Sequence 50, Appl
20	42	45.2	1147	2	US-09-949-016-8616	Sequence 8616, Ap
21	42	45.2	1464	1	US-08-231-193A-11	Sequence 11, Appl
22	42	45.2	1464	1	US-08-486-273A-11	Sequence 11, Appl
23	42	45.2	1464	2	US-08-940-086A-11	Sequence 11, Appl
24	42	45.2	1464	2	US-08-436-332B-10	Sequence 10, Appl
25	42	45.2	1464	2	US-08-940-035A-11	Sequence 11, Appl
26	42	45.2	1464	2	US-08-935-105A-11	Sequence 11, Appl
27	42	45.2	1464	2	US-09-648-797-11	Sequence 11, Appl
28	42	45.2	1464	2	US-08-217-704C-2	Sequence 2, Appli
29	42	45.2	1464	2	US-09-386-123-11	Sequence 11, Appl
30	42	45.2	1464	2	US-09-949-016-8311	Sequence 8311, Ap
31	42	45.2	1464	2	US-10-038-937-11	Sequence 11, Appl
32	42	45.2	1464	2	US-10-007-747-11	Sequence 11, Appl
33	42	45.2	1464	2	US-09-945-901-11	Sequence 11, Appl
34	41	44.1	117	2	US-08-965-903B-6	Sequence 6, Appli
35	41	44.1	139	2	US-08-965-903B-20	Sequence 20, Appl
36	41	44.1	139	2	US-09-370-398-4	Sequence 4, Appli
37	41	44.1	139	2	US-10-090-190-4	Sequence 4, Appli
38	41	44.1	139	2	US-10-082-902-4	Sequence 4, Appli
39	40.5	43.5	797	2	US-09-198-452A-636	Sequence 636, App
40	40.5	43.5	814	2	US-09-438-185A-596	Sequence 596, App
41	40	43.0	158	2	US-10-104-047-3221	Sequence 3221, Ap
42	40	43.0	305	2	US-09-248-796A-17837	Sequence 17837, A
43	40	43.0	789	2	US-09-949-016-7164	Sequence 7164, Ap
44	40	43.0	1500	2	US-09-949-016-5878	Sequence 5878, Ap
45	40	43.0	1620	2	US-09-949-016-7242	Sequence 7242, Ap
46	39	41.9	238	2	US-08-858-207A-420	Sequence 420, App
47	39	41.9	320	2	US-09-330-970-3	Sequence 3, Appli
48	39	41.9	390	2	US-09-949-016-10020	Sequence 10020, A
49	39	41.9	502	2	US-09-330-970-1	Sequence 1, Appli
50	39	41.9	659	2	US-09-583-110-4043	Sequence 4043, Ap
51	39	41.9	661	2	US-09-107-433-3700	Sequence 3700, Ap
52	39	41.9	741	2	US-08-943-956A-2	Sequence 2, Appli
53	38.5	41.4	355	2	US-09-498-520A-8	Sequence 8, Appli
54	38.5	41.4	355	2	US-09-498-520A-48	Sequence 48, Appl
55	38.5	41.4	393	2	US-08-956-171E-5248	Sequence 5248, Ap
56	38.5	41.4	393	2	US-08-781-986A-5248	Sequence 5248, Ap
57	38	40.9	193	2	US-09-949-016-10446	Sequence 10446, A
58	38	40.9	197	2	US-09-270-767-47012	Sequence 47012, A
59	38	40.9	291	2	US-09-198-452A-624	Sequence 624, App
60	38	40.9	291	2	US-09-438-185A-584	Sequence 584, App
61	38	40.9	339	2	US-08-758-280-1	Sequence 1, Appli
62	38	40.9	339	2	US-08-758-280-2	Sequence 2, Appli
63	38	40.9	339	2	US-08-964-614A-1	Sequence 1, Appli
64	38	40.9	339	2	US-08-964-614A-2	Sequence 2, Appli
65	38	40.9	339	2	US-09-538-092-1274	Sequence 1274, Ap
66	38	40.9	349	2	US-09-270-767-43051	Sequence 43051, A
67	38	40.9	395	2	US-09-949-016-8564	Sequence 8564, Ap
68	38	40.9	400	2	US-09-107-532A-4562	Sequence 4562, Ap
69	38	40.9	448	2	US-08-476-509B-2	Sequence 2, Appli
70	38	40.9	486	2	US-08-348-518C-2	Sequence 2, Appli
71	38	40.9	498	1	US-07-688-352C-20	Sequence 20, Appl
72	38	40.9	498	1	US-08-474-379C-20	Sequence 20, Appl
73	38	40.9	498	2	US-09-146-249A-20	Sequence 20, Appl
74	38	40.9	498	2	US-08-206-188B-20	Sequence 20, Appl
75	38	40.9	700	2	US-09-252-991A-23746	Sequence 23746, A
76	38	40.9	757	2	US-09-538-092-520	Sequence 520, App
77	38	40.9	772	2	US-10-148-806-37	Sequence 37, Appl
78	38	40.9	852	2	US-09-248-796A-14890	Sequence 14890, A
79	38	40.9	940	2	US-09-252-991A-24639	Sequence 24639, A
80	38	40.9	981	2	US-09-902-540-9848	Sequence 9848, Ap
81	38	40.9	1068	2	US-09-538-092-1111	Sequence 1111, Ap
82	38	40.9	1069	1	US-08-162-081B-37	Sequence 37, Appl
83	38	40.9	1069	1	US-08-780-872-37	Sequence 37, Appl
84	38	40.9	1069	2	US-09-085-957-37	Sequence 37, Appl
85	38	40.9	1080	1	US-08-162-081B-36	Sequence 36, Appl
86	38	40.9	1080	1	US-08-780-872-36	Sequence 36, Appl
87	38	40.9	1080	2	US-09-085-957-36	Sequence 36, Appl
88	37.5	40.3	15	1	US-08-522-326-6	Sequence 6, Appli
89	37.5	40.3	375	2	US-09-270-767-39877	Sequence 39877, A
90	37.5	40.3	375	2	US-09-270-767-55094	Sequence 55094, A
91	37	39.8	75	2	US-09-248-796A-24305	Sequence 24305, A
92	37	39.8	104	2	US-09-634-238-312	Sequence 312, App
93	37	39.8	116	2	US-08-965-903B-9	Sequence 9, Appli
94	37	39.8	191	2	US-09-270-767-35892	Sequence 35892, A
95	37	39.8	191	2	US-09-270-767-51109	Sequence 51109, A
96	37	39.8	277	2	US-09-328-352-7936	Sequence 7936, Ap
97	37	39.8	315	2	US-08-965-903B-8	Sequence 8, Appli
98	37	39.8	315	2	US-09-370-398-3	Sequence 3, Appli
99	37	39.8	315	2	US-09-370-398-6	Sequence 6, Appli

100	37	39.8	315	2	US-10-090-190-3	Sequence 3, Appli
101	37	39.8	315	2	US-10-090-190-6	Sequence 6, Appli
102	37	39.8	315	2	US-10-082-902-3	Sequence 3, Appli
103	37	39.8	315	2	US-10-082-902-6	Sequence 6, Appli
104	37	39.8	326	2	US-09-520-781-75	Sequence 75, Appl
105	37	39.8	326	2	US-09-957-187-75	Sequence 75, Appl
106	37	39.8	326	2	US-09-991-053-75	Sequence 75, Appl
107	37	39.8	339	2	US-09-134-000C-5209	Sequence 5209, Ap
108	37	39.8	363	2	US-09-205-258-278	Sequence 278, App
109	37	39.8	363	2	US-10-004-860-278	Sequence 278, App
110	37	39.8	370	2	US-09-205-258-558	Sequence 558, App
111	37	39.8	370	2	US-10-004-860-558	Sequence 558, App
112	37	39.8	380	2	US-09-248-796A-14486	Sequence 14486, A
113	37	39.8	393	1	US-08-933-750C-11	Sequence 11, Appl
114	37	39.8	393	2	US-09-234-613-11	Sequence 11, Appl
115	37	39.8	393	2	US-09-663-600A-199	Sequence 199, App
116	37	39.8	416	2	US-09-205-258-461	Sequence 461, App
117	37	39.8	416	2	US-10-004-860-461	Sequence 461, App
118	37	39.8	494	2	US-10-290-579A-175	Sequence 175, App
119	37	39.8	510	2	US-09-370-368-5	Sequence 5, Appli
120	37	39.8	549	2	US-09-107-532A-6840	Sequence 6840, Ap
121	37	39.8	579	1	US-08-448-196A-8	Sequence 8, Appli
122	37	39.8	707	2	US-10-094-749-2693	Sequence 2693, Ap
123	37	39.8	1713	3	US-10-114-270-194	Sequence 194, App
124	36.5	39.2	291	2	US-09-489-039A-8172	Sequence 8172, Ap
125	36.5	39.2	657	2	US-09-653-465B-2	Sequence 2, Appli
126	36.5	39.2	672	2	US-09-949-016-8895	Sequence 8895, Ap
127	36	38.7	70	2	US-09-513-999C-6629	Sequence 6629, Ap
128	36	38.7	90	2	US-09-188-930-134	Sequence 134, App
129	36	38.7	90	2	US-09-312-283C-134	Sequence 134, App
130	36	38.7	101	1	US-08-670-354-4	Sequence 4, Appli
131	36	38.7	101	2	US-09-320-424-4	Sequence 4, Appli
132	36	38.7	101	2	US-09-374-454-17	Sequence 17, Appl
133	36	38.7	101	2	US-09-825-563-4	Sequence 4, Appli
134	36	38.7	101	5	PCT-US96-10895-4	Sequence 4, Appli
135	36	38.7	120	2	US-09-569-611C-32	Sequence 32, Appl
136	36	38.7	121	2	US-09-513-999C-7833	Sequence 7833, Ap
137	36	38.7	122	2	US-09-569-611C-31	Sequence 31, Appl
138	36	38.7	125	2	US-09-198-452A-1172	Sequence 1172, Ap
139	36	38.7	157	2	US-09-270-767-40741	Sequence 40741, A
140	36	38.7	157	2	US-09-270-767-55957	Sequence 55957, A
141	36	38.7	161	2	US-09-270-767-48702	Sequence 48702, A
142	36	38.7	169	2	US-09-569-611C-29	Sequence 29, Appl
143	36	38.7	185	2	US-10-104-047-1972	Sequence 1972, Ap
144	36	38.7	208	2	US-09-521-335-11	Sequence 11, Appl
145	36	38.7	225	2	US-09-949-016-11297	Sequence 11297, A
146	36	38.7	225	2	US-09-949-016-11298	Sequence 11298, A
147	36	38.7	241	2	US-09-915-789A-11	Sequence 11, Appl
148	36	38.7	250	2	US-09-124-141-17	Sequence 17, Appl
149	36	38.7	250	2	US-09-902-540-13813	Sequence 13813, A
150	36	38.7	252	1	US-08-834-655-7	Sequence 7, Appli
151	36	38.7	252	2	US-08-834-033A-8	Sequence 8, Appli
152	36	38.7	252	2	US-09-363-574-7	Sequence 7, Appli
153	36	38.7	252	2	US-09-363-526-7	Sequence 7, Appli
154	36	38.7	261	2	US-09-270-767-47059	Sequence 47059, A
155	36	38.7	266	2	US-09-645-415A-10	Sequence 10, Appl
156	36	38.7	271	2	US-09-569-611C-30	Sequence 30, Appl
157	36	38.7	279	2	US-09-072-993C-3	Sequence 3, Appli
158	36	38.7	281	1	US-08-670-354-2	Sequence 2, Appli
159	36	38.7	281	2	US-08-584-031-1	Sequence 1, Appli
160	36	38.7	281	2	US-08-780-496-1	Sequence 1, Appli
161	36	38.7	281	2	US-08-883-086-10	Sequence 10, Appl
162	36	38.7	281	2	US-09-320-424-2	Sequence 2, Appli
163	36	38.7	281	2	US-09-333-593A-6	Sequence 6, Appli
164	36	38.7	281	2	US-09-157-864-11	Sequence 11, Appl
165	36	38.7	281	2	US-09-825-563-2	Sequence 2, Appli
166	36	38.7	281	2	US-09-919-039-118	Sequence 118, App
167	36	38.7	281	2	US-09-582-450-1	Sequence 1, Appli
168	36	38.7	281	2	US-09-934-465-1	Sequence 1, Appli
169	36	38.7	281	2	US-10-011-125A-4	Sequence 4, Appli
170	36	38.7	281	2	US-09-459-808-1	Sequence 1, Appli
171	36	38.7	281	5	PCT-US96-10895-2	Sequence 2, Appli
172	36	38.7	302	2	US-09-915-789A-18	Sequence 18, Appl
173	36	38.7	309	2	US-09-667-135-6	Sequence 6, Appli
174	36	38.7	309	2	US-09-910-174B-7	Sequence 7, Appli
175	36	38.7	309	2	US-09-620-461-7	Sequence 7, Appli
176	36	38.7	352	2	US-09-710-279-216	Sequence 216, App
177	36	38.7	359	2	US-09-949-016-5912	Sequence 5912, Ap
178	36	38.7	377	2	US-09-489-039A-12546	Sequence 12546, A
179	36	38.7	403	2	US-09-540-236-2573	Sequence 2573, Ap
180	36	38.7	411	2	US-09-188-930-302	Sequence 302, App
181	36	38.7	411	2	US-09-312-283C-302	Sequence 302, App
182	36	38.7	450	2	US-09-949-016-8496	Sequence 8496, Ap
183	36	38.7	459	3	US-10-433-794-3	Sequence 3, Appli
184	36	38.7	478	2	US-09-570-454-2	Sequence 2, Appli
185	36	38.7	478	2	US-09-867-521-2	Sequence 2, Appli
186	36	38.7	490	2	US-09-667-135-28	Sequence 28, Appl
187	36	38.7	558	2	US-09-667-135-31	Sequence 31, Appl
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189	36	38.7	594	1	US-08-592-696-4	Sequence 4, Appli
190	36	38.7	594	1	US-09-027-536-2	Sequence 2, Appli
191	36	38.7	594	1	US-09-027-536-4	Sequence 4, Appli
192	36	38.7	594	2	US-09-028-148-2	Sequence 2, Appli
193	36	38.7	594	2	US-09-028-148-4	Sequence 4, Appli
194	36	38.7	594	2	US-09-124-141-15	Sequence 15, Appl
195	36	38.7	594	2	US-09-124-141-23	Sequence 23, Appl
196	36	38.7	625	1	US-08-242-689-2	Sequence 2, Appli
197	36	38.7	625	2	US-08-468-583-2	Sequence 2, Appli
198	36	38.7	640	2	US-09-134-000C-5035	Sequence 5035, Ap
199	36	38.7	646	2	US-09-710-279-676	Sequence 676, App
200	36	38.7	648	2	US-09-949-016-11296	Sequence 11296, A
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202	36	38.7	741	1	US-08-436-771-2	Sequence 2, Appli
203	36	38.7	741	1	US-08-436-771-4	Sequence 4, Appli
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205	36	38.7	741	1	US-08-434-998-4	Sequence 4, Appli
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207	36	38.7	741	1	US-08-487-797-4	Sequence 4, Appli
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212	36	38.7	741	5	PCT-US95-02058-4	Sequence 4, Appli
213	36	38.7	747	2	US-09-949-016-7955	Sequence 7955, Ap
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215	36	38.7	870	2	US-09-374-454-6	Sequence 6, Appli
216	36	38.7	2789	2	US-09-949-016-8208	Sequence 8208, Ap
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219	35	37.6	28	2	US-09-880-132-12	Sequence 12, Appl
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224	35	37.6	157	2	US-09-306-454-7	Sequence 7, Appli
225	35	37.6	157	2	US-09-306-454-9	Sequence 9, Appli
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227	35	37.6	178	1	US-08-446-822-6	Sequence 6, Appli
228	35	37.6	178	2	US-09-328-314-6	Sequence 6, Appli
229	35	37.6	178	5	PCT-US93-12586-6	Sequence 6, Appli
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232	35	37.6	199	2	US-09-232-201-85	Sequence 85, Appl
233	35	37.6	199	2	US-09-232-195-85	Sequence 85, Appl
234	35	37.6	199	3	US-09-405-504A-85	Sequence 85, Appl
235	35	37.6	202	2	US-09-543-681A-6592	Sequence 6592, Ap
236	35	37.6	203	2	US-09-124-141-9	Sequence 9, Appli
237	35	37.6	253	2	US-09-248-796A-14363	Sequence 14363, A
238	35	37.6	254	2	US-10-126-279-27	Sequence 27, Appl
239	35	37.6	254	2	US-10-286-606-27	Sequence 27, Appl
240	35	37.6	254	2	US-10-891-383A-27	Sequence 27, Appl
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242	35	37.6	261	2	US-09-328-314-15	Sequence 15, Appl
243	35	37.6	261	5	PCT-US93-12586-15	Sequence 15, Appl
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258	35	37.6	364	2	US-09-270-767-43337	Sequence 43337, A
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262	35	37.6	380	2	US-09-826-509-441	Sequence 441, App
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264	35	37.6	388	1	US-08-446-822-8	Sequence 8, Appli
265	35	37.6	388	2	US-09-328-314-8	Sequence 8, Appli
266	35	37.6	388	2	US-09-826-509-439	Sequence 439, App
267	35	37.6	388	5	PCT-US93-12586-8	Sequence 8, Appli
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277	35	37.6	569	2	US-08-685-212-2	Sequence 2, Appli
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292	35	37.6	758	2	US-09-438-185A-926	Sequence 926, App
293	35	37.6	760	2	US-09-555-313B-2	Sequence 2, Appli
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298	35	37.6	902	2	US-10-282-162-36	Sequence 36, Appl
299	35	37.6	902	2	US-10-282-162-38	Sequence 38, Appl
300	35	37.6	902	2	US-10-282-162-42	Sequence 42, Appl
301	35	37.6	902	2	US-10-282-162-44	Sequence 44, Appl
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303	35	37.6	910	2	US-10-282-162-28	Sequence 28, Appl
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310	35	37.6	1175	1	US-08-639-923A-36	Sequence 36, Appl
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312	35	37.6	1279	2	US-09-364-425B-58	Sequence 58, Appl
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318	35	37.6	2368	1	US-08-870-693-15	Sequence 15, Appl
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321	34.5	37.1	826	2	US-09-949-016-9213	Sequence 9213, Ap
322	34.5	37.1	826	2	US-09-949-016-9214	Sequence 9214, Ap
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334	34	36.6	117	2	US-09-248-796A-19723	Sequence 19723, A
335	34	36.6	120	2	US-09-248-796A-16151	Sequence 16151, A
336	34	36.6	130	2	US-09-621-976-4013	Sequence 4013, Ap
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342	34	36.6	154	2	US-09-435-242-22	Sequence 22, Appl
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348	34	36.6	188	2	US-09-710-279-152	Sequence 152, App
349	34	36.6	198	2	US-10-094-749-1831	Sequence 1831, Ap
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351	34	36.6	224	2	US-09-270-767-33261	Sequence 33261, A
352	34	36.6	224	2	US-09-830-230A-349	Sequence 349, App
353	34	36.6	245	2	US-09-602-787A-22	Sequence 22, Appl
354	34	36.6	246	2	US-09-107-532A-5040	Sequence 5040, Ap
355	34	36.6	254	2	US-09-248-796A-21484	Sequence 21484, A
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357	34	36.6	308	2	US-09-134-000C-6494	Sequence 6494, Ap
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371	34	36.6	330	2	US-09-301-217-10	Sequence 10, Appl
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446	34	36.6	672	2	US-09-083-587-2	Sequence 2, Appli
447	34	36.6	672	2	US-10-094-749-2290	Sequence 2290, Ap
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452	34	36.6	735	5	PCT-US94-01624-4	Sequence 4, Appli
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734	33	35.5	28	2	US-09-880-132-11	Sequence 11, Appl
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737	33	35.5	29	2	US-09-880-132-52	Sequence 52, Appl
738	33	35.5	29	2	US-09-880-132-55	Sequence 55, Appl
739	33	35.5	33	2	US-09-227-357-651	Sequence 651, App
740	33	35.5	33	2	US-09-973-278-369	Sequence 369, App
741	33	35.5	56	2	US-09-270-767-57450	Sequence 57450, A
742	33	35.5	64	2	US-09-107-532A-4990	Sequence 4990, Ap
743	33	35.5	73	2	US-09-949-016-9293	Sequence 9293, Ap
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745	33	35.5	74	2	US-09-139-600-58	Sequence 58, Appl
746	33	35.5	74	2	US-09-989-903-63	Sequence 63, Appl
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753	33	35.5	90	2	US-09-433-043B-29	Sequence 29, Appl
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757	33	35.5	121	2	US-09-621-976-7091	Sequence 7091, Ap
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763	33	35.5	122	2	US-09-433-043B-28	Sequence 28, Appl
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769	33	35.5	140	2	US-09-170-996-16	Sequence 16, Appl
770	33	35.5	146	2	US-09-436-699C-14	Sequence 14, Appl
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773	33	35.5	167	2	US-09-248-796A-17420	Sequence 17420, A
774	33	35.5	170	2	US-09-621-976-7090	Sequence 7090, Ap
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777	33	35.5	186	2	US-09-248-796A-17741	Sequence 17741, A
778	33	35.5	188	2	US-09-438-185A-957	Sequence 957, App
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789	33	35.5	230	2	US-09-270-767-32425	Sequence 32425, A
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808	33	35.5	303	2	US-09-489-039A-11552	Sequence 11552, A
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862	33	35.5	541	2	US-10-191-780A-2	Sequence 2, Appli
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871	33	35.5	663	2	US-09-398-184-5	Sequence 5, Appli
872	33	35.5	664	1	US-08-421-661-6	Sequence 6, Appli
873	33	35.5	664	2	US-09-917-254-78	Sequence 78, Appl
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909	33	35.5	946	2	US-09-969-528-4	Sequence 4, Appli
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ALIGNMENTS

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; Sequence 258, Application US/09991181
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 93; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 9e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 258, Application US/09990444
; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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Best Local Similarity 100.0%; Pred. No. 9e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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; Patent No. 6953836
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; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
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; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 93; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 9e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSLVEEDQFSQNPISCFE 18
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Db 32 VSLVEEDQFSQNPISCFE 49

RESULT 4
US-09-992-598-258

; Sequence 258, Application US/09992598
; Patent No. 6956108
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 93; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 9e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSLVEEDQFSQNPISCFE 18
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Db 32 VSLVEEDQFSQNPISCFE 49

RESULT 5
US-09-989-735-258
; Sequence 258, Application US/09989735
; Patent No. 6972185
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C61
; CURRENT APPLICATION NUMBER: US/09/989,735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 93; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 9e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSLVEEDQFSQNPISCFE 18
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Db 32 VSLVEEDQFSQNPISCFE 49

RESULT 6
US-09-989-726-258
; Sequence 258, Application US/09989726
; Patent No. 7018811
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.

; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C60
; CURRENT APPLICATION NUMBER: US/09/989,726
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 93; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 9e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSLVEEDQFSQNPISCFE 18
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Db 32 VSLVEEDQFSQNPISCFE 49

RESULT 7
US-09-997-514-258
; Sequence 258, Application US/09997514
; Patent No. 7019116
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C46
; CURRENT APPLICATION NUMBER: US/09/997,514
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-07
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Query Match 100.0%; Score 93; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 9e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db         32 VSLVEEDQFSQNPISCFE 49
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RESULT 8
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; Sequence 258, Application US/09989728
; Patent No. 7029873
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
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; APPLICANT: Gurney,Austin L.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C72
; CURRENT APPLICATION NUMBER: US/09/989,728
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Query Match 100.0%; Score 93; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 9e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 32 VSLVEEDQFSQNPISCFE 49

RESULT 9
US-09-997-349-258
; Sequence 258, Application US/09997349
; Patent No. 7034106
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
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; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C37
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; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
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Query Match 100.0%; Score 93; DB 3; Length 229;
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 258, Application US/09997653
; Patent No. 7034122
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
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; APPLICANT: Goddard,Audrey
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; APPLICANT: Gurney,Austin L.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C38
; CURRENT APPLICATION NUMBER: US/09/997,653
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
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; Patent No. 7034136
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
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; APPLICANT: Eaton,Dan L.
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
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;  PRIOR FILING DATE: 1998-07-09

  Query Match             100.0%;  Score 93;  DB 3;  Length 229;
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  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         32 VSLVEEDQFSQNPISCFE 49


RESULT 12
US-08-118-441-29
; Sequence 29, Application US/08118441
; Patent No. 5578493
;  GENERAL INFORMATION:
;    APPLICANT:  Gilliam, T. Conrad
;    APPLICANT:  Tanzi, Rudolph E.
;    TITLE OF INVENTION:  ISOLATION AND USES OF A WILSON'S DISEASE
;    TITLE OF INVENTION:  GENE
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10112
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/118,441
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  0575/44011
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 977-9550
;      TELEFAX:  (212) 664-0525
;      TELEX:  422523 COOP UI
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1110 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-118-441-29

  Query Match             46.2%;  Score 43;  DB 1;  Length 1110;
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Qy          1 VSLVEEDQFSQNP 13
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Db        590 VKLVEEAQMSKNP 602


RESULT 13
US-08-338-579A-29
; Sequence 29, Application US/08338579A
; Patent No. 6068975
;  GENERAL INFORMATION:
;    APPLICANT:  Gilliam, T. Conrad
;    APPLICANT:  Tanzi, Rudolph E.
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;    TITLE OF INVENTION:  ISOLATION AND USES OF A WILSON'S
;    TITLE OF INVENTION:  DISEASE GENE
;    NUMBER OF SEQUENCES:  107
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/338,579A
;      FILING DATE:  June 17, 1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  0575/44011-A-PCT-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1110 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-338-579A-29

  Query Match             46.2%;  Score 43;  DB 2;  Length 1110;
  Best Local Similarity   69.2%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 VSLVEEDQFSQNP 13
              | |||| | |:||
Db        590 VKLVEEAQMSKNP 602


RESULT 14
PCT-US94-09851-29
; Sequence 29, Application PC/TUS9409851
;  GENERAL INFORMATION:
;    APPLICANT:  Gilliam, T. Conrad
;    APPLICANT:  Tanzi, Rudolph E.
;    TITLE OF INVENTION:  ISOLATION AND USES OF A WILSON'S
;    TITLE OF INVENTION:  DISEASE GENE
;    NUMBER OF SEQUENCES:  92
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10112
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/09851
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  0575/44011-PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 977-9550
;      TELEFAX:  (212) 664-0525
;      TELEX:  422523 COOP UI
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1110 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US94-09851-29

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Db        590 VKLVEEAQMSKNP 602


RESULT 15
US-08-398-590A-40
; Sequence 40, Application US/08398590A
; Patent No. 5935811
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, David J.
;    APPLICANT:  Schoenherr, Christopher J.
;    TITLE OF INVENTION:  Neuron-Restrictive Silencer Factor
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/398,590A
;      FILING DATE:  03-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/103,445
;      FILING DATE:  06-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Silva, Robin M.
;      REGISTRATION NUMBER:  38,304
;      REFERENCE/DOCKET NUMBER:  A-60897/RFT/RMS
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  676 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-398-590A-40

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Db        284 STAEEGDFSKGPIRC 298
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OM protein - protein search, using sw model

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SUMMARIES

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787	42	45.2	1464	5	US-10-473-127-242	Sequence 242, App
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918	38	40.9	228	4	US-10-424-599-228931	Sequence 228931,
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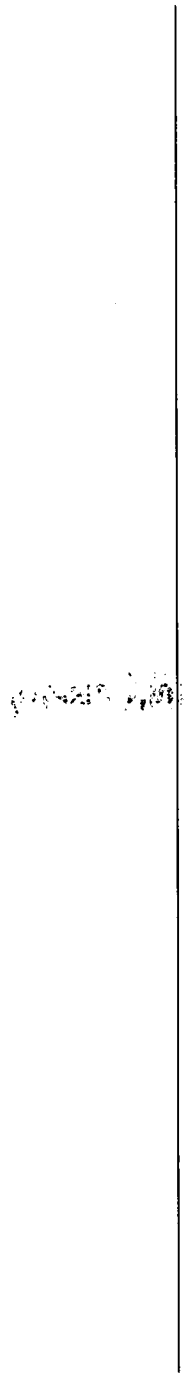
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1292	36	38.7	309	4	US-10-051-874-143	Sequence 143, App
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1445	35.5	38.2	589	4	US-10-282-122A-72457	Sequence 72457, A
1446	35.5	38.2	742	4	US-10-369-493-18643	Sequence 18643, A
1447	35.5	38.2	742	5	US-10-732-923-23192	Sequence 23192, A
1448	35.5	38.2	742	5	US-10-732-923-23277	Sequence 23277, A
1449	35.5	38.2	742	6	US-11-188-298-10239	Sequence 10239, A
1450	35.5	38.2	742	6	US-11-188-298-19716	Sequence 19716, A
1451	35.5	38.2	789	6	US-11-098-686-10148	Sequence 10148, A
1452	35	37.6	28	3	US-09-880-149-12	Sequence 12, Appl
1453	35	37.6	28	3	US-09-880-132-12	Sequence 12, Appl
1454	35	37.6	28	4	US-10-345-281-12	Sequence 12, Appl
1455	35	37.6	34	4	US-10-424-599-163588	Sequence 163588,
1456	35	37.6	37	3	US-09-764-847-664	Sequence 664, App
1457	35	37.6	37	4	US-10-092-154-664	Sequence 664, App
1458	35	37.6	37	4	US-10-424-599-212056	Sequence 212056,
1459	35	37.6	39	4	US-10-425-115-222391	Sequence 222391,
1460	35	37.6	42	4	US-10-425-115-355812	Sequence 355812,
1461	35	37.6	47	3	US-09-864-761-37293	Sequence 37293, A
1462	35	37.6	52	4	US-10-437-963-170135	Sequence 170135,
1463	35	37.6	55	4	US-10-424-599-193997	Sequence 193997,
1464	35	37.6	60	4	US-10-437-963-187245	Sequence 187245,
1465	35	37.6	61	4	US-10-424-599-190588	Sequence 190588,
1466	35	37.6	64	4	US-10-425-115-363783	Sequence 363783,
1467	35	37.6	67	3	US-09-764-860-482	Sequence 482, App
1468	35	37.6	67	4	US-10-074-095-482	Sequence 482, App
1469	35	37.6	67	4	US-10-212-872-482	Sequence 482, App
1470	35	37.6	71	4	US-10-050-704-112	Sequence 112, App
1471	35	37.6	71	4	US-10-798-512-112	Sequence 112, App
1472	35	37.6	72	4	US-10-425-115-323086	Sequence 323086,
1473	35	37.6	80	4	US-10-437-963-104123	Sequence 104123,
1474	35	37.6	87	4	US-10-424-599-174578	Sequence 174578,
1475	35	37.6	87	4	US-10-425-115-356460	Sequence 356460,
1476	35	37.6	89	4	US-10-424-599-245934	Sequence 245934,
1477	35	37.6	89	4	US-10-437-963-140565	Sequence 140565,
1478	35	37.6	89	6	US-11-096-568A-4507	Sequence 4507, Ap
1479	35	37.6	94	4	US-10-106-698-4972	Sequence 4972, Ap
1480	35	37.6	94	4	US-10-424-599-187006	Sequence 187006,
1481	35	37.6	96	4	US-10-425-115-195885	Sequence 195885,
1482	35	37.6	99	4	US-10-424-599-181233	Sequence 181233,
1483	35	37.6	100	6	US-11-188-298-11083	Sequence 11083, A
1484	35	37.6	101	4	US-10-424-599-262302	Sequence 262302,
1485	35	37.6	102	6	US-11-096-568A-4506	Sequence 4506, Ap
1486	35	37.6	107	4	US-10-437-963-158886	Sequence 158886,
1487	35	37.6	111	4	US-10-656-769-76	Sequence 76, Appl
1488	35	37.6	118	4	US-10-424-599-143016	Sequence 143016,
1489	35	37.6	118	4	US-10-425-115-293283	Sequence 293283,
1490	35	37.6	140	3	US-09-764-868-703	Sequence 703, App
1491	35	37.6	140	3	US-09-764-875-1105	Sequence 1105, Ap
1492	35	37.6	140	6	US-11-096-568A-21198	Sequence 21198, A
1493	35	37.6	144	4	US-10-264-237-2247	Sequence 2247, Ap
1494	35	37.6	161	4	US-10-425-114-58207	Sequence 58207, A
1495	35	37.6	178	3	US-09-989-861-6	Sequence 6, Appli
1496	35	37.6	179	3	US-09-864-761-43175	Sequence 43175, A
1497	35	37.6	187	4	US-10-424-599-168140	Sequence 168140,
1498	35	37.6	189	4	US-10-437-963-112042	Sequence 112042,
1499	35	37.6	192	4	US-10-369-493-14929	Sequence 14929, A
1500	35	37.6	198	4	US-10-369-493-14776	Sequence 14776, A

Search completed: November 21, 2006, 20:47:22
Job time : 31.1743 secs



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OM protein - protein search, using sw model

Run on: November 21, 2006, 19:59:58 ; Search time 3.3578 Seconds
(without alignments)
515.785 Million cell updates/sec

Title: US-10-063-553-48_COPY_32_49
Perfect score: 93
Sequence: 1 VSLVEEDQFSQNPISCFE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	44	47.3	1249	2	F86909	probable DNA gyras
2	44	47.3	1273	2	T10006	DNA topoisomerase
3	43	46.2	221	2	T29509	hypothetical prote
4	43	46.2	518	2	E84536	hypothetical prote
5	43	46.2	601	2	S38171	peptide transport
6	42	45.2	316	2	I38754	transcription fact
7	42	45.2	420	2	T45592	hypothetical prote
8	42	45.2	478	2	A49228	trypsin-like prote
9	42	45.2	681	2	I38755	transcription fact
10	42	45.2	1097	2	A56138	transcription fact
11	42	45.2	1356	2	T16754	hypothetical prote
12	42	45.2	1464	2	S47555	N-methyl-D-asparta
13	41.5	44.6	353	2	S37138	protoporphyrin IX
14	41.5	44.6	355	2	A89858	hypothetical prote
15	41.5	44.6	632	2	T16128	hypothetical prote
16	41	44.1	449	2	H84870	probable glucosylt
17	41	44.1	502	2	T29729	hypothetical prote
18	41	44.1	766	1	WZBEC5	infected cell prot
19	41	44.1	925	2	T37831	hypothetical prote
20	40.5	43.5	792	2	G86564	phenylalanyl tRNA
21	40.5	43.5	792	2	H72058	phenylalanine-tRNA
22	40.5	43.5	792	2	D81608	phenylalanine-tRNA
23	40	43.0	235	2	S73609	MG381 homolog H03_
24	40	43.0	317	2	A47336	R-phycoerythrin ga
25	40	43.0	574	2	T29615	hypothetical prote
26	40	43.0	1491	1	S43793	copper-transportin
27	40	43.0	1500	2	S36149	copper-transportin
28	40	43.0	1985	2	I61776	Munc13-2 - rat
29	39.5	42.5	778	2	T40570	probable nuclear p
30	39.5	42.5	1137	2	G84581	copia-like retroel
31	39	41.9	70	2	T32770	hypothetical prote
32	39	41.9	71	2	T17765	hypothetical prote
33	39	41.9	165	2	C95036	PTS system, IIA co
34	39	41.9	214	2	A81697	hypothetical prote
35	39	41.9	277	2	F65014	xanthosine phospho
36	39	41.9	324	2	S73000	hypothetical prote
37	39	41.9	428	2	AD3593	dihydroorotase (EC
38	39	41.9	450	2	JC7266	3',5'-cyclic-nucle
39	39	41.9	505	2	T51403	hypothetical prote
40	39	41.9	659	2	G97906	transcription anti
41	39	41.9	929	2	T17392	vrlL protein - Dic
42	39	41.9	1411	2	S40525	copper-transportin
43	39	41.9	1451	1	I58124	copper-transportin
44	39	41.9	1465	1	S78555	copper-transportin
45	39	41.9	1743	2	T26859	hypothetical prote
46	38	40.9	100	2	G71950	hypothetical prote
47	38	40.9	225	2	C86563	CT465 hypothetical
48	38	40.9	225	2	C72062	conserved hypothet
49	38	40.9	287	2	H90314	conserved hypothet
50	38	40.9	288	2	H81309	hypothetical prote
51	38	40.9	339	2	I58295	RAD51 protein homo
52	38	40.9	339	2	A48221	RAD51 protein homo
53	38	40.9	345	2	S64151	hypothetical prote
54	38	40.9	361	2	A95089	conserved hypothet
55	38	40.9	385	2	T22666	hypothetical prote
56	38	40.9	395	2	S44454	transcription fact
57	38	40.9	414	2	S62462	protein phosphatas
58	38	40.9	430	2	T44851	molybdopterin co-f
59	38	40.9	436	2	T39837	MAD box transcript
60	38	40.9	446	2	C86459	probable serine ca
61	38	40.9	448	2	I50730	yes-associated pro
62	38	40.9	498	2	A47286	3',5'-cyclic-AMP p
63	38	40.9	503	2	G85432	transcription init
64	38	40.9	551	2	T05667	probable growth re
65	38	40.9	558	2	T10672	aspartate-tRNA lig
66	38	40.9	653	2	A39922	potassium channel
67	38	40.9	654	2	S11049	potassium channel
68	38	40.9	660	2	S24125	potassium channel
69	38	40.9	757	1	S64742	dynamin-related pr
70	38	40.9	772	2	S22660	excision repair pr
71	38	40.9	844	2	T38730	probable helicase
72	38	40.9	913	2	T15474	hypothetical prote
73	38	40.9	997	2	JC6067	CCAAT-binding fact
74	38	40.9	998	2	A36368	transcription fact
75	38	40.9	1068	1	A43322	1-phosphatidylinos
76	38	40.9	1068	1	I38110	1-phosphatidylinos
77	38	40.9	1276	2	S69048	probable membrane
78	38	40.9	1364	2	T40839	hypothetical prote
79	38	40.9	2201	2	AH0095	probable sideropho
80	37.5	40.3	372	2	B84262	hypothetical prote
81	37.5	40.3	838	2	A96557	probable receptor
82	37	39.8	193	2	H86404	probable lipid tra
83	37	39.8	194	2	C82244	hypothetical prote
84	37	39.8	249	2	A97227	polyferredoxin [im
85	37	39.8	256	2	T30932	hypothetical prote
86	37	39.8	265	2	T31245	transglycosylase h
87	37	39.8	271	2	C75060	hydrogenase (EC 1.
88	37	39.8	341	2	T48858	acetylpolyamine am
89	37	39.8	365	2	C86700	phosphoserine tran
90	37	39.8	377	2	AC3426	mannosyltransferas
91	37	39.8	386	2	T18890	hypothetical prote
92	37	39.8	404	2	G87757	protein D1007.8 [i
93	37	39.8	420	2	S62541	hypothetical prote
94	37	39.8	425	2	T33111	hypothetical prote
95	37	39.8	445	2	D83932	aminotransferase (
96	37	39.8	447	2	I49126	protein-tyrosine-p
97	37	39.8	463	2	S43787	glutamate-1-semial
98	37	39.8	465	2	T02698	Nicotiana tabacum
99	37	39.8	505	2	T41303	hypothetical prote
100	37	39.8	509	2	E86273	hypothetical prote
101	37	39.8	510	1	FOLJTM	gag polyprotein -
102	37	39.8	529	2	B49993	glycylpeptide N-te

103	37	39.8	608	1	ABXL68	68K serum albumin
104	37	39.8	647	2	S48471	probable membrane
105	37	39.8	652	2	T16582	hypothetical prote
106	37	39.8	731	1	A32621	gelsolin, cytosoli
107	37	39.8	870	2	T25338	hypothetical prote
108	37	39.8	930	2	T20817	hypothetical prote
109	37	39.8	989	2	T46659	period clock prote
110	37	39.8	1047	2	B71402	hypothetical prote
111	37	39.8	1064	2	F86182	hypothetical prote
112	37	39.8	1082	2	T15269	hypothetical prote
113	37	39.8	1170	2	I45914	integrin alpha 2 s
114	37	39.8	1735	2	A57607	Muncl3-1 - rat
115	37	39.8	13055	2	T16580	hypothetical prote
116	36.5	39.2	78	2	F97852	hypothetical prote
117	36.5	39.2	238	2	T15817	hypothetical prote
118	36.5	39.2	657	2	A53545	protein p84 - huma
119	36.5	39.2	804	2	AD0958	DNA gyrase chain B
120	36.5	39.2	832	1	S71788	P/CAF protein - hu
121	36.5	39.2	1756	2	T07566	hypothetical prote
122	36.5	39.2	1889	2	T50069	dynein heavy chain
123	36.5	39.2	4196	2	T43274	dynein heavy chain
124	36	38.7	15	2	A61612	allatostatin - tob
125	36	38.7	68	2	A81968	hypothetical prote
126	36	38.7	108	2	C64516	hypothetical prote
127	36	38.7	121	2	JC7630	C-type allatostati
128	36	38.7	166	2	F59091	hypothetical prote
129	36	38.7	168	2	AG2198	hypothetical prote
130	36	38.7	176	2	T48292	hypothetical prote
131	36	38.7	218	2	D71693	hypothetical prote
132	36	38.7	227	2	T00671	probable methyl ch
133	36	38.7	246	2	AB1345	hypothetical prote
134	36	38.7	268	2	T40101	hypothetical prote
135	36	38.7	271	2	AG0757	probable cobalt tr
136	36	38.7	282	2	S39972	leucine-rich prote
137	36	38.7	297	2	S66102	protein secretion
138	36	38.7	327	2	A81839	probable periplasm
139	36	38.7	327	2	D81103	hypothetical prote
140	36	38.7	332	2	A23083	L-lactate dehydrog
141	36	38.7	361	2	T49337	hypothetical prote
142	36	38.7	363	2	T22594	hypothetical prote
143	36	38.7	387	2	S12773	mitochondrial impo
144	36	38.7	393	2	A49008	paired box transcr
145	36	38.7	403	2	T38078	hypothetical prote
146	36	38.7	440	2	F64904	hipA protein - Esc
147	36	38.7	449	2	B84871	probable glucosylt
148	36	38.7	483	2	AB0072	tagaturonate reduc
149	36	38.7	506	1	FOLJG3	gag polyprotein -
150	36	38.7	543	2	T37570	WD repeat protein
151	36	38.7	562	2	E81069	glutaminyl-tRNA sy
152	36	38.7	562	2	T27807	hypothetical prote
153	36	38.7	573	2	D81799	glutamine-tRNA lig
154	36	38.7	579	2	A84227	hypothetical prote
155	36	38.7	581	2	T41210	hypothetical prote
156	36	38.7	593	2	S48135	glutamate decarbox
157	36	38.7	593	2	S51776	glutamate decarbox
158	36	38.7	594	1	A46758	glutamate decarbox
159	36	38.7	594	2	S51775	glutamate decarbox
160	36	38.7	594	2	JC4065	glutamate dècarbox
161	36	38.7	622	2	E97126	DNA mismatch repai
162	36	38.7	644	2	A36325	epidermal growth f
163	36	38.7	644	2	C86747	topoisomerase IV s
164	36	38.7	646	2	S47929	signal recognition
165	36	38.7	654	2	B75587	probable N-glycosi
166	36	38.7	695	2	T39242	hypothetical prote
167	36	38.7	725	2	T19994	hypothetical prote
168	36	38.7	741	2	A45771	2-5A-dependent RNA
169	36	38.7	792	2	AB0038	probable outer mem
170	36	38.7	817	2	T24063	hypothetical prote
171	36	38.7	852	2	S57984	probable membrane
172	36	38.7	912	2	T02892	hypothetical prote
173	36	38.7	967	2	D72308	conserved hypothet
174	36	38.7	1003	2	T24545	hypothetical prote
175	36	38.7	1012	2	T13712	dof protein - frui
176	36	38.7	1072	2	AD1280	SNF2-type helicase
177	36	38.7	1072	2	AD1643	SNF2-type helicase
178	36	38.7	1144	2	T13749	dof protein - frui
179	36	38.7	1181	2	A41052	parasporal crystal
180	36	38.7	1204	2	A96676	hypothetical prote
181	36	38.7	1210	2	A53183	epidermal growth f
182	36	38.7	1320	2	G81961	phosphoribosylform
183	36	38.7	1645	2	AG1897	two-component hybr
184	36	38.7	1722	2	E89753	protein F11C7.4 [i
185	36	38.7	2156	1	RRVUNE	genome polyprotein
186	36	38.7	2195	2	S61103	SEC16 protein - ye
187	36	38.7	4753	1	A47437	LDL-receptor-relat
188	35.5	38.2	278	2	B82388	probable maltose o
189	35.5	38.2	349	2	T00526	probable GDSL-moti
190	35.5	38.2	356	2	S73315	protoporphyrin IX
191	35.5	38.2	401	2	F86754	prophage pi2 prote
192	35.5	38.2	591	2	E81687	ATP synthase, chai
193	35.5	38.2	591	2	B71531	probable ATP synth
194	35.5	38.2	742	1	S47018	cdcH protein - Hal
195	35.5	38.2	742	2	C84319	cell division cycl
196	35.5	38.2	1258	2	F96753	Similar to downy m
197	35	37.6	42	2	I48240	LDH-A - mouse (fra
198	35	37.6	89	2	S78744	protein YDR363w-a
199	35	37.6	130	2	H72642	hypothetical prote
200	35	37.6	144	2	S66493	serotonin receptor
201	35	37.6	147	2	D27733	hypothetical prote
202	35	37.6	157	2	H64965	DNA gyrase inhibit
203	35	37.6	157	2	C90980	SbmC protein [impo
204	35	37.6	157	2	H85825	SbmC protein [impo
205	35	37.6	161	2	T22222	hypothetical prote
206	35	37.6	161	2	T41833	AcMNPV orf93 - Bom
207	35	37.6	219	2	T08083	H+-transporting tw
208	35	37.6	223	2	I59173	glutamate decarbox
209	35	37.6	245	2	T28148	class II histocomp
210	35	37.6	245	2	S09666	psbG protein - whe
211	35	37.6	254	2	C70682	probable cysH - My
212	35	37.6	259	2	T28147	class II histocomp
213	35	37.6	266	2	C71531	hypothetical prote
214	35	37.6	267	1	JQ1324	DNA excision repai
215	35	37.6	267	2	JG0191	XPA protein - Afri
216	35	37.6	278	2	E81426	parB family protei
217	35	37.6	281	2	JC4295	heat-shock protein
218	35	37.6	284	2	G82234	conserved hypothet
219	35	37.6	296	2	G90063	hypothetical prote
220	35	37.6	297	2	G88035	protein M01D1.8 [i
221	35	37.6	309	2	T41494	zinc finger, ADP-r
222	35	37.6	313	2	T48439	probable RNA-bindi
223	35	37.6	324	2	T05273	hypothetical prote
224	35	37.6	342	2	T18474	hypothetical prote
225	35	37.6	344	2	F69272	hypothetical prote
226	35	37.6	344	2	C70208	conserved hypothet
227	35	37.6	344	2	T50895	prephytoene pyroph
228	35	37.6	349	2	D64134	peptide transport
229	35	37.6	351	2	A86045	sepL [imported] -
230	35	37.6	351	2	E91198	type III secretion
231	35	37.6	362	2	A39714	G protein-coupled
232	35	37.6	362	2	A30341	G protein-coupled
233	35	37.6	364	2	G69377	bacteriochlorophyl
234	35	37.6	365	2	AD2669	chorismate synthas
235	35	37.6	368	2	B97451	chorismate synthas
236	35	37.6	376	2	T16147	hypothetical prote
237	35	37.6	380	2	E81302	probable type I re
238	35	37.6	391	2	T23227	hypothetical prote
239	35	37.6	405	1	F69611	cytochrome P450 cy
240	35	37.6	408	2	T42650	hypothetical prote
241	35	37.6	411	2	B91220	probable arylsulfa
242	35	37.6	411	2	D86066	probable arylsulfa
243	35	37.6	411	2	A65184	arylsulfatase acti
244	35	37.6	411	2	D88037	protein K02E7.2 [i
245	35	37.6	411	2	T03897	hypothetical prote
246	35	37.6	411	2	B89024	protein R02D1.1 [i
247	35	37.6	414	2	T34000	hypothetical prote
248	35	37.6	414	2	G82174	hypothetical prote

249	35	37.6	421	2	T35205	citrate synthase-1
250	35	37.6	426	2	F70343	enolase - Aquifex
251	35	37.6	431	2	G81179	oxidoreductase; pr
252	35	37.6	440	2	T01115	probable protein d
253	35	37.6	440	2	I49624	gap junction prote
254	35	37.6	441	2	T20840	hypothetical prote
255	35	37.6	443	1	A46248	dihydroorotate oxi
256	35	37.6	444	2	S57989	probable membrane
257	35	37.6	451	2	S44446	GDP dissociation i
258	35	37.6	454	2	H85293	hypothetical prote
259	35	37.6	454	2	A56954	yes-associated pro
260	35	37.6	455	2	T05804	hypothetical prote
261	35	37.6	458	2	T19941	hypothetical prote
262	35	37.6	461	1	DCHUO	ornithine decarbox
263	35	37.6	472	2	I64098	glutamate-ammonia
264	35	37.6	505	2	S50567	hypothetical prote
265	35	37.6	506	2	S55786	DNA nucleotidylexo
266	35	37.6	511	2	E90083	t-complex protein1
267	35	37.6	514	2	B64055	periplasmic oligop
268	35	37.6	541	2	G90192	conserved hypothet
269	35	37.6	543	2	S73820	type I restriction
270	35	37.6	564	2	S44611	C02F5.9 protein -
271	35	37.6	569	2	A36187	interleukin-1 rece
272	35	37.6	580	2	T43310	glycerone kinase (
273	35	37.6	580	2	F84471	hypothetical prote
274	35	37.6	585	2	S61534	glutamate decarbox
275	35	37.6	593	1	A41367	glutamate decarbox
276	35	37.6	594	1	B41935	glutamate decarbox
277	35	37.6	599	2	S47928	signal recognition
278	35	37.6	611	1	W1WLEP	E1 protein - Europ
279	35	37.6	613	1	W1WLDP	E1 protein - deer
280	35	37.6	616	1	A40457	replication protei
281	35	37.6	618	2	T39985	probable arginyl-t
282	35	37.6	622	2	T37257	hypothetical prote
283	35	37.6	643	2	T19199	hypothetical prote
284	35	37.6	649	2	S74823	N-acetylmuramoyl-L
285	35	37.6	702	2	C86268	F13B4.2 protein -
286	35	37.6	711	2	T05148	protein kinase hom
287	35	37.6	716	2	G01627	androgen receptor
288	35	37.6	723	2	S70098	probable membrane
289	35	37.6	728	2	A86453	CDS protein F9L11.
290	35	37.6	749	2	B86606	primosomal protein
291	35	37.6	749	2	C72018	primosomal protein
292	35	37.6	773	2	T42575	infected cell prot
293	35	37.6	781	2	B64135	ribonucleoside-dip
294	35	37.6	802	2	B84560	hypothetical prote
295	35	37.6	831	2	G91036	probable PTS syste
296	35	37.6	831	2	A85881	hypothetical prote
297	35	37.6	831	2	D65012	probable phosphoen
298	35	37.6	916	2	G81797	preprotein translo
299	35	37.6	916	2	D81072	preprotein translo
300	35	37.6	958	2	T51148	hypothetical prote
301	35	37.6	993	2	S21964	mating-type switch
302	35	37.6	1081	2	T31329	receptor tyrosine
303	35	37.6	1135	2	JS0605	M polyprotein - Ha
304	35	37.6	1155	2	A26513	parasporal crystal
305	35	37.6	1181	2	C82500	IcmF-related prote
306	35	37.6	1190	2	F86677	pyruvate-flavodoxi
307	35	37.6	1217	2	D88996	protein C17B7.7 [i
308	35	37.6	1464	1	S29159	glutamate receptor
309	35	37.6	1464	2	A43274	N-methyl D-asparta
310	35	37.6	1704	2	T43141	vitellogenin 1 - m
311	35	37.6	1945	2	T13937	plexin A - fruit f
312	35	37.6	2368	2	S46005	ESR1 protein - yea
313	35	37.6	4767	2	T31345	hypothetical prote
314	34.5	37.1	58	2	S58628	hypothetical prote
315	34.5	37.1	145	2	D64202	DNA-directed RNA p
316	34.5	37.1	389	2	E82618	hypothetical prote
317	34.5	37.1	537	2	D89889	conserved hypothet
318	34.5	37.1	804	1	ISECTB	DNA topoisomerase
319	34.5	37.1	804	2	B91208	DNA gyrase subunit
320	34.5	37.1	804	2	D86054	hypothetical prote
321	34.5	37.1	1297	2	S25714	son-of-sevenless-2
322	34	36.6	63	1	FEDV2V	ferredoxin [4Fe-4S
323	34	36.6	96	2	T04223	hypothetical prote
324	34	36.6	101	2	B86645	Glu-tRNA amidotran
325	34	36.6	107	2	A82815	hypothetical prote
326	34	36.6	114	2	AE1349	hypothetical prote
327	34	36.6	133	2	T08447	hypothetical prote
328	34	36.6	145	2	S34574	gene 70 protein -
329	34	36.6	176	2	A97808	hypothetical prote
330	34	36.6	179	2	AI3477	hypothetical cytos
331	34	36.6	224	2	D64454	proteasome beta su
332	34	36.6	224	2	G70119	hypothetical prote
333	34	36.6	227	2	T00672	hypothetical prote
334	34	36.6	230	2	AF3113	transcription regu
335	34	36.6	234	2	G98173	probable transcrip
336	34	36.6	237	2	JU0176	lectin alpha chain
337	34	36.6	238	2	T30945	hypothetical prote
338	34	36.6	241	2	T33932	hypothetical prote
339	34	36.6	257	2	T28946	hypothetical prote
340	34	36.6	266	2	F81687	conserved hypothet
341	34	36.6	273	2	T51512	hypothetical prote
342	34	36.6	285	1	QQECHF	hydrogenase-1 cofa
343	34	36.6	285	2	E90770	hypothetical prote
344	34	36.6	285	2	A85633	hypothetical prote
345	34	36.6	287	2	B84039	hypothetical prote
346	34	36.6	289	2	A84058	formyltetrahydrofo
347	34	36.6	303	2	E83096	ketopantoate reduc
348	34	36.6	309	2	A36064	basic fibroblast g
349	34	36.6	313	2	F96493	probable transposo
350	34	36.6	314	2	G85575	hypothetical prote
351	34	36.6	314	2	G90724	hypothetical prote
352	34	36.6	317	2	S77827	probable DNA-direc
353	34	36.6	322	2	B81336	pseudouridylate sy
354	34	36.6	323	2	S43850	melanocortin 3 rec
355	34	36.6	323	2	S36636	melanocortin recep
356	34	36.6	325	2	T40264	zinc-binding dehyd
357	34	36.6	330	2	T51834	transcription fact
358	34	36.6	334	2	C69148	dTDP-glucose 4,6-d
359	34	36.6	334	2	T19519	hypothetical prote
360	34	36.6	339	2	S35642	RAD51 protein homo
361	34	36.6	341	2	E83779	iron (III) dicitra
362	34	36.6	347	2	H86743	heat-inducible tra
363	34	36.6	348	2	T39358	DNA-directed RNA p
364	34	36.6	351	2	AC2289	hypothetical prote
365	34	36.6	359	2	A48857	angiotensin II rec
366	34	36.6	367	2	JC6087	helix-loop-helix t
367	34	36.6	380	2	T19280	hypothetical prote
368	34	36.6	382	2	S74947	hypothetical prote
369	34	36.6	387	2	AI1567	hypothetical prote
370	34	36.6	388	2	D82023	probable lipoprote
371	34	36.6	388	2	E81244	conserved hypothet
372	34	36.6	411	1	OXRTL	protein-lysine 6-o
373	34	36.6	422	2	T38764	aureobasidin a res
374	34	36.6	424	1	G69641	histidine-tRNA lig
375	34	36.6	424	2	AH0301	probable exported
376	34	36.6	425	2	D64542	apolipoprotein N-a
377	34	36.6	425	2	D71965	apolipoprotein n-a
378	34	36.6	428	2	JQ1864	hypothetical 47.0K
379	34	36.6	431	2	T24597	hypothetical prote
380	34	36.6	435	2	E72342	pmbA-related prote
381	34	36.6	449	2	T47950	delta-8 sphingolip
382	34	36.6	450	2	T38465	probable dolichyl-
383	34	36.6	465	2	E69788	hypothetical prote
384	34	36.6	467	2	D83055	poly(A) polymerase
385	34	36.6	472	2	A33312	sarcoplasmic retic
386	34	36.6	474	2	T27566	hypothetical prote
387	34	36.6	479	2	E69613	ATP-dependent RNA
388	34	36.6	480	2	S46153	probable membrane
389	34	36.6	481	2	A89102	protein F25E5.4 [i
390	34	36.6	498	2	T51430	dolichyl-phosphate
391	34	36.6	503	2	A28415	steroid 11beta-mon
392	34	36.6	503	2	JX0151	steroid 11beta-mon
393	34	36.6	503	2	JX0071	steroid 11beta-mon
394	34	36.6	503	2	S52085	steroid 11-beta-hy

395	34	36.6	516	2	G95406	probable ABC trans
396	34	36.6	520	2	T20007	hypothetical prote
397	34	36.6	530	2	D82412	chaperonin, 60 Kd
398	34	36.6	543	2	A72292	hypothetical prote
399	34	36.6	544	2	S62527	probable amino-aci
400	34	36.6	544	2	H86828	fructuronate reduc
401	34	36.6	554	2	T43211	cytoplasmic signal
402	34	36.6	557	1	WZBYI	isocitrate lyase (
403	34	36.6	560	1	RGNVPM	trans-activating t
404	34	36.6	560	2	T10414	immediate early pr
405	34	36.6	564	2	E64241	threonine-tRNA lig
406	34	36.6	578	2	AF1958	L-aspartate oxidas
407	34	36.6	584	2	T18908	hypothetical prote
408	34	36.6	594	2	D64676	oligopeptide ABC t
409	34	36.6	607	2	H64041	probable long-chai
410	34	36.6	608	2	A53195	afamin precursor -
411	34	36.6	615	2	T15423	hypothetical prote
412	34	36.6	616	2	T38717	probable GTP-bindi
413	34	36.6	623	2	D71435	hypothetical prote
414	34	36.6	623	2	T28051	hypothetical prote
415	34	36.6	632	2	G88109	protein T24E12.10
416	34	36.6	638	1	YSBST2	threonine-tRNA lig
417	34	36.6	638	2	T21321	hypothetical prote
418	34	36.6	640	1	UZADP7	terminal protein p
419	34	36.6	658	2	A86231	hypothetical prote
420	34	36.6	660	2	T38294	sec-7 cytohesin-li
421	34	36.6	666	2	T43171	cytoplasmic signal
422	34	36.6	670	2	H96707	probable receptor
423	34	36.6	672	2	T24507	hypothetical prote
424	34	36.6	715	2	JC4560	methylmalonyl-CoA
425	34	36.6	716	2	A86181	hypothetical prote
426	34	36.6	739	2	T15215	hypothetical prote
427	34	36.6	755	2	G84791	probable ABC trans
428	34	36.6	757	2	C70034	conserved hypothet
429	34	36.6	764	2	I39934	protective antigen
430	34	36.6	764	2	S64951	hypothetical prote
431	34	36.6	804	2	T18014	hypothetical prote
432	34	36.6	818	2	F97348	heavy-metal transp
433	34	36.6	857	2	S33821	median body protei
434	34	36.6	861	2	B84885	probable transcrip
435	34	36.6	876	2	T33176	hypothetical prote
436	34	36.6	908	2	A33280	sarcalumenin precu
437	34	36.6	957	2	A49847	nitrite reductase
438	34	36.6	962	2	D70661	probable membranep
439	34	36.6	967	2	G96637	hypothetical prote
440	34	36.6	981	2	T51921	hypothetical prote
441	34	36.6	997	2	S44457	period clock prote
442	34	36.6	1010	2	S45389	probable membrane
443	34	36.6	1014	2	H71602	protein with DnaJ
444	34	36.6	1036	2	S73601	protein P200 - Myc
445	34	36.6	1058	2	AG2541	cation efflux syst
446	34	36.6	1075	2	G59434	KIAA0411 protein [
447	34	36.6	1075	2	C96682	protein F1E22.16 [
448	34	36.6	1133	2	S54496	probable membrane
449	34	36.6	1135	1	GNVUH7	M polyprotein - Ha
450	34	36.6	1135	1	GNVUHV	M polyprotein - Ha
451	34	36.6	1155	2	S02134	parasporal crystal
452	34	36.6	1155	2	I39838	parasporal crystal
453	34	36.6	1155	2	JD0002	parasporal crystal
454	34	36.6	1156	2	A29125	parasporal crystal
455	34	36.6	1156	2	A29838	parasporal crystal
456	34	36.6	1165	2	S11446	parasporal crystal
457	34	36.6	1166	2	S32645	parasporal crystal
458	34	36.6	1171	2	A37829	parasporal crystal
459	34	36.6	1171	2	I40572	parasporal crystal
460	34	36.6	1172	2	S32689	parasporal crystal
461	34	36.6	1174	2	A42459	parasporal crystal
462	34	36.6	1176	2	A48970	parasporal crystal
463	34	36.6	1182	2	T30189	myelin transcripti
464	34	36.6	1187	2	T46637	transcription fact
465	34	36.6	1188	2	T46608	zinc finger protei
466	34	36.6	1189	2	S00944	parasporal crystal
467	34	36.6	1190	2	T38636	tat binding homolo
468	34	36.6	1212	2	T13804	shs protein - frui
469	34	36.6	1214	2	T18549	DNA polymerase hom
470	34	36.6	1214	2	T30941	DNA polymerase - c
471	34	36.6	1239	2	G71266	probable ATP-depen
472	34	36.6	1263	2	T13805	spalt-related prot
473	34	36.6	1299	2	A86366	T26J12.6 protein -
474	34	36.6	1328	2	T23007	hypothetical prote
475	34	36.6	1345	2	T44204	capsid protein U57
476	34	36.6	1345	2	T44017	major capsid prote
477	34	36.6	1397	2	T10466	DNA topoisomerase
478	34	36.6	1536	1	RGBYS3	regulatory protein
479	34	36.6	1557	2	T28811	hypothetical prote
480	34	36.6	1658	2	S55101	hypothetical prote
481	34	36.6	1787	2	F84528	probable retroelem
482	34	36.6	1919	2	T40032	hypothetical prote
483	34	36.6	2049	2	T43161	sodium channel pro
484	34	36.6	2180	2	A47651	zinc-finger protei
485	34	36.6	2761	2	T29285	hypothetical prote
486	34	36.6	2907	2	A57278	fibrillin-2 precur
487	34	36.6	3507	2	T34513	hypothetical prote
488	34	36.6	3724	2	T18427	hypothetical prote
489	33.5	36.0	78	2	T17963	hypothetical prote
490	33.5	36.0	168	2	A28476	myosin heavy chain
491	33.5	36.0	168	2	B25217	myosin heavy chain
492	33.5	36.0	169	2	A25217	myosin heavy chain
493	33.5	36.0	258	2	T35147	glutamate uptake s
494	33.5	36.0	294	2	C75574	conserved hypothet
495	33.5	36.0	359	2	D81711	phospholipase D fa
496	33.5	36.0	374	2	AH1825	protoporphyrin IX
497	33.5	36.0	493	2	T05105	hypothetical prote
498	33.5	36.0	508	2	AG2206	serine/threonine k
499	33.5	36.0	523	2	H90529	potassium uptake p
500	33.5	36.0	838	2	S38156	hypothetical prote
501	33.5	36.0	953	2	F96498	hypothetical prote
502	33.5	36.0	1776	2	G86280	protein T5E21.13 [
503	33.5	36.0	1804	2	AF2250	serine/threonine k
504	33.5	36.0	1938	1	JX0178	myosin heavy chain
505	33.5	36.0	1940	2	A29320	myosin heavy chain
506	33	35.5	74	2	AF3436	hypothetical prote
507	33	35.5	75	2	C90601	hypothetical prote
508	33	35.5	76	2	AD1442	gp37-1 (Bacterioph
509	33	35.5	103	2	T13589	distal tail fiber
510	33	35.5	108	2	T00420	probable small nuc
511	33	35.5	110	2	H64512	hypothetical prote
512	33	35.5	113	2	AH3438	hypothetical prote
513	33	35.5	115	2	T38514	small nuclear ribo
514	33	35.5	118	2	I38861	small nuclear ribo
515	33	35.5	128	2	AF2143	hypothetical prote
516	33	35.5	135	2	C69446	hypothetical prote
517	33	35.5	137	2	AI1375	hypothetical prote
518	33	35.5	152	2	T07858	glycine-rich prote
519	33	35.5	155	2	S75888	hypothetical prote
520	33	35.5	161	2	T00729	hypothetical prote
521	33	35.5	161	2	F72861	AcOrf-93 protein -
522	33	35.5	162	2	D84959	small protein B [i
523	33	35.5	164	2	S73814	probable 5-formyl
524	33	35.5	167	2	T12580	GTP-binding protei
525	33	35.5	177	2	A86610	frame-shift with C
526	33	35.5	188	2	F81808	hypothetical prote
527	33	35.5	188	2	AC3613	probable s-adenosy
528	33	35.5	195	2	I46272	trophoblast interf
529	33	35.5	195	2	A96731	unknown protein F5
530	33	35.5	200	2	S55609	hypothetical prote
531	33	35.5	210	2	T05541	heat shock protein
532	33	35.5	216	1	TLBPX2	tail fiber protein
533	33	35.5	220	2	A41662	hypothetical prote
534	33	35.5	223	2	S06576	finger protein (cl
535	33	35.5	237	2	A45587	lectin - Dioclea l
536	33	35.5	237	2	T27145	hypothetical prote
537	33	35.5	243	2	C64124	molybdopterin bios
538	33	35.5	247	1	D24706	nodulation protein
539	33	35.5	247	2	H95319	phosphoadenylyl-su
540	33	35.5	249	2	C85592	molybdopterin bios

541	33	35.5	249	2	H90741	molybdopterin bios
542	33	35.5	257	2	D81086	FrpC operon protei
543	33	35.5	258	2	G96798	hypothetical prote
544	33	35.5	263	2	AF2534	hypothetical prote
545	33	35.5	267	2	T00114	exodeoxyribonuclea
546	33	35.5	271	2	B81182	FrpC operon protei
547	33	35.5	275	2	A82257	oxidoreductase, sh
548	33	35.5	284	2	S52672	hypothetical prote
549	33	35.5	287	2	S25259	streptomycin resis
550	33	35.5	289	2	A84790	probable RNA-bindi
551	33	35.5	294	2	T24776	hypothetical prote
552	33	35.5	298	2	C82073	signal peptidase I
553	33	35.5	299	2	T25596	hypothetical prote
554	33	35.5	301	2	B69815	CDP-glucose 4,6-de
555	33	35.5	304	2	T09357	hypothetical prote
556	33	35.5	305	2	C89915	hypothetical prote
557	33	35.5	305	2	A89721	protein T10B10.4 [
558	33	35.5	307	2	T16457	hypothetical prote
559	33	35.5	309	2	I48125	syndecan-1 - Chine
560	33	35.5	310	2	S43101	SED5 protein - fru
561	33	35.5	314	2	B95034	dihydropteroate sy
562	33	35.5	314	2	B97905	dihydropteroate sy
563	33	35.5	316	1	A43661	dihydropteroate sy
564	33	35.5	326	2	AS4497	surface membrane p
565	33	35.5	330	2	AD2854	conserved hypothet
566	33	35.5	336	2	H70328	hypothetical prote
567	33	35.5	338	2	E95251	ornithine carbamoy
568	33	35.5	338	2	B98116	ornithine carbamoy
569	33	35.5	349	2	T23931	hypothetical prote
570	33	35.5	356	2	AE2729	cytochrome oxidase
571	33	35.5	363	2	A85700	probable GTP-bindi
572	33	35.5	363	2	AB0721	probable ATP/GTP-b
573	33	35.5	363	2	H64866	probable GTP-bindi
574	33	35.5	363	2	D90842	probable GTP-bindi
575	33	35.5	363	2	I64150	probable GTP-bindi
576	33	35.5	363	2	AD0245	conserved hypothet
577	33	35.5	367	1	I69653	UDPgalactopyranose
578	33	35.5	371	2	G87644	hypothetical prote
579	33	35.5	372	2	F97510	BA483f11.2.1 (cox1
580	33	35.5	373	2	F81438	probable periplasm
581	33	35.5	383	1	C53309	prgY protein - Ent
582	33	35.5	386	2	A97631	hypothetical 37.4K
583	33	35.5	387	2	S77268	carboxynorspermidi
584	33	35.5	391	2	T40029	hypothetical prote
585	33	35.5	396	2	D64022	hypothetical prote
586	33	35.5	401	2	H84828	hypothetical prote
587	33	35.5	408	2	T01006	hypothetical prote
588	33	35.5	410	1	IXBE10	alpha trans-induci
589	33	35.5	410	2	H69307	bacteriochlorophyl
590	33	35.5	413	2	A97173	flagellar switch p
591	33	35.5	417	2	F71238	hypothetical prote
592	33	35.5	418	2	S44646	hypothetical prote
593	33	35.5	419	2	S06784	hypothetical prote
594	33	35.5	420	2	A45166	protein-lysine 6-o
595	33	35.5	422	2	S37280	cyclin A - mouse
596	33	35.5	422	2	S38501	cyclin A2 - mouse
597	33	35.5	423	2	AC3553	4-aminobutyrate tr
598	33	35.5	426	2	S16416	gene E46 protein -
599	33	35.5	433	2	T19632	hypothetical prote
600	33	35.5	434	2	D71309	47K integral membr
601	33	35.5	436	2	T00908	hypothetical prote
602	33	35.5	443	2	AI3525	4-aminobutyrate tr
603	33	35.5	445	2	T28988	hypothetical prote
604	33	35.5	450	1	DCCHO	ornithine decarbox
605	33	35.5	453	2	JC5607	replication initia
606	33	35.5	455	1	DCHYOC	ornithine decarbox
607	33	35.5	455	2	F72326	hemolysin-related
608	33	35.5	455	2	T52155	threonyl-tRNA synt
609	33	35.5	459	2	T04808	hypothetical prote
610	33	35.5	465	2	D86166	protein F21B7.12 [
611	33	35.5	466	2	S44878	ZC262.6 protein -
612	33	35.5	468	2	T41294	hypothetical prote
613	33	35.5	469	2	C86170	hypothetical prote
614	33	35.5	469	2	A71369	probable sugar ABC
615	33	35.5	470	2	C70641	hypothetical prote
616	33	35.5	475	2	T20706	hypothetical prote
617	33	35.5	477	2	S74716	hypothetical prote
618	33	35.5	480	2	A86371	hypothetical prote
619	33	35.5	498	2	A97061	uncharacterized pr
620	33	35.5	505	2	AC2107	hypothetical prote
621	33	35.5	514	2	S72847	hypothetical prote
622	33	35.5	514	2	E84145	transposase (22) B
623	33	35.5	536	2	S06548	finger protein (cl
624	33	35.5	541	2	T13162	cytosolic phosphol
625	33	35.5	554	2	C70512	hypothetical prote
626	33	35.5	556	2	T49501	hypothetical prote
627	33	35.5	565	1	HMIVE5	hemagglutinin prec
628	33	35.5	565	2	A25226	RAD7 protein - yea
629	33	35.5	584	2	F75090	archaeosine trna-r
630	33	35.5	591	2	T43443	hypothetical prote
631	33	35.5	615	2	S06546	finger protein (cl
632	33	35.5	618	2	T44595	alcaligin synthesi
633	33	35.5	643	1	FOVZZW	major core protein
634	33	35.5	643	2	G89008	protein T27C4.2 [i
635	33	35.5	644	1	FOVZ5R	major core protein
636	33	35.5	644	2	T37390	major core protein
637	33	35.5	644	2	A72164	A4L protein - vari
638	33	35.5	644	2	D36848	major core protein
639	33	35.5	644	2	T28545	hypothetical prote
640	33	35.5	649	2	B75317	threonyl-tRNA synt
641	33	35.5	651	2	C86333	hypothetical prote
642	33	35.5	660	2	AB0794	probable lipopolys
643	33	35.5	660	2	F85865	probable transform
644	33	35.5	660	2	G91021	probable transform
645	33	35.5	660	2	E64996	hypothetical prote
646	33	35.5	661	2	B75084	ferrous iron trans
647	33	35.5	662	2	E83201	conserved hypothet
648	33	35.5	663	2	S54426	DNA topoisomerase
649	33	35.5	664	2	S60062	hevin precursor -
650	33	35.5	665	2	B89911	topoisomerase IV s
651	33	35.5	667	2	AD0295	probable formyl tr
652	33	35.5	672	2	B84782	probable receptor-
653	33	35.5	677	2	T19281	hypothetical prote
654	33	35.5	681	2	JX0338	rabphilin-3A - mou
655	33	35.5	682	2	T10319	envelope protein E
656	33	35.5	684	2	I58166	rabphilin-3A - rat
657	33	35.5	686	2	E87624	phospholipase C [i
658	33	35.5	693	2	C84495	hypothetical prote
659	33	35.5	702	2	T01763	threonine-tRNA lig
660	33	35.5	704	2	A48097	rabphilin-3A - bov
661	33	35.5	709	2	T51624	threonine-tRNA lig
662	33	35.5	712	1	YSHUT	threonine-tRNA lig
663	33	35.5	734	1	YSBYTC	threonine-tRNA lig
664	33	35.5	745	1	S75354	probable copper-tr
665	33	35.5	746	1	QRECFC	ferrienterochelin
666	33	35.5	746	2	G90706	hypothetical prote
667	33	35.5	746	2	B85557	hypothetical prote
668	33	35.5	747	2	T23882	hypothetical prote
669	33	35.5	753	2	T19338	hypothetical prote
670	33	35.5	765	2	T29582	hypothetical prote
671	33	35.5	766	1	B43684	probable RNA-direc
672	33	35.5	776	2	T20896	hypothetical prote
673	33	35.5	787	2	E82323	organic solvent to
674	33	35.5	790	1	G69071	heavy-metal-transp
675	33	35.5	790	2	T15709	hypothetical prote
676	33	35.5	802	2	F90060	copper-transportin
677	33	35.5	803	1	E70041	probable copper-tr
678	33	35.5	812	2	E95029	formate acetyltran
679	33	35.5	815	2	H97900	formate C-acetyltr
680	33	35.5	815	2	G82861	conjugal transfer
681	33	35.5	821	2	T24728	hypothetical prote
682	33	35.5	825	2	I46078	endothelin convert
683	33	35.5	826	2	G97073	uncharacterized pr
684	33	35.5	863	2	F84504	probable retroelem
685	33	35.5	870	2	T30110	hypothetical prote
686	33	35.5	904	2	T40072	P Type Copper ATPa

687	33	35.5	910	2	G84648	probable disease r
688	33	35.5	915	2	B59433	chromosome 5 GAP-1
689	33	35.5	921	2	D82513	malT regulatory pr
690	33	35.5	944	2	T38130	probable helicase
691	33	35.5	946	2	S48433	inositol-1,4,5-tri
692	33	35.5	987	2	AI2011	peptide synthetase
693	33	35.5	1011	2	T17430	tol protein - Neur
694	33	35.5	1015	2	T32186	hypothetical prote
695	33	35.5	1040	2	T39936	probable helicase
696	33	35.5	1045	2	S60571	integrin alpha v c
697	33	35.5	1071	1	PXBYVA	H+-exporting ATPas
698	33	35.5	1081	2	T20698	hypothetical prote
699	33	35.5	1081	2	S51899	probable protein k
700	33	35.5	1083	2	T26844	hypothetical prote
701	33	35.5	1088	2	A46080	H+-exporting ATPas
702	33	35.5	1093	2	B86748	hypothetical prote
703	33	35.5	1093	2	T50652	AP-3 complex beta3
704	33	35.5	1094	2	T50651	AP3-complex beta-3
705	33	35.5	1099	2	A59311	myosin VIII, ZMM3
706	33	35.5	1099	2	AE1065	conserved hypothet
707	33	35.5	1116	2	B88612	protein Y76A2A.2 [
708	33	35.5	1135	2	T42723	probable DNA-direc
709	33	35.5	1135	2	T42368	DNA-directed RNA p
710	33	35.5	1152	2	T27531	hypothetical prote
711	33	35.5	1168	2	T37496	probable pre-mRNA
712	33	35.5	1176	2	A22617	parasporal crystal
713	33	35.5	1176	2	JC2219	parasporal crystal
714	33	35.5	1176	2	JT0241	parasporal crystal
715	33	35.5	1176	2	S02215	parasporal crystal
716	33	35.5	1177	2	A49785	parasporal crystal
717	33	35.5	1178	1	USBSXH	parasporal crystal
718	33	35.5	1189	2	AI2493	WD-repeat protein
719	33	35.5	1191	2	T31091	hypothetical prote
720	33	35.5	1195	2	S38174	probable purine nu
721	33	35.5	1220	2	S17179	Ca2+-transporting
722	33	35.5	1238	1	JC5573	copper-transportin
723	33	35.5	1287	2	A41685	SIL protein - huma
724	33	35.5	1320	2	G81017	phosphoribosylform
725	33	35.5	1332	2	S41552	probable transcrip
726	33	35.5	1341	2	S50366	probable membrane
727	33	35.5	1345	1	VCBEH6	major capsid prote
728	33	35.5	1480	2	T05566	hypothetical prote
729	33	35.5	1523	2	T13953	MEGF5 protein - ra
730	33	35.5	1529	2	T16779	hypothetical prote
731	33	35.5	1531	2	T42218	slit-1 protein hom
732	33	35.5	1549	2	T13940	ankyrin - fruit fl
733	33	35.5	1619	2	S67083	hypothetical prote
734	33	35.5	1715	2	T30559	resistance protein
735	33	35.5	1744	2	JH0720	tanabin - African
736	33	35.5	1761	2	T13675	hypothetical prote
737	33	35.5	1792	2	T20363	hypothetical prote
738	33	35.5	1838	2	H86337	protein F5M15.26 [
739	33	35.5	2123	2	F86348	hypothetical prote
740	33	35.5	2185	1	S60200	acetyl-CoA carboxy
741	33	35.5	2324	1	A29924	acetyl-CoA carboxy
742	33	35.5	2364	2	A56577	microtubule-associ
743	33	35.5	2427	2	T16613	hypothetical prote
744	33	35.5	2464	1	QRMSP1	microtubule-associ
745	33	35.5	2717	2	A34203	DNA-binding protei
746	33	35.5	2918	2	A54105	fibrillin-2 precur
747	33	35.5	4687	1	A39638	plectin - rat
748	32.5	34.9	136	2	T45080	hypothetical prote
749	32.5	34.9	207	2	AI2505	hypothetical prote
750	32.5	34.9	238	2	H82084	aerobic respiratio
751	32.5	34.9	241	2	F97202	hypothetical prote
752	32.5	34.9	247	2	E86723	transcription regu
753	32.5	34.9	332	2	T51269	hypothetical prote
754	32.5	34.9	352	2	T05106	hypothetical prote
755	32.5	34.9	371	2	C97355	uncharacterized pr
756	32.5	34.9	411	2	T29475	hypothetical prote
757	32.5	34.9	412	2	T09313	immediate-early pr
758	32.5	34.9	413	1	S16426	tyrosine-tRNA liga
759	32.5	34.9	441	2	F88930	protein R11G11.12
760	32.5	34.9	443	2	AH2415	two-component hybr
761	32.5	34.9	491	2	T01856	hypothetical prote
762	32.5	34.9	499	2	T03213	probable ribosomal
763	32.5	34.9	532	2	AB1369	conserved hypothet
764	32.5	34.9	538	2	T03232	probable ribosomal
765	32.5	34.9	590	2	A96656	unknown protein, 3
766	32.5	34.9	635	2	T23465	hypothetical prote
767	32.5	34.9	681	2	AD3318	DNA primase (EC 2.
768	32.5	34.9	695	1	VHIWMV	nucleocapsid prote
769	32.5	34.9	695	2	S44049	nucleocapsid prote
770	32.5	34.9	759	2	S62067	Ty1 enhancer activ
771	32.5	34.9	770	2	B48910	desmocollin 1b pre
772	32.5	34.9	781	2	T26080	hypothetical prote
773	32.5	34.9	824	2	A48910	desmocollin 1a pre
774	32.5	34.9	840	2	I37281	Dsc1a precursor -
775	32.5	34.9	893	2	F86476	protein F15O4.39 [
776	32.5	34.9	894	2	I37282	Dsc1b precursor -
777	32.5	34.9	932	2	S65214	probable alpha/gam
778	32.5	34.9	1356	2	JC1402	protein-tyrosine k
779	32.5	34.9	1367	2	A41228	protein-tyrosine k
780	32.5	34.9	1417	2	T18418	hypothetical prote
781	32.5	34.9	1946	2	AC2141	serine/threonine k
782	32.5	34.9	3020	2	A43932	mucin 2 precursor,
783	32	34.4	50	2	H82588	hypothetical prote
784	32	34.4	73	2	T25926	hypothetical prote
785	32	34.4	98	2	T26046	hypothetical prote
786	32	34.4	104	2	S50936	probable membrane
787	32	34.4	109	2	T00234	hypothetical prote
788	32	34.4	110	2	S41557	hypothetical prote
789	32	34.4	115	2	A55827	blue copper protei
790	32	34.4	125	2	T49512	hypothetical prote
791	32	34.4	136	1	B64956	flagellar protein
792	32	34.4	136	2	H90961	flagellar protein
793	32	34.4	136	2	H85809	hypothetical prote
794	32	34.4	145	2	H82498	hypothetical prote
795	32	34.4	154	2	E83634	hypothetical prote
796	32	34.4	158	2	T09295	probable heat shoc
797	32	34.4	159	2	E75151	molybdenum cofacto
798	32	34.4	165	2	H71649	hypothetical prote
799	32	34.4	166	2	AH2568	hypothetical prote
800	32	34.4	168	2	E69198	Ni,Fe-Hydrogenase
801	32	34.4	174	2	T50419	hypothetical prote
802	32	34.4	175	2	AC2876	conserved hypothet
803	32	34.4	177	2	E97652	hypothetical prote
804	32	34.4	180	1	A39167	placental protein
805	32	34.4	185	2	AE0736	probable bacteriop
806	32	34.4	186	2	T39759	hypothetical prote
807	32	34.4	191	2	S78155	ribosomal protein
808	32	34.4	192	2	D69061	precorrin-8W decar
809	32	34.4	196	2	G89950	conserved hypothet
810	32	34.4	200	2	T25406	hypothetical prote
811	32	34.4	203	2	T48718	mitochondrial ribo
812	32	34.4	204	2	T01447	hypothetical prote
813	32	34.4	204	2	T28939	hypothetical prote
814	32	34.4	205	2	A71567	probable GMP kinas
815	32	34.4	212	2	F72752	hypothetical prote
816	32	34.4	213	2	D82849	cell division prot
817	32	34.4	213	2	D70211	lipoprotein homolo
818	32	34.4	215	2	E70350	probable thiamin p
819	32	34.4	219	1	TLBPT2	tail fiber protein
820	32	34.4	221	1	TLBP64	tail fiber protein
821	32	34.4	226	2	AC0176	probable exported
822	32	34.4	230	1	TLBPK3	tail fiber protein
823	32	34.4	231	2	T45566	hypothetical prote
824	32	34.4	237	2	E81298	hypothetical prote
825	32	34.4	242	2	E89813	hypothetical prote
826	32	34.4	246	2	T19850	hypothetical prote
827	32	34.4	247	2	T49991	probable protein p
828	32	34.4	254	2	H89772	hypothetical prote
829	32	34.4	255	2	H83700	transcription acti
830	32	34.4	255	2	AC3292	glucose-1-phosphat
831	32	34.4	257	2	C81206	FrpC operon protei
832	32	34.4	259	2	T36172	hypothetical prote

833	32	34.4	259	2	H88969	protein F15E11.5 [
834	32	34.4	261	2	T51243	Scl1 protein [impo
835	32	34.4	264	2	AB2326	hypothetical prote
836	32	34.4	265	2	G37271	metalloproteinase
837	32	34.4	268	2	F37271	metalloproteinase
838	32	34.4	268	2	T32775	hypothetical prote
839	32	34.4	271	2	S35026	hypothetical prote
840	32	34.4	278	2	C69854	conserved hypothet
841	32	34.4	278	2	AD2325	hypothetical prote
842	32	34.4	278	2	T22640	hypothetical prote
843	32	34.4	278	2	AH2981	hypothetical prote
844	32	34.4	278	2	H98301	dipeptide transpor
845	32	34.4	281	2	AI0126	conserved hypothet
846	32	34.4	281	2	D82554	tRNA/rRNA methyltr
847	32	34.4	281	2	C82547	hypothetical prote
848	32	34.4	285	2	B82459	hypothetical prote
849	32	34.4	287	2	T40403	hypothetical prote
850	32	34.4	288	2	D82781	conserved hypothet
851	32	34.4	289	2	E69207	conserved hypothet
852	32	34.4	290	2	E37271	metalloproteinase
853	32	34.4	291	2	S48252	serine-rich protei
854	32	34.4	294	2	T20338	hypothetical prote
855	32	34.4	297	2	C96524	F11A17.4 [imported
856	32	34.4	300	2	AE0762	conserved hypothet
857	32	34.4	304	2	S12975	coat protein - pot
858	32	34.4	304	2	AG0926	hypothetical prote
859	32	34.4	304	2	T48281	hypothetical prote
860	32	34.4	306	2	S19997	hypothetical prote
861	32	34.4	307	2	G69211	conserved hypothet
862	32	34.4	308	2	A86246	hypothetical prote
863	32	34.4	308	2	T46294	hypothetical prote
864	32	34.4	308	2	H89839	hypothetical prote
865	32	34.4	310	1	S37695	calcium-binding pr
866	32	34.4	311	2	E96714	probable DNA-bindi
867	32	34.4	313	2	F71285	hypothetical prote
868	32	34.4	323	2	T28951	hypothetical prote
869	32	34.4	328	2	AE0301	conserved hypothet
870	32	34.4	330	2	T39698	protein tyrosine p
871	32	34.4	330	2	AG2129	iron(III) dicitrat
872	32	34.4	331	2	A83678	hypothetical prote
873	32	34.4	332	1	DEMSLM	L-lactate dehydrog
874	32	34.4	335	2	T49145	hypothetical prote
875	32	34.4	337	2	T46742	ornithine carbamoy
876	32	34.4	340	2	F85724	hypothetical prote
877	32	34.4	341	2	T47338	hypothetical prote
878	32	34.4	341	2	H90797	probable tellurium
879	32	34.4	344	2	B83605	probable acetylpol
880	32	34.4	345	2	H90515	lipoate-protein li
881	32	34.4	346	2	T30463	hypothetical prote
882	32	34.4	348	2	AI3626	inositol 2-dehydro
883	32	34.4	354	2	JC4212	nitrilase (EC 3.5.
884	32	34.4	358	2	AC0740	probable integrase
885	32	34.4	359	2	JC2134	angiotensin II rec
886	32	34.4	361	2	AG0335	chorismate synthas
887	32	34.4	361	2	D97956	conserved hypothet
888	32	34.4	363	2	D81037	GTP-binding protei
889	32	34.4	366	2	A83061	conserved hypothet
890	32	34.4	367	2	T10207	oleoyl-[acyl-carri
891	32	34.4	367	2	B56598	endothelial kinase
892	32	34.4	370	2	I40085	gtcS protein - Bac
893	32	34.4	372	2	T08273	conserved hypothet
894	32	34.4	373	2	JC7289	G-protein coupled
895	32	34.4	379	2	C86821	hypothetical prote
896	32	34.4	383	2	H75129	probable transamin
897	32	34.4	383	2	S53379	probable membrane
898	32	34.4	385	2	A85607	hypothetical prote
899	32	34.4	386	2	E71001	probable transamin
900	32	34.4	387	2	E71711	probable o-sialogl
901	32	34.4	390	2	G01936	Abl binding protei
902	32	34.4	391	2	D64366	hypothetical prote
903	32	34.4	397	2	T35361	hypothetical prote
904	32	34.4	401	2	A57226	mei-S332 protein -
905	32	34.4	402	2	S55465	chalcone synthase
906	32	34.4	402	2	B82982	DNA/pantothenate m
907	32	34.4	403	2	S53477	IMP dehydrogenase
908	32	34.4	404	2	D86321	hypothetical prote
909	32	34.4	405	2	T37022	probable lycopene
910	32	34.4	410	2	T36610	hypothetical prote
911	32	34.4	412	1	B70125	hemolysin homolog
912	32	34.4	412	2	JC4921	double C2 protein
913	32	34.4	415	2	T48171	hypothetical prote
914	32	34.4	416	2	D69251	hypothetical prote
915	32	34.4	421	2	T43534	transcription fact
916	32	34.4	421	2	T05032	protein kinase hom
917	32	34.4	424	2	B95201	3-hydroxy-3-methyl
918	32	34.4	424	2	H98067	hydroxymethylgluta
919	32	34.4	424	2	S27783	hypothetical prote
920	32	34.4	426	2	H87462	enolase [imported]
921	32	34.4	427	2	T46265	hypothetical prote
922	32	34.4	428	2	A81841	phosphopyruvate hy
923	32	34.4	428	2	D81100	enolase NMB1285 [i
924	32	34.4	431	2	C95023	competence-induced
925	32	34.4	435	2	T24074	hypothetical prote
926	32	34.4	437	2	E71953	hypothetical prote
927	32	34.4	440	2	S37303	sox-4 protein - mo
928	32	34.4	443	2	A70438	flagellar export p
929	32	34.4	444	2	E70201	pantothenate perme
930	32	34.4	447	2	G86940	probable enolase [
931	32	34.4	451	2	C49898	cellobiose phospho
932	32	34.4	453	2	F82702	conserved hypothet
933	32	34.4	455	2	AH0794	o-succinylbenzoate
934	32	34.4	456	2	AE3341	cobG protein (EC 1
935	32	34.4	460	2	T27770	hypothetical prote
936	32	34.4	461	2	F82700	enolase XF1291 [im
937	32	34.4	461	2	T51458	hypothetical prote
938	32	34.4	461	2	A46394	suppressor protein
939	32	34.4	465	2	T26146	hypothetical prote
940	32	34.4	466	2	T44350	hypothetical prote
941	32	34.4	466	2	AI1707	transcription regu
942	32	34.4	468	1	B64896	hypothetical prote
943	32	34.4	468	2	D85734	hypothetical prote
944	32	34.4	468	2	C90884	probable transcrip
945	32	34.4	469	1	P2WL35	L2 protein - human
946	32	34.4	469	2	S36525	L2 protein - human
947	32	34.4	470	2	B86165	hypothetical prote
948	32	34.4	471	1	S62590	peptidyl-prolyl ci
949	32	34.4	472	1	B53236	transcription fact
950	32	34.4	472	2	S36519	L2 protein - human
951	32	34.4	474	2	AF0669	probable regulator
952	32	34.4	474	2	I38240	transcription fact
953	32	34.4	475	1	JN0327	sulfate adenylyltr
954	32	34.4	475	2	E91079	hypothetical prote
955	32	34.4	475	2	F85924	hypothetical prote
956	32	34.4	478	1	FOVWVL	gag polyprotein -
957	32	34.4	481	2	S56299	hypothetical prote
958	32	34.4	481	2	AD1337	transcription regu
959	32	34.4	498	2	D83994	xylose kinase xylB
960	32	34.4	498	2	T09436	gag polyprotein -
961	32	34.4	500	1	FOVWLV	gag polyprotein -
962	32	34.4	500	1	A44001	gag polyprotein -
963	32	34.4	500	2	G71836	anthranilate synth
964	32	34.4	500	2	B64680	anthranilate synth
965	32	34.4	500	2	S33979	gag polyprotein -
966	32	34.4	502	1	FOVWA2	gag polyprotein -
967	32	34.4	503	2	S54302	zinc transporter Z
968	32	34.4	506	1	A38068	gag polyprotein -
969	32	34.4	507	2	T11559	gag protein - simi
970	32	34.4	507	2	S04237	gag polyprotein -
971	32	34.4	508	1	FOLJSI	gag polyprotein -
972	32	34.4	511	2	AI3112	hypothetical prote
973	32	34.4	511	2	D98174	oligopeptide ABC t
974	32	34.4	512	1	FOVWH3	gag polyprotein -
975	32	34.4	512	2	T44982	methylmalonyl-CoA
976	32	34.4	512	2	B71474	probable hsp60 cha
977	32	34.4	512	2	H85878	multidrug resistan
978	32	34.4	512	2	F91034	multidrug resistan

979	32	34.4	512	2	D65010	multidrug resistan
980	32	34.4	515	2	B89648	protein lin-14 [im
981	32	34.4	518	2	G70174	hypothetical prote
982	32	34.4	520	2	C81273	hypothetical prote
983	32	34.4	521	1	FOLJCA	gag polyprotein -
984	32	34.4	521	1	FOLJST	gag polyprotein -
985	32	34.4	521	2	JC5220	protein-tyrosine-p
986	32	34.4	521	2	S53091	gag polyprotein -
987	32	34.4	521	2	S08435	gag polyprotein -
988	32	34.4	521	2	S12152	gag polyprotein -
989	32	34.4	522	1	FOLJG2	gag polyprotein -
990	32	34.4	522	2	B71807	DNA repair protein
991	32	34.4	523	1	S48997	IMP dehydrogenase
992	32	34.4	523	1	S59402	IMP dehydrogenase
993	32	34.4	524	2	A64694	DNA repair protein
994	32	34.4	526	2	F82873	hypothetical prote
995	32	34.4	527	2	T25131	hypothetical prote
996	32	34.4	529	2	B23595	DNA nucleotidylexo
997	32	34.4	537	2	T25268	embryonic nuclear
998	32	34.4	538	2	H96008	hypothetical prote
999	32	34.4	539	2	A40581	embryonic nuclear
1000	32	34.4	542	2	S58837	hypothetical prote
1001	32	34.4	553	2	S22954	finger protein zfp
1002	32	34.4	554	2	S46346	gag polyprotein -
1003	32	34.4	554	2	T33294	hypothetical prote
1004	32	34.4	556	2	D88700	protein K02B2.4 [i
1005	32	34.4	559	2	T29693	hypothetical prote
1006	32	34.4	565	2	H72253	DNA primase - Ther
1007	32	34.4	577	1	VGBEGI	glycoprotein E - s
1008	32	34.4	579	2	E96496	unknown protein, 5
1009	32	34.4	582	2	H70588	probable proS prot
1010	32	34.4	583	2	AH1922	hypothetical prote
1011	32	34.4	585	2	S38155	hypothetical prote
1012	32	34.4	587	2	A86203	hypothetical prote
1013	32	34.4	591	1	S22664	virulence-associat
1014	32	34.4	593	2	S15215	virulence-associat
1015	32	34.4	598	2	T40659	probable peroxisom
1016	32	34.4	600	2	T24626	hypothetical prote
1017	32	34.4	602	2	T50974	related to hxB pro
1018	32	34.4	604	2	I36917	glycoprotein IIb -
1019	32	34.4	614	2	T19963	hypothetical prote
1020	32	34.4	617	2	AE0394	probable acçessory
1021	32	34.4	621	2	D70762	probable transfera
1022	32	34.4	621	2	A71516	hypothetical prote
1023	32	34.4	622	2	D71078	aldehyde-ferredoxi
1024	32	34.4	623	2	T02007	ABC1 protein homol
1025	32	34.4	623	2	T52128	ABC1 protein homol
1026	32	34.4	624	2	S50650	hypothetical prote
1027	32	34.4	631	2	T40189	probable biotin-pr
1028	32	34.4	633	2	D82527	proteinase IV XF26
1029	32	34.4	635	2	A81656	threonyl-tRNA synt
1030	32	34.4	637	2	D97708	cell division prot
1031	32	34.4	637	2	C71712	cell division prot
1032	32	34.4	638	2	D84453	hypothetical prote
1033	32	34.4	640	2	B84478	probable replicati
1034	32	34.4	642	2	A82479	threonyl-tRNA synt
1035	32	34.4	644	2	A96721	probable peptide t
1036	32	34.4	650	2	T00081	hypothetical prote
1037	32	34.4	651	2	C75014	hypothetical prote
1038	32	34.4	660	2	G71497	threonine-tRNA lig
1039	32	34.4	677	2	T40145	probable beta-adap
1040	32	34.4	686	2	T15795	hypothetical prote
1041	32	34.4	692	2	A36143	phospholipase C (E
1042	32	34.4	692	2	E83230	non-hemolytic phos
1043	32	34.4	694	2	F82511	vgrG protein VCA00
1044	32	34.4	694	2	F90609	exodeoxyribonuclea
1045	32	34.4	700	2	T10566	probable serine/th
1046	32	34.4	703	2	T39997	Ths1p - fission ye
1047	32	34.4	711	2	S68443	double-stranded RN
1048	32	34.4	711	2	G86526	hypothetical prote
1049	32	34.4	711	2	A72098	hypothetical prote
1050	32	34.4	715	2	D84549	probable selenium-
1051	32	34.4	718	2	G70978	probable copper-tr
1052	32	34.4	721	2	T41530	hypothetical prote
1053	32	34.4	726	2	AG0837	TonB-dependent out
1054	32	34.4	729	2	AF0808	probable membrane
1055	32	34.4	736	2	T49652	glycerol-3-phospha
1056	32	34.4	744	2	H71643	cell division prot
1057	32	34.4	750	2	E84475	probable Athila re
1058	32	34.4	751	2	I48748	semaphorin E - mou
1059	32	34.4	751	2	F85043	hypothetical prote
1060	32	34.4	764	2	I36916	glycoprotein IIb -
1061	32	34.4	764	2	T07608	chloride channel p
1062	32	34.4	775	2	T49817	hypothetical prote
1063	32	34.4	776	2	S67053	probable membrane
1064	32	34.4	782	2	S62583	probable transcrip
1065	32	34.4	785	2	AD1893	hydrogenase matura
1066	32	34.4	792	2	C85359	hypothetical prote
1067	32	34.4	793	2	T24270	hypothetical prote
1068	32	34.4	806	2	JC4835	beta-catenin - Hyd
1069	32	34.4	808	2	T16564	hypothetical prote
1070	32	34.4	822	2	AD3232	conjugal transfer
1071	32	34.4	822	2	T09221	exocyst complex pr
1072	32	34.4	826	2	A60385	monocyte surface a
1073	32	34.4	830	2	S25198	vacuolar membrane
1074	32	34.4	839	2	S62963	hypothetical prote
1075	32	34.4	847	2	G75270	cation-transportin
1076	32	34.4	850	2	S20462	RNA12 protein - ye
1077	32	34.4	873	2	F71092	ATP-dependent RNA
1078	32	34.4	891	2	T19915	hypothetical prote
1079	32	34.4	906	2	T45158	pre-mRNA splicing
1080	32	34.4	922	2	B82168	insulinase-type zi
1081	32	34.4	929	2	A32495	rep-1 protein, for
1082	32	34.4	935	2	S66306	hypothetical prote
1083	32	34.4	939	2	AE2275	hypothetical prote
1084	32	34.4	944	2	T28734	hypothetical prote
1085	32	34.4	947	2	T00340	hypothetical prote
1086	32	34.4	962	2	I70165	adenosine triphosp
1087	32	34.4	968	2	F70746	probable mmpL2 pro
1088	32	34.4	974	2	T14076	probable villin [i
1089	32	34.4	982	2	S10340	DNA-directed RNA p
1090	32	34.4	986	2	T10754	cis-Golgi matrix p
1091	32	34.4	994	2	A70776	probable glnE - My
1092	32	34.4	1022	2	E84792	probable kinesin h
1093	32	34.4	1029	2	T28956	hypothetical prote
1094	32	34.4	1053	2	S72194	hydroxymethylgluta
1095	32	34.4	1055	2	H64577	type I restriction
1096	32	34.4	1070	2	C75506	hypothetical prote
1097	32	34.4	1072	2	T37876	probable (Xeroderm
1098	32	34.4	1074	2	T24877	hypothetical prote
1099	32	34.4	1076	2	T24887	hypothetical prote
1100	32	34.4	1098	2	T28816	hypothetical prote
1101	32	34.4	1119	2	B70126	surface-located me
1102	32	34.4	1124	2	G91055	hypothetical prote
1103	32	34.4	1124	2	C85900	hypothetical prote
1104	32	34.4	1124	2	D65032	hypothetical prote
1105	32	34.4	1126	2	JC4019	DNA mismatch repai
1106	32	34.4	1129	2	D84022	ATP-dependent nucl
1107	32	34.4	1131	2	T19442	hypothetical prote
1108	32	34.4	1131	2	AD2166	two-component sens
1109	32	34.4	1135	2	JQ2163	hypothetical 126.5
1110	32	34.4	1145	2	T13810	DNA-directed DNA p
1111	32	34.4	1145	2	T13808	DNA-directed DNA p
1112	32	34.4	1146	2	S46837	hypothetical prote
1113	32	34.4	1162	2	B97852	hypothetical prote
1114	32	34.4	1163	2	D82202	vgrG protein VC141
1115	32	34.4	1169	2	C71639	hypothetical prote
1116	32	34.4	1176	2	A28065	Ca2+-transporting
1117	32	34.4	1200	2	T48194	hypothetical prote
1118	32	34.4	1206	2	T34021	protein kinase SK2
1119	32	34.4	1220	2	A30802	Ca2+-transporting
1120	32	34.4	1220	2	I55491	adenosine triphosp
1121	32	34.4	1220	2	S13057	Ca2+-transporting
1122	32	34.4	1224	2	H96615	hypothetical prote
1123	32	34.4	1231	2	T18532	serine/threoine pr
1124	32	34.4	1233	2	T14157	serine/threonine p

1125	32	34.4	1257	2	A88536	protein B0523.5 [i
1126	32	34.4	1263	2	F44466	DNA-directed RNA p
1127	32	34.4	1283	2	T13799	neurexin IV - frui
1128	32	34.4	1300	2	S73679	probable lipoprote
1129	32	34.4	1379	2	JC4954	vascular endotheli
1130	32	34.4	1384	2	T26656	hypothetical prote
1131	32	34.4	1405	2	T04426	hypothetical prote
1132	32	34.4	1416	2	E88550	protein ZC84.1 [im
1133	32	34.4	1466	2	G84516	probable retroelem
1134	32	34.4	1499	2	B59431	Rho GTPase activat
1135	32	34.4	1501	2	T42724	p190-B protein - m
1136	32	34.4	1509	2	T19486	hypothetical prote
1137	32	34.4	1513	1	RNRZC2	DNA-directed RNA p
1138	32	34.4	1520	2	B82274	conserved hypothet
1139	32	34.4	1547	2	S69842	TyB protein - yeas
1140	32	34.4	1560	2	T02885	peroxisome prolife
1141	32	34.4	1571	2	T14155	zinc finger protei
1142	32	34.4	1616	2	G64242	cytadherence-acces
1143	32	34.4	1727	2	T50073	myosin-like coiled
1144	32	34.4	1735	1	S22812	DNA-directed RNA p
1145	32	34.4	1759	2	T18868	myoblast city prot
1146	32	34.4	1825	2	T42725	actin binding prot
1147	32	34.4	1872	2	JC4976	plexin 3 precursor
1148	32	34.4	1885	2	T30847	actin binding prot
1149	32	34.4	1927	2	A59236	embryonic muscle m
1150	32	34.4	2033	2	T30849	actin binding prot
1151	32	34.4	2042	2	T18399	variant-specific s
1152	32	34.4	2090	2	S26058	probable transform
1153	32	34.4	2207	2	T42759	Munc13-3 protein -
1154	32	34.4	2287	2	T21312	hypothetical prote
1155	32	34.4	2297	2	AB2494	hypothetical prote
1156	32	34.4	2561	1	I40456	peptide synthetase
1157	32	34.4	2824	2	T22759	hypothetical prote
1158	32	34.4	2844	2	S28291	hypothetical prote
1159	32	34.4	3227	2	T37964	probable ubiquitin
1160	32	34.4	3603	1	D69681	peptide synthetase
1161	32	34.4	3744	2	S46715	hypothetical prote
1162	32	34.4	6486	2	T31076	tyrocidine synthet
1163	31.5	33.9	60	2	S35180	cytochrome P450 (c
1164	31.5	33.9	91	2	S17627	Ig kappa chain V r
1165	31.5	33.9	143	2	T36669	probable anti-sigm
1166	31.5	33.9	168	2	AE1238	E. coli YbdM prote
1167	31.5	33.9	168	2	AI1600	E. coli YbdM prote
1168	31.5	33.9	200	2	AG2261	transcription regu
1169	31.5	33.9	220	2	T20059	hypothetical prote
1170	31.5	33.9	274	2	AH2462	biotin acetyl-CoA
1171	31.5	33.9	277	2	T20065	hypothetical prote
1172	31.5	33.9	296	2	S75601	hypothetical prote
1173	31.5	33.9	302	2	T32234	hypothetical prote
1174	31.5	33.9	320	2	C83628	probable oxidoredu
1175	31.5	33.9	330	2	T22411	hypothetical prote
1176	31.5	33.9	331	2	G02431	geranylgeranyl tra
1177	31.5	33.9	340	1	C64360	conserved hypothet
1178	31.5	33.9	357	2	T46868	protoporphyrin IX
1179	31.5	33.9	357	2	S75252	protoporphyrin IX
1180	31.5	33.9	370	2	AB3334	daunorubicin resis
1181	31.5	33.9	374	2	JC2123	major allergen Cry
1182	31.5	33.9	380	2	G69893	butyryl-CoA dehydr
1183	31.5	33.9	380	2	T44811	acyl-CoA dehydroge
1184	31.5	33.9	380	2	A83458	hypothetical prote
1185	31.5	33.9	392	2	T35487	hypothetical prote
1186	31.5	33.9	401	2	A81335	tyrosine-tRNA liga
1187	31.5	33.9	438	2	D72404	flagellum-specific
1188	31.5	33.9	559	1	R3ZMS3	ribosomal protein
1189	31.5	33.9	559	2	T20709	hypothetical prote
1190	31.5	33.9	591	2	B72121	ATP synthase, chai
1191	31.5	33.9	591	2	H86501	ATP synthase subun
1192	31.5	33.9	595	2	JC8012	G protein-coupled
1193	31.5	33.9	607	2	E84827	hypothetical prote
1194	31.5	33.9	673	2	T06294	hypothetical prote
1195	31.5	33.9	673	2	H69828	ABC transporter (A
1196	31.5	33.9	693	2	T00256	hypothetical prote
1197	31.5	33.9	696	2	JC7361	follitropin recept
1198	31.5	33.9	827	2	S75622	hypothetical prote
1199	31.5	33.9	840	2	I48968	major fibrous shea
1200	31.5	33.9	849	2	I49060	major 80,000 Mr fi
1201	31.5	33.9	861	2	T41945	primase - human he
1202	31.5	33.9	1024	2	G72041	exodeoxyribonuclea
1203	31.5	33.9	1024	2	F86582	exodeoxyribonuclea
1204	31.5	33.9	1024	2	D81624	exodeoxyribonuclea
1205	31.5	33.9	1025	2	I59331	thyrotropin-releas
1206	31.5	33.9	1150	2	H96501	probable retroelem
1207	31.5	33.9	1175	2	S52417	E-selectin ligand-
1208	31.5	33.9	1226	2	S69078	hypothetical prote
1209	31.5	33.9	1381	2	S55619	capsid protein 25
1210	31.5	33.9	1484	2	T42632	breast cancer tumo
1211	31.5	33.9	1672	2	C81675	polymorphic membra
1212	31.5	33.9	1787	2	AC2009	serine/threonine k
1213	31.5	33.9	1796	2	AC1895	serine/threonine k
1214	31.5	33.9	4588	2	T28667	dynein beta heavy
1215	31	33.3	66	2	AG1908	hypothetical prote
1216	31	33.3	82	2	AG0714	hypothetical prote
1217	31	33.3	98	2	S06671	cinnamomin - Phyto
1218	31	33.3	101	2	T21657	hypothetical prote
1219	31	33.3	103	2	A72713	hypothetical prote
1220	31	33.3	110	2	B41323	ribulose-bisphosph
1221	31	33.3	111	2	B71115	hypothetical prote
1222	31	33.3	111	2	S10222	hypothetical prote
1223	31	33.3	111	2	S12179	transcription fact
1224	31	33.3	113	2	S12184	transcription fact
1225	31	33.3	114	2	S40340	Ig kappa chain V-J
1226	31	33.3	114	2	S12185	transcription fact
1227	31	33.3	114	2	F90557	hypothetical prote
1228	31	33.3	115	2	S12187	transcription fact
1229	31	33.3	118	1	B70021	arsenate reductase
1230	31	33.3	118	2	AH0986	phage-like lysozym
1231	31	33.3	118	2	S26611	transcription fact
1232	31	33.3	120	2	S16445	transcription fact
1233	31	33.3	122	2	JN0441	Shaking-B neural p
1234	31	33.3	123	2	S26610	transcription fact
1235	31	33.3	124	2	S76185	hypothetical prote
1236	31	33.3	127	2	H82181	hypothetical prote
1237	31	33.3	135	2	T40281	gtp-binding protei
1238	31	33.3	136	2	JU0266	envelope polyprote
1239	31	33.3	136	2	JT0954	envelope polyprote
1240	31	33.3	139	2	S06550	finger protein (cl
1241	31	33.3	142	2	S25093	phospholipase A2 (
1242	31	33.3	142	2	G75109	hypothetical prote
1243	31	33.3	145	2	S30247	Hin-1 protein - hu
1244	31	33.3	152	2	T32784	hypothetical prote
1245	31	33.3	153	2	A26092	myosin L1 regulato
1246	31	33.3	153	2	S77187	hypothetical prote
1247	31	33.3	154	2	B84973	aspartate carbamoy
1248	31	33.3	154	2	S28181	transcription fact
1249	31	33.3	160	2	C69355	hypothetical prote
1250	31	33.3	165	2	AH3295	acetyltransferase
1251	31	33.3	169	2	JC6013	hypothetical k pro
1252	31	33.3	171	2	E97074	probable acetyltra
1253	31	33.3	171	2	T48393	hypothetical prote
1254	31	33.3	173	2	S10548	lectin - barnacle
1255	31	33.3	178	2	S74564	hypothetical prote
1256	31	33.3	184	2	A83316	hypothetical prote
1257	31	33.3	184	2	G85955	hypothetical prote
1258	31	33.3	192	2	D64481	hypothetical prote
1259	31	33.3	194	2	A72167	A28L protein - var
1260	31	33.3	199	2	E86081	hypothetical prote
1261	31	33.3	199	2	S40863	hypothetical 21.8K
1262	31	33.3	199	2	E91234	hypothetical prote
1263	31	33.3	203	2	AD1369	hypothetical prote
1264	31	33.3	207	2	S59142	mudrB protein - ma
1265	31	33.3	208	2	C81160	uracil phosphoribo
1266	31	33.3	209	2	F82483	hypothetical prote
1267	31	33.3	212	2	S03070	gag protein - huma
1268	31	33.3	212	2	D82383	conserved hypothet
1269	31	33.3	213	2	T06333	probable glutathio
1270	31	33.3	217	2	H64956	yedG protein - Esc

1271	31	33.3	218	2	JC7147	trichothecene bios
1272	31	33.3	219	2	G86620	dethiobiotin synth
1273	31	33.3	219	2	F72004	dethiobiotin synth
1274	31	33.3	220	2	A81311	probable periplasm
1275	31	33.3	221	2	T43159	ubiquitin-protein
1276	31	33.3	221	2	AF2316	endonuclease V [im
1277	31	33.3	222	2	F90962	hypothetical prote
1278	31	33.3	222	2	F85810	hypothetical prote
1279	31	33.3	226	2	A35968	tox regulon transc
1280	31	33.3	227	2	T37499	probable ubiquitin
1281	31	33.3	228	2	T15236	hypothetical prote
1282	31	33.3	229	1	H64098	probable pyridoxam
1283	31	33.3	230	2	B83325	probable transport
1284	31	33.3	231	2	B64249	tRNA (guanine-N1-)
1285	31	33.3	231	2	S73286	phycobilisome rod-
1286	31	33.3	231	2	S33552	hypothetical prote
1287	31	33.3	232	1	JH0597	transcription fact
1288	31	33.3	234	2	A41178	heparin-binding gr
1289	31	33.3	236	2	E84307	glucose 1-dehydrog
1290	31	33.3	237	2	S46685	hypothetical prote
1291	31	33.3	238	2	S78571	transcription fact
1292	31	33.3	239	2	AF0750	RNA polymerase sig
1293	31	33.3	239	2	E90961	RNA polymerase sig
1294	31	33.3	239	2	JC4346	RNA polymerase sig
1295	31	33.3	239	2	E85809	RNA polymerase sig
1296	31	33.3	239	2	S11895	transcription init
1297	31	33.3	241	1	JQ1641	phosphoprotein P -
1298	31	33.3	241	2	T23428	hypothetical prote
1299	31	33.3	241	2	A87551	glutathione S-tran
1300	31	33.3	241	2	T16802	hypothetical prote
1301	31	33.3	242	2	A96794	unknown protein F1
1302	31	33.3	245	2	S10658	hypothetical prote
1303	31	33.3	245	2	H86151	hypothetical prote
1304	31	33.3	246	2	C64054	tRNA (guanine-N1-)
1305	31	33.3	247	2	C82307	tRNA (guanine-N1)-
1306	31	33.3	249	2	C81180	tRNA (guanine-N1)-
1307	31	33.3	249	2	A81924	probable tRNA (gua
1308	31	33.3	249	2	T32566	hypothetical prote
1309	31	33.3	251	2	H82864	conserved hypothet
1310	31	33.3	252	2	C83178	tRNA (guanine-N1)-
1311	31	33.3	252	2	F65084	hypothetical prote
1312	31	33.3	252	2	S30292	mating-type switch
1313	31	33.3	255	2	T24406	hypothetical prote
1314	31	33.3	256	2	AI1119	transcription regu
1315	31	33.3	256	2	AD1480	transcription regu
1316	31	33.3	257	2	C97109	specialized DNA-de
1317	31	33.3	257	2	I40621	probable transcrip
1318	31	33.3	257	2	T40880	hypothetical prote
1319	31	33.3	258	2	T34422	hypothetical prote
1320	31	33.3	261	2	T41508	hypothetical prote
1321	31	33.3	261	2	D90562	hypothetical prote
1322	31	33.3	262	2	B83126	probable transcrip
1323	31	33.3	263	2	G81272	hypothetical prote
1324	31	33.3	263	4	I67792	probable glucosylc
1325	31	33.3	266	1	WQECMP	phosphotransferase
1326	31	33.3	266	2	H90944	mannose-specific P
1327	31	33.3	266	2	C85793	PTS enzyme IIC, ma
1328	31	33.3	268	2	AB1087	PTS system mannose
1329	31	33.3	268	2	AI1450	PTS system mannose
1330	31	33.3	268	2	H83320	probable transcrip
1331	31	33.3	272	2	T33515	hypothetical prote
1332	31	33.3	272	2	F70979	hypothetical prote
1333	31	33.3	273	2	T50938	DitR protein [impo
1334	31	33.3	274	2	I76777	O9 mannan biosynth
1335	31	33.3	276	2	T38825	hypothetical prote
1336	31	33.3	278	2	A56570	homeobox protein D
1337	31	33.3	280	2	I55577	Fc gamma (IgG) rec
1338	31	33.3	281	1	T15613	probable phosphoes
1339	31	33.3	281	2	T50351	probable methyltra
1340	31	33.3	282	2	B84984	geranyltranstransf
1341	31	33.3	283	2	S42634	homeoprotein, IDX-
1342	31	33.3	284	2	D81075	conserved hypothet
1343	31	33.3	284	2	S39581	IPF1 protein - mou
1344	31	33.3	287	2	T27056	hypothetical prote
1345	31	33.3	290	2	T50434	hypothetical prote
1346	31	33.3	291	2	AI3092	hypothetical prote
1347	31	33.3	296	2	AB0557	cytochrome o ubiqu
1348	31	33.3	296	2	E42226	heme O synthase -
1349	31	33.3	296	2	F85539	Protoheme IX farne
1350	31	33.3	296	2	B90689	Protoheme IX farne
1351	31	33.3	297	2	F64206	lipopolysaccharide
1352	31	33.3	297	2	F90287	antibiotic ABC tra
1353	31	33.3	303	2	JS0379	hypothetical 35.5K
1354	31	33.3	304	2	A89905	hypothetical prote
1355	31	33.3	305	2	A71324	conserved hypothet
1356	31	33.3	310	2	T31799	hypothetical prote
1357	31	33.3	312	2	H97297	probable transcrip
1358	31	33.3	314	2	AG3410	chlorAMPhenicol-se
1359	31	33.3	314	2	F90569	conserved hypothet
1360	31	33.3	318	2	A99510	hypothetical prote
1361	31	33.3	318	2	A85066	hypothetical prote
1362	31	33.3	320	1	C71071	hypothetical prote
1363	31	33.3	323	2	AI2024	hypothetical prote
1364	31	33.3	326	1	S17954	alkanal monooxygen
1365	31	33.3	326	2	JC4196	36K hydrophobic nu
1366	31	33.3	326	2	A96608	hypothetical prote
1367	31	33.3	327	2	JC4195	36k hydrophobic nu
1368	31	33.3	328	2	F72260	hypothetical prote
1369	31	33.3	330	2	S49471	transcription init
1370	31	33.3	330	2	AG0855	RNA polymerase sig
1371	31	33.3	330	2	S47534	transcription init
1372	31	33.3	331	2	JQ2018	hypothetical 36.5K
1373	31	33.3	331	2	A86278	hypothetical prote
1374	31	33.3	331	2	A99179	conserved hypothet
1375	31	33.3	332	1	DEHULM	L-lactate dehydrog
1376	31	33.3	332	2	T00847	probable membrane
1377	31	33.3	334	2	F89008	protein W08A12.4 [
1378	31	33.3	335	2	A40267	interleukin-5 rece
1379	31	33.3	336	2	G95051	ketol-acid reducto
1380	31	33.3	336	2	AD1566	hypothetical prote
1381	31	33.3	337	2	AI2723	naphthalene 1,2-di
1382	31	33.3	337	2	E97505	phenol hydroxylase
1383	31	33.3	337	2	D70132	hypothetical prote
1384	31	33.3	338	2	A82890	hypothetical prote
1385	31	33.3	340	2	B86778	ketol-acid reducto
1386	31	33.3	340	2	C97922	ketol-acid reducto
1387	31	33.3	343	2	G71499	probable D-Ala-D-A
1388	31	33.3	343	2	T19082	hypothetical prote
1389	31	33.3	343	2	T22053	hypothetical prote
1390	31	33.3	344	1	S35140	probable ketol-aci
1391	31	33.3	347	2	T40599	hypothetical prote
1392	31	33.3	347	2	AD3513	channel protein vi
1393	31	33.3	348	1	B46216	transcription fact
1394	31	33.3	349	2	A25952	glycerol-3-phospha
1395	31	33.3	349	2	D69856	conserved hypothet
1396	31	33.3	351	2	D48552	orf US1053 - infec
1397	31	33.3	351	2	S52708	hypothetical prote
1398	31	33.3	354	2	B55733	G protein-coupled
1399	31	33.3	354	2	AG3315	lipopolysaccharide
1400	31	33.3	355	2	G88216	protein B0495.1 [i
1401	31	33.3	355	2	F96940	beta-mannanase [im
1402	31	33.3	357	2	S63142	hypothetical prote
1403	31	33.3	357	2	A96194	hypothetical prote
1404	31	33.3	358	2	S45911	hypothetical prote
1405	31	33.3	359	2	T02608	hypothetical prote
1406	31	33.3	360	2	AE0172	probable outer mem
1407	31	33.3	361	2	A53860	chondroadherin pre
1408	31	33.3	363	2	G70145	glycerol-3-phospha
1409	31	33.3	363	2	C70462	DNA polymerase III
1410	31	33.3	363	2	S66114	creatine kinase ho
1411	31	33.3	364	1	JT0741	GTP-binding protei
1412	31	33.3	364	1	A55014	GTP-binding protei
1413	31	33.3	366	2	AH2237	septum site-determ
1414	31	33.3	368	1	S64487	GTP-binding protei
1415	31	33.3	370	2	A27098	larvicidal toxin 4
1416	31	33.3	370	2	S07712	larvicidal toxin 4

1417	31	33.3	370	2	D28211	larvicidal toxin 4
1418	31	33.3	370	2	G90122	hypothetical prote
1419	31	33.3	370	2	T52141	hypothetical prote
1420	31	33.3	372	2	T06745	hypothetical prote
1421	31	33.3	374	1	LQBPR4	RNA ligase (ATP) (
1422	31	33.3	374	1	A39878	Fc gamma (IgG) rec
1423	31	33.3	375	2	AH1685	hypothetical prote
1424	31	33.3	376	2	T28935	hypothetical prote
1425	31	33.3	380	2	A86401	protein T22C5.1 [i
1426	31	33.3	381	2	T10707	adenosylmethionine
1427	31	33.3	381	2	T49544	hypothetical prote
1428	31	33.3	382	2	C83337	hypothetical prote
1429	31	33.3	383	2	JC2472	brain and reproduc
1430	31	33.3	384	2	S58446	sigma S - Salmonel
1431	31	33.3	384	2	A86324	protein F14D16.19
1432	31	33.3	385	2	S66292	actin-crosslinking
1433	31	33.3	386	2	D59237	probable citrate s
1434	31	33.3	387	2	S55550	5-HT4S receptor -
1435	31	33.3	387	2	G64489	hypothetical prote
1436	31	33.3	388	2	T31306	hypothetical prote
1437	31	33.3	390	2	B84727	molybdopterin synt
1438	31	33.3	390	2	T41199	dom34 protein homo
1439	31	33.3	391	2	H97491	alanine racemase (
1440	31	33.3	391	2	AG2709	alanine racemase [
1441	31	33.3	392	2	T01617	probable protein k
1442	31	33.3	393	2	AE0216	phosphoribosylglyc
1443	31	33.3	396	2	H72224	hypothetical prote
1444	31	33.3	397	2	JE0082	GPI-linked recepto
1445	31	33.3	397	2	AC2006	hypothetical prote
1446	31	33.3	398	2	S56699	naringenin-chalcon
1447	31	33.3	399	2	AD2917	conserved hypothet
1448	31	33.3	399	2	G97691	hypothetical prote
1449	31	33.3	400	1	S22539	transcription fact
1450	31	33.3	402	2	D75592	hypothetical prote
1451	31	33.3	403	1	S35541	transcription fact
1452	31	33.3	404	2	T21251	hypothetical prote
1453	31	33.3	406	2	S55549	serotonin 4 recept
1454	31	33.3	410	2	S68515	probable arginine
1455	31	33.3	410	2	A41465	arginine deiminase
1456	31	33.3	411	1	OXMSL	protein-lysine 6-o
1457	31	33.3	412	2	T41552	hypothetical prote
1458	31	33.3	412	2	B81356	ankyrin repeat-con
1459	31	33.3	413	2	E86400	protein T17H3.4 [i
1460	31	33.3	413	2	AC3614	dtdp-4-dehydrorham
1461	31	33.3	414	2	T38742	hypothetical prote
1462	31	33.3	417	1	OXHUL	protein-lysine 6-o
1463	31	33.3	417	2	A96610	probable pectinace
1464	31	33.3	418	2	E86395	hypothetical prote
1465	31	33.3	420	2	S21052	interleukin-5 rece
1466	31	33.3	421	2	C82253	folylpolyglutamate
1467	31	33.3	423	2	E72004	adenosylmethionine
1468	31	33.3	423	2	F86620	hypothetical prote
1469	31	33.3	423	2	T09338	DnaJ-like protein
1470	31	33.3	424	2	F82503	proton/glutamate s
1471	31	33.3	425	2	I64250	hypothetical prote
1472	31	33.3	425	2	F83990	lactose transport
1473	31	33.3	426	2	T41682	hypothetical prote
1474	31	33.3	429	2	B90576	hemolysin c [impor
1475	31	33.3	429	2	T45040	hypothetical prote
1476	31	33.3	430	1	A46216	transcription fact
1477	31	33.3	431	1	JC2002	transcription fact
1478	31	33.3	432	2	T34154	hypothetical prote
1479	31	33.3	434	2	AI2379	hypothetical prote
1480	31	33.3	435	2	T23364	hypothetical prote
1481	31	33.3	436	2	S72701	adenosylmethionine
1482	31	33.3	437	2	B70540	probable adenosylm
1483	31	33.3	438	2	T45602	glucosyltransferas
1484	31	33.3	438	2	I38946	melanoma ubiquitou
1485	31	33.3	438	2	F81659	D-alanyl-D-alanine
1486	31	33.3	440	2	T32151	hypothetical prote
1487	31	33.3	440	2	S69728	hypothetical prote
1488	31	33.3	441	2	T48960	vacuolar H(+)-ATPa
1489	31	33.3	443	2	H84414	hypothetical prote
1490	31	33.3	444	2	H83624	probable porin PA0
1491	31	33.3	445	2	S27492	hypothetical prote
1492	31	33.3	445	2	T26762	hypothetical prote
1493	31	33.3	446	2	D71418	hypothetical prote
1494	31	33.3	447	2	T12978	hypothetical prote
1495	31	33.3	447	2	T39170	probable cis-mucon
1496	31	33.3	447	2	AH0536	conserved hypothet
1497	31	33.3	448	2	F95036	PTS system, IIC co
1498	31	33.3	448	2	B97907	phosphotransferase
1499	31	33.3	449	2	G89841	hypothetical prote
1500	31	33.3	450	2	H84448	probable MYB famil

ALIGNMENTS

RESULT 1
F86909
probable DNA gyrase subunit A [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: F86909
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squ
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: F86909
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1249 <STO>
A;Cross-references: UNIPARC:UPI0000165F27; GB:AL450380; NID:g13092418; PIDN:CAC29514.1; C
C;Genetics:
A;Gene: gyrA

Query Match 47.3%; Score 44; DB 2; Length 1249;
Best Local Similarity 46.7%; Pred. No. 39;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

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Qy          4 VEEDQFSQNPISCFE 18
              |||| |:|: : | :
Db        469 VEEDSFNQHNVDCVQ 483
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RESULT 2
T10006
DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) A - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10006
R;Cole, S.T.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z16916
A;Accession: T10006
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1273 <COL>
A;Cross-references: UNIPROT:Q57532; UNIPARC:UPI000016FAEB; EMBL:Z70722; NID:e1059634; PII
C;Genetics:
A;Gene: gyrA
C;Keywords: isomerase

Query Match 47.3%; Score 44; DB 2; Length 1273;
Best Local Similarity 46.7%; Pred. No. 40;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

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Qy          4 VEEDQFSQNPISCFE 18
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Db        469 VEEDSFNQHNVDCVQ 483
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RESULT 3
T29509
hypothetical protein W05H7.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T29509
R;Wohldmann, P.; Le, T.T.
submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosmid W05H7.
A;Reference number: Z20630
A;Accession: T29509
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-221 <WOH>
A;Cross-references: UNIPARC:UPI000017935A; EMBL:U97552; PIDN:AAB52865.1; GSPDB:GN00028;
A;Experimental source: strain Bristol N2; clone W05H7
C;Genetics:
A;Gene: CESP:W05H7.5
A;Map position: X
A;Introns: 30/1; 61/1; 172/3; 183/1
C;Superfamily: Caenorhabditis elegans hypothetical protein W05H7.5

  Query Match             46.2%;  Score 43;  DB 2;  Length 221;
  Best Local Similarity   53.3%;  Pred. No. 8.4;
  Matches    8;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 SLVEEDQFSQNPISC 16
              |:|    || :||||
Db        152 SIVNPHHFSDSPISC 166


RESULT 4
E84536
hypothetical protein At2g16090 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: E84536
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: E84536
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-518 <STO>
A;Cross-references: UNIPROT:Q9XII0; UNIPARC:UPI000009CCB6; GB:AE002093; NID:g4678205; PI
C;Genetics:
A;Gene: At2g16090
A;Map position: 2

  Query Match             46.2%;  Score 43;  DB 2;  Length 518;
  Best Local Similarity   53.8%;  Pred. No. 22;
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Qy          4 VEEDQFSQNPISC 16
              ||:|: | :| ||
Db        216 VEDDELSHSPCSC 228


RESULT 5
S38171
peptide transport protein PTR2 - yeast (Saccharomyces cerevisiae)
N;Alternate names: peptide permease PTR2; protein YKR093w; protein YKR413
C;Species: Saccharomyces cerevisiae
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: S38171; S40646; S37700
R;Baladron, V.; Ballesta, J.P.G.; Bou, G.; del Rey, F.; Esteban, P.F.; Garcia-Cantalejo,
submitted to the Protein Sequence Database, March 1994
A;Reference number: S38158
A;Accession: S38171
A;Molecule type: DNA
A;Residues: 1-601 <BAL>
A;Cross-references: UNIPROT:P32901; UNIPARC:UPI00001329B5; EMBL:Z28318; NID:g486582; PID:
A;Experimental source: strain S288C
R;Bou, G.; Esteban, P.F.; Baladron, V.; Gonzalez, G.A.; Cantalejo, J.G.; Remacha, M.; Jin
Yeast 9, 1349-1354, 1993
A;Title: The complete sequence of a 15 820 bp segment of Saccharomyces cerevisiae chromos
A;Reference number: S40644; MUID:94205265; PMID:8154186
A;Accession: S40646
A;Molecule type: DNA
A;Residues: 1-601 <BOU>
A;Cross-references: UNIPARC:UPI00001329B5; EMBL:X73541; NID:g450550; PIDN:CAA51947.1; PII
A;Experimental source: strain S288C
A;Note: the authors did not translate the codon for residue 200
R;Becker, J.M.; Perry, J.R.; Basrai, M.A.; Naider, F.R.
submitted to the EMBL Data Library, March 1993
A;Description: Isolation and characterization of a Saccharomyces cerevisiae peptide trans
A;Reference number: S37700
A;Accession: S37700
A;Molecule type: DNA
A;Residues: 1-38,'T',40-466,'LLANTRICLDFFFRDLCLYHWVG',470,'RLFQS',471,'SFHEIVY',473-474,'
A;Cross-references: UNIPARC:UPI000017B2F9; EMBL:L11994
C;Genetics:
A;Gene: SGD:PTR2
A;Cross-references: SGD:S0001801; MIPS:YKR093w
A;Map position: 11R
C;Keywords: membrane protein

  Query Match             46.2%;  Score 43;  DB 2;  Length 601;
  Best Local Similarity   72.7%;  Pred. No. 26;
  Matches    8;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 EEDQFSQNPIS 15
              |||:|  ||||
Db        569 EEDEFDLNPIS 579


RESULT 6
I38754
transcription factor REST (version 1) - human (fragment)
N;Alternate names: neural-restrictive silencer factor; RE1-silencing transcription factor
C;Species: Homo sapiens (man)
C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Accession: I38754
R;Schoenherr, C.J.; Anderson, D.J.
Science 267, 1360-1363, 1995
A;Title: The neuron-restrictive silencer factor (NRSF): a coordinate repressor of multipl
A;Reference number: I38754; MUID:95176234; PMID:7871435
A;Accession: I38754
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-316 <RES>
A;Cross-references: UNIPROT:Q12956; UNIPARC:UPI0000070017; EMBL:U13877; NID:g606943; PIDN
C;Genetics:
A;Gene: GDB:REST; NRSF
A;Cross-references: GDB:702138
A;Map position: 4q12-4q12
C;Keywords: transcription regulation

  Query Match             45.2%;  Score 42;  DB 2;  Length 316;
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  Matches    8;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 SLVEEDQFSQNPISC 16
              |  ||  ||: || |
Db        207 STAEEGDFSKGPIRC 221


RESULT 7
T45592
hypothetical protein F12A12.70 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 31-Dec-2004
C;Accession: T45592
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R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa
submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23008
A;Accession: T45592
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-420 <CHO>
A;Cross-references: UNIPROT:Q9SNC3; UNIPARC:UPI00000A91C1; EMBL:AL133314
A;Experimental source: cultivar Columbia; BAC clone F12A12
C;Genetics:
A;Map position: 3
A;Note: F12A12.70
C;Superfamily: pollen surface protein

  Query Match             45.2%;  Score 42;  DB 2;  Length 420;
  Best Local Similarity   41.2%;  Pred. No. 26;
  Matches    7;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VSLVEEDQFSQNPISCF 17
              :::| :  | |||:| |
Db        329 LAVVTQTAFDQNPVSVF 345


RESULT 8
A49228
trypsin-like proteinase prtT - Porphyromonas gingivalis
C;Species: Porphyromonas gingivalis
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 03-Mar-1995
C;Accession: A49228
R;Otogoto, J.; Kuramitsu, H.K.
Infect. Immun. 61, 117-123, 1993
A;Title: Isolation and characterization of the Porphyromonas gingivalis prtT gene, codin
A;Reference number: A49228; MUID:93114862; PMID:8093357
A;Accession: A49228
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-478 <OTO>
A;Cross-references: UNIPARC:UPI000017AB4E
A;Experimental source: ATCC 53977
A;Note: sequence extracted from NCBI backbone (NCBIN:121603, NCBIP:121604)

  Query Match             45.2%;  Score 42;  DB 2;  Length 478;
  Best Local Similarity   38.9%;  Pred. No. 30;
  Matches    7;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VSLVEEDQFSQNPISCFE 18
              | : |:: :  : |||||
Db        169 VDVKEDEDYPSSAISCFE 186


RESULT 9
I38755
transcription factor REST (version 2) - human (fragment)
N;Alternate names: neural-restrictive silencer factor; RE1-silencing transcription factc
C;Species: Homo sapiens (man)
C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Accession: I38755
R;Schoenherr, C.J.; Anderson, D.J.
Science 267, 1360-1363, 1995
A;Title: The neuron-restrictive silencer factor (NRSF): a coordinate repressor of multip
A;Reference number: I38754; MUID:95176234; PMID:7871435
A;Accession: I38755
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-681 <RES>
A;Cross-references: UNIPROT:Q12957; UNIPARC:UPI000006F634; EMBL:U13879; NID:g606947; PID
C;Genetics:
A;Gene: GDB:REST; NRSF
A;Cross-references: GDB:702138
A;Map position: 4q12-4q12
C;Keywords: transcription regulation

  Query Match             45.2%;  Score 42;  DB 2;  Length 681;
  Best Local Similarity   53.3%;  Pred. No. 45;
  Matches    8;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 SLVEEDQFSQNPISC 16
              |  ||  ||: || |
Db        286 STAEEGDFSKGPIRC 300


RESULT 10
A56138
transcription factor REST (version 3) - human
N;Alternate names: neural-restrictive silencer factor; RE1-silencing transcription factor
C;Species: Homo sapiens (man)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 09-Jul-2004
C;Accession: A56138
R;Chong, J.A.; Tapia-Ramirez, J.; Kim, S.; Toledo-Aral, J.J.; Zheng, Y.; Boutros, M.C.; H
Cell 80, 949-957, 1995
A;Title: REST: a mammalian silencer protein that restricts sodium channel gene expressior
A;Reference number: A56138; MUID:95211846; PMID:7697725
A;Accession: A56138
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1097 <CHO>
A;Cross-references: UNIPROT:Q13127; UNIPARC:UPI000017C3E1; GB:U22314
C;Genetics:
A;Gene: GDB:REST; NRSF
A;Cross-references: GDB:702138
A;Map position: 4q12-4q12

  Query Match             45.2%;  Score 42;  DB 2;  Length 1097;
  Best Local Similarity   53.3%;  Pred. No. 76;
  Matches    8;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 SLVEEDQFSQNPISC 16
              |  ||  ||: || |
Db        204 STAEEGDFSKGPIRC 218


RESULT 11
T16754
hypothetical protein R144.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16754
R;Favello, T.
submitted to the EMBL Data Library, March 1995
A;Description: The sequence of C. elegans cosmid R144.
A;Reference number: Z18571
A;Accession: T16754
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1356 <FAV>
A;Cross-references: UNIPARC:UPI000017BB2D; EMBL:U23515; NID:g746492; PID:g746500; PIDN:AA
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:R144.7
A;Introns: 71/1; 180/3; 238/1; 256/2; 273/2; 337/3; 528/2; 656/3; 683/2; 749/3; 808/3; 95

  Query Match             45.2%;  Score 42;  DB 2;  Length 1356;
  Best Local Similarity   53.3%;  Pred. No. 97;
  Matches    8;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 VSLVEEDQFSQNPIS 15
              :||::||:| ||  |
Db        889 ISLLQEDRFVQNVYS 903


RESULT 12
S47555
N-methyl-D-aspartate receptor modulatory chain hNR2A - human
C;Species: Homo sapiens (man)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S47555
```

```
R;Foldes, R.L.; Adams, S.L.; Fantaske, R.P.; Kamboj, R.K.
Biochim. Biophys. Acta 1223, 155-159, 1994
A;Title: Human N-methyl-D-aspartate receptor modulatory subunit hNR2A: cloning and seque
A;Reference number: S47555; MUID:94339179; PMID:8061049
A;Accession: S47555
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1464 <FOL>
A;Cross-references: UNIPROT:Q12879; UNIPARC:UPI000000D7AB; GB:U09002; NID:g558748; PIDN:
C;Superfamily: N-methyl-D-aspartate receptor 2A; glutamate receptor homology
F;428-854/Domain: glutamate receptor homology <GRH>

  Query Match             45.2%;  Score 42;  DB 2;  Length 1464;
  Best Local Similarity   46.7%;  Pred. No. 1.1e+02;
  Matches    7;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VSLVEEDQFSQNPIS 15
              |  : :|  ||||:|
Db       1018 VDSIRQDSLSQNPVS 1032


RESULT 13
S37138
protoporphyrin IX magnesium chelatase (EC 4.99.1.-) - Cryptomonas sp.
C;Species: Cryptomonas sp.
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S37138
R;Douglas, S.E.; Reith, M.
submitted to the EMBL Data Library, March 1993
A;Description: A bchI homolog, encoding a subunit of Mg chelatase, is located on the pla
A;Reference number: S37138
A;Accession: S37138
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-353 <DOU>
A;Cross-references: UNIPROT:Q39516; UNIPARC:UPI0000127871; EMBL:Z21976; NID:g398949; PID
C;Genetics:
A;Start codon: GTG
C;Superfamily: magnesium chelatase, subunit ChlI
C;Keywords: lyase

  Query Match             44.6%;  Score 41.5;  DB 2;  Length 353;
  Best Local Similarity   42.1%;  Pred. No. 26;
  Matches    8;  Conservative    5;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 VSLVEE-DQFSQNPISCFE 18
              | :||:  :| :|| :| |
Db        225 VKIVEQRSEFDKNPSACLE 243


RESULT 14
A89858
hypothetical protein SA0781 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: A89858
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: A89858
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-355 <KUR>
A;Cross-references: UNIPROT:Q99VP6; UNIPARC:UPI00000C7F68; GB:BA000018; PID:g13700723; P
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA0781

  Query Match             44.6%;  Score 41.5;  DB 2;  Length 355;
  Best Local Similarity   34.6%;  Pred. No. 26;
  Matches    9;  Conservative    3;  Mismatches    5;  Indels    9;  Gaps    1;

Qy          1 VSLVEEDQF---------SQNPISCF 17
              | ::|| ||          | |: ||
Db        106 VKIIEEQQFKCHIDTIIKKQVPVCCF 131


RESULT 15
T16128
hypothetical protein F21H12.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16128
R;Favello, T.
submitted to the EMBL Data Library, July 1995
A;Description: The sequence of C. elegans cosmid F21H12.
A;Reference number: Z18464
A;Accession: T16128
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-632 <FAV>
A;Cross-references: UNIPROT:Q09312; UNIPARC:UPI000012A562; EMBL:U23176; NID:g726404; PID:
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:F21H12.5
A;Introns: 14/3; 92/3; 151/2; 235/3; 440/2; 483/2; 551/2

  Query Match             44.6%;  Score 41.5;  DB 2;  Length 632;
  Best Local Similarity   56.2%;  Pred. No. 50;
  Matches    9;  Conservative    2;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          2 SLVEEDQFSQNPISCF 17
              | :| | |||| : ||
Db        115 SRLESDDFSQN-VRCF 129


Search completed: November 21, 2006, 20:09:22
Job time : 22.3578 secs
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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: November 21, 2006, 19:59:24 ; Search time 26.367 Seconds
(without alignments)
631.482 Million cell updates/sec

Title: US-10-063-553-48_COPY_32_49
Perfect score: 93
Sequence: 1 VSLVEEDQFSQNPISCFE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	93	100.0	229	2	Q53R12_HUMAN	Q53r12 homo sapien
2	93	100.0	229	2	Q5U609_HUMAN	Q5u609 homo sapien
3	93	100.0	229	2	Q6UWS1_HUMAN	Q6uws1 homo sapien
4	93	100.0	229	2	Q9H5X9_HUMAN	Q9h5x9 homo sapien
5	71	76.3	230	2	Q3T0Z4_BOVIN	Q3t0z4 bos taurus
6	70	75.3	226	2	Q9CQY8_MOUSE	Q9cqy8 m 11 days p
7	70	75.3	226	2	Q9D3Q0_MOUSE	Q9d3q0 mus musculu
8	70	75.3	226	2	Q9D3R0_MOUSE	Q9d3r0 mus musculu
9	48	51.6	445	2	Q3FNJ8_9BURK	Q3fnj8 rhodoferax
10	48	51.6	505	2	Q43H61_9CHLB	Q43h61 chlorobium
11	47	50.5	126	2	Q9C252_NEUCR	Q9c252 neurospora
12	46	49.5	601	2	Q7V7K2_PROMM	Q7v7k2 prochloroco
13	45.5	48.9	299	2	Q3IFH2_PSEHT	Q3ifh2 pseudoalter
14	45	48.4	143	2	Q4N5J1_THEPA	Q4n5j1 theileria p
15	45	48.4	238	2	Q7T301_BRARE	Q7t301 brachydanio
16	45	48.4	410	2	Q9VDK6_DROME	Q9vdk6 drosophila
17	45	48.4	575	2	Q61CF7_CAEBR	Q61cf7 caenorhabdi
18	45	48.4	805	2	Q55DX2_DICDI	Q55dx2 dictyosteli
19	44	47.3	1273	1	GYRA_MYCLE	Q57532 mycobacteri
20	44	47.3	1710	2	Q4RM05_TETNG	Q4rm05 tetraodon n
21	43.5	46.8	1144	2	Q612X4_CAEBR	Q612x4 caenorhabdi
22	43	46.2	124	2	Q8ILR4_PLAF7	Q8ilr4 plasmodium
23	43	46.2	216	2	Q58AT8_CAEEL	Q58at8 caenorhabdi
24	43	46.2	435	2	Q54F45_DICDI	Q54f45 dictyosteli
25	43	46.2	491	2	Q90D04_9HIV1	Q90d04 human immun
26	43	46.2	518	2	Q9XII0_ARATH	Q9xii0 arabidopsis
27	43	46.2	601	1	PTR2_YEAST	P32901 saccharomyc
28	43	46.2	889	2	Q36EJ0_9GAMM	Q36ej0 shewanella
29	43	46.2	890	2	Q87GP6_VIBPA	Q87gp6 vibrio para
30	43	46.2	1112	2	Q4N6M1_THEPA	Q4n6m1 theileria p
31	43	46.2	1418	2	Q86HT4_DICDI	Q86ht4 dictyosteli
32	43	46.2	1466	2	Q554X7_DICDI	Q554x7 dictyosteli
33	43	46.2	1679	2	Q7PHR1_ANOGA	Q7phr1 anopheles g
34	43	46.2	1749	2	Q7RGH9_PLAYO	Q7rgh9 plasmodium
35	43	46.2	3005	2	Q50LG3_ALTAL	Q50lg3 alternaria
36	42.5	45.7	209	2	Q8W1X7_ALLCE	Q8w1x7 allium cepa
37	42	45.2	87	2	Q57L77_SALCH	Q57177 salmonella
38	42	45.2	182	2	Q582P7_9TRYP	Q582p7 trypanosoma
39	42	45.2	226	2	Q5LZL6_STRT1	Q5lzl6 streptococc
40	42	45.2	226	2	Q5M469_STRT2	Q5m469 streptococc
41	42	45.2	264	2	Q3MF69_ANAVT	Q3mf69 anabaena va
42	42	45.2	316	2	Q12956_HUMAN	Q12956 homo sapien
43	42	45.2	388	2	Q8KLJ8_STRTO	Q8klj8 streptomyce
44	42	45.2	420	2	Q9SNC3_ARATH	Q9snc3 arabidopsis
45	42	45.2	454	2	Q8IWI3_HUMAN	Q8iwi3 homo sapien
46	42	45.2	467	2	Q40KH4_EHRCH	Q40kh4 ehrlichia c
47	42	45.2	472	2	Q50VT4_ENTHI	Q50vt4 entamoeba h
48	42	45.2	480	2	Q3GK57_CHLVI	Q3gk57 prosthecoch
49	42	45.2	519	2	Q3U0W0_MOUSE	Q3u0w0 mus musculu
50	42	45.2	522	2	Q60694_MOUSE	Q60694 mus musculu
51	42	45.2	525	2	Q4VAD6_MOUSE	Q4vad6 mus musculu
52	42	45.2	549	2	Q8JTM8_LSDV	Q8jtm8 lumpy skin
53	42	45.2	550	2	Q91ML3_LSDV	Q91ml3 lumpy skin
54	42	45.2	551	2	Q8JTY6_LSDV	Q8jty6 lumpy skin
55	42	45.2	681	2	Q12957_HUMAN	Q12957 homo sapien
56	42	45.2	762	2	Q6AMC0_DESPS	Q6amc0 desulfotale
57	42	45.2	808	2	Q34YJ8_9GAMM	Q34yj8 alkalilimni
58	42	45.2	853	2	Q9CW43_MOUSE	Q9cw43 mus musculu
59	42	45.2	868	2	Q21992_CAEEL	Q21992 caenorhabdi
60	42	45.2	900	2	Q6EQM5_ORYSA	Q6eqm5 oryza sativ
61	42	45.2	925	2	Q336Q1_ORYSA	Q336q1 oryza sativ
62	42	45.2	948	2	Q8S7M6_ORYSA	Q8s7m6 oryza sativ
63	42	45.2	1027	2	Q4CXP0_TRYCR	Q4cxp0 trypanosoma
64	42	45.2	1065	2	Q2L6Y2_CAEEL	Q2l6y2 caenorhabdi
65	42	45.2	1082	2	Q8VIG1_MOUSE	Q8vig1 mus musculu
66	42	45.2	1097	2	Q13127_HUMAN	Q13127 homo sapien
67	42	45.2	1126	2	Q59ER1_HUMAN	Q59er1 homo sapien
68	42	45.2	1464	1	NMDE1_HUMAN	Q12879 homo sapien
69	42	45.2	1464	1	NMDE1_PANTR	Q5is45 pan troglod
70	42	45.2	1464	2	Q547U9_HUMAN	Q547u9 homo sapien
71	42	45.2	1491	2	Q59EW6_HUMAN	Q59ew6 homo sapien
72	42	45.2	1587	2	Q53P23_ORYSA	Q53p23 oryza sativ
73	42	45.2	2418	2	Q8I1R9_PLAF7	Q8i1r9 plasmodium
74	42	45.2	3602	2	Q4DEC1_TRYCR	Q4dec1 trypanosoma
75	42	45.2	4337	2	Q54B24_DICDI	Q54b24 dictyosteli
76	41.5	44.6	353	1	CHLI_GUITH	Q39516 guillardia
77	41.5	44.6	355	2	Q931V4_STAAM	Q931v4 staphylococ
78	41.5	44.6	355	2	Q99VF6_STAAN	Q99vf6 staphylococ
79	41.5	44.6	632	1	FBF2_CAEEL	Q09312 caenorhabdi
80	41	44.1	32	2	Q3DPG0_STRAG	Q3dpg0 streptococc
81	41	44.1	115	2	Q2U636_ASPOR	Q2u636 aspergillus
82	41	44.1	160	2	Q4XX10_PLACH	Q4xx10 plasmodium
83	41	44.1	187	2	Q5TF17_HUMAN	Q5tf17 homo sapien
84	41	44.1	239	1	GRPE_PROMP	Q7v3q4 prochloroco
85	41	44.1	254	2	Q76930_9HIV2	Q76930 human immun
86	41	44.1	259	2	Q5C507_SCHJA	Q5c507 schistosoma
87	41	44.1	260	2	Q8LFC3_ARATH	Q8lfc3 arabidopsis
88	41	44.1	300	2	Q2RZH0_9SPHI	Q2rzh0 salinibacte
89	41	44.1	302	2	O54964_RAT	O54964 rattus norv
90	41	44.1	316	2	Q6PNE0_HUMAN	Q6pne0 homo sapien
91	41	44.1	319	1	SPY1_HUMAN	O43609 homo sapien
92	41	44.1	326	1	MPPD1_HUMAN	O15442 homo sapien
93	41	44.1	326	1	MPPD1_MOUSE	Q91zg2 mus musculu
94	41	44.1	326	2	Q3TMS4_MOUSE	Q3tms4 mus musculu
95	41	44.1	326	2	Q3TYC7_MOUSE	Q3tyc7 mus musculu
96	41	44.1	334	2	Q50SV9_ENTHI	Q50sv9 entamoeba h
97	41	44.1	339	2	Q6FEN2_ACIAD	Q6fen2 acinetobact
98	41	44.1	351	2	Q44J37_CHRSL	Q44j37 chromohalob
99	41	44.1	362	2	Q54EV8_DICDI	Q54ev8 dictyosteli
100	41	44.1	388	2	Q4SXK3_TETNG	Q4sxk3 tetraodon n
101	41	44.1	400	2	Q5RGZ5_BRARE	Q5rgz5 brachydanio
102	41	44.1	402	2	Q9SRU1_ARATH	Q9sru1 arabidopsis
103	41	44.1	416	2	Q467V5_METBA	Q467v5 methanosarc
104	41	44.1	421	2	Q38HR7_HIRME	Q38hr7 hirudo medi

105	41	44.1	421	2	Q5E9M2_BOVIN	Q5e9m2	bos taurus
106	41	44.1	421	2	Q5E9P4_BOVIN	Q5e9p4	bos taurus
107	41	44.1	421	2	Q5EAB8_BOVIN	Q5eab8	bos taurus
108	41	44.1	439	2	Q38KG0_TETTH	Q38kg0	tetrahymena
109	41	44.1	449	2	O22822_ARATH	O22822	arabidopsis
110	41	44.1	452	2	Q2TA94_MOUSE	Q2ta94	mus musculu
111	41	44.1	454	2	Q41EX1_9BACI	Q41ex1	exiguobacte
112	41	44.1	496	1	CBLC_MOUSE	Q80xl1	mus musculu
113	41	44.1	510	2	Q4RUC1_TETNG	Q4ruc1	tetraodon n
114	41	44.1	512	2	Q93ZR8_ARATH	Q93zr8	arabidopsis
115	41	44.1	526	2	Q4S3S8_TETNG	Q4s3s8	tetraodon n
116	41	44.1	545	2	Q9HEK1_NEUCR	Q9hek1	neurospora
117	41	44.1	559	2	Q53PG5_ORYSA	Q53pg5	oryza sativ
118	41	44.1	564	2	Q7RVW0_NEUCR	Q7rvw0	neurospora
119	41	44.1	595	2	Q2WK51_CLOBE	Q2wk51	clostridium
120	41	44.1	606	2	Q6Y9B1_BORHE	Q6y9b1	borrelia he
121	41	44.1	606	2	Q8BI29_MOUSE	Q8bi29	mus musculu
122	41	44.1	609	2	Q7R0R9_GIALA	Q7r0r9	giardia lam
123	41	44.1	739	2	Q4T141_TETNG	Q4t141	tetraodon n
124	41	44.1	766	1	PRTP_EHV1	P68351	equine herp
125	41	44.1	766	1	PRTP_EHV1B	Q6dlh9	equine herp
126	41	44.1	766	1	PRTP_EHV1V	Q6s6n9	equine herp
127	41	44.1	793	1	LHR2A_MOUSE	Q99kc8	mus musculu
128	41	44.1	793	2	Q3TTU2_MOUSE	Q3ttu2	mus musculu
129	41	44.1	793	2	Q3UVU1_MOUSE	Q3uvu1	mus musculu
130	41	44.1	793	2	Q3V3F2_MOUSE	Q3v3f2	mus musculu
131	41	44.1	794	2	Q2UCR0_ASPOR	Q2ucr0	aspergillus
132	41	44.1	822	1	LHR2A_RAT	Q75we7	rattus norv
133	41	44.1	822	2	Q4S8A9_TETNG	Q4s8a9	tetraodon n
134	41	44.1	837	1	SYFB_PROMA	Q7vbx6	prochloroco
135	41	44.1	925	1	YE9G_SCHPO	O13776	schizosacch
136	41	44.1	929	2	Q4RW90_TETNG	Q4rw90	tetraodon n
137	41	44.1	1069	2	O54963_RAT	O54963	rattus norv
138	41	44.1	1117	2	Q9SED7_AEGVE	Q9sed7	aegilops ve
139	41	44.1	1337	2	Q4WHR7_ASPFU	Q4whr7	aspergillus
140	41	44.1	1447	2	Q5CFG8_CRYHO	Q5cfg8	cryptospori
141	41	44.1	2270	2	Q6BGF9_PARTE	Q6bgf9	paramecium
142	41	44.1	11696	2	Q5CV09_CRYPV	Q5cv09	cryptospori
143	40.5	43.5	496	2	Q4UEB8_THEAN	Q4ueb8	theileria a
144	40.5	43.5	792	1	SYFB_CHLPN	Q9z7w0	chlamydia p
145	40.5	43.5	801	2	Q95LI3_BOVIN	Q95li3	bos taurus
146	40.5	43.5	894	2	Q9BJD6_STRPU	Q9bjd6	strongyloce
147	40.5	43.5	2274	2	Q54W13_DICDI	Q54w13	dictyosteli
148	40	43.0	95	1	SCR23_ARATH	P82642	arabidopsis
149	40	43.0	235	1	Y559_MYCPN	P75219	mycoplasma
150	40	43.0	242	2	Q4KL96_XENLA	Q4kl96	xenopus lae
151	40	43.0	245	2	Q3F7G6_9BURK	Q3f7g6	burkholderi
152	40	43.0	251	2	Q43IL4_9CHLB	Q43il4	chlorobium
153	40	43.0	267	2	Q9D9F7_MOUSE	Q9d9f7	mus musculu
154	40	43.0	276	2	Q50TC5_ENTHI	Q50tc5	entamoeba h
155	40	43.0	277	1	LGT_BACSK	Q5wdh2	bacillus cl
156	40	43.0	312	2	Q93RA5_THETH	Q93ra5	thermus the
157	40	43.0	317	1	PHEG_AGLNE	P34784	aglaothamni
158	40	43.0	323	2	Q4CMT4_TRYCR	Q4cmt4	trypanosoma
159	40	43.0	332	2	Q8QFN6_ELAQU	Q8qfn6	elaphe quad
160	40	43.0	332	2	Q8QFN7_ELAQU	Q8qfn7	elaphe quad
161	40	43.0	348	2	Q6QHD1_ORYSA	Q6qhd1	oryza sativ
162	40	43.0	348	2	Q6IEL0_ORYSA	Q6iel0	oryza sativ
163	40	43.0	356	2	Q962C9_PODCA	Q962c9	podocoryne
164	40	43.0	369	2	Q8JV08_CSV	Q8jv08	campoletis
165	40	43.0	370	2	Q5F3Z4_CHICK	Q5f3z4	gallus gall
166	40	43.0	373	2	Q3TQG0_MOUSE	Q3tqg0	mus musculu
167	40	43.0	373	2	Q8BQU1_MOUSE	Q8bqu1	mus musculu
168	40	43.0	390	2	Q6L5S8_STROR	Q6l5s8	streptococc
169	40	43.0	392	2	Q4L5J4_STAHJ	Q4l5j4	staphylococ
170	40	43.0	398	2	Q7SYC4_BRARE	Q7syc4	brachydanio
171	40	43.0	405	2	Q5AVS5_EMENI	Q5avs5	aspergillus
172	40	43.0	405	2	Q31DB1_PROM9	Q31db1	prochloroco
173	40	43.0	419	2	Q4B9S3_BURVI	Q4b9s3	burkholderi
174	40	43.0	421	2	Q9NXT9_HUMAN	Q9nxt9	homo sapien
175	40	43.0	430	2	Q93KW3_STRVR	Q93kw3	streptomyce
176	40	43.0	445	2	Q86YG4_HUMAN	Q86yg4	homo sapien
177	40	43.0	446	2	Q5AD28_CANAL	Q5ad28	candida alb
178	40	43.0	456	2	Q4RR95_TETNG	Q4rr95	tetraodon n
179	40	43.0	457	2	Q99KJ4_MOUSE	Q99kj4	mus musculu
180	40	43.0	484	2	Q78J30_MOUSE	Q78j30	mus musculu
181	40	43.0	510	2	Q61LS7_CAEBR	Q61ls7	caenorhabdi
182	40	43.0	510	2	Q8JAI1_SIVCZ	Q8jai1	chimpanzee
183	40	43.0	512	2	Q8JAH2_SIVCZ	Q8jah2	chimpanzee
184	40	43.0	527	2	Q9NIV0_DICDI	Q9niv0	dictyosteli
185	40	43.0	534	2	Q6NRT8_XENLA	Q6nrt8	xenopus lae
186	40	43.0	578	2	Q57V46_9TRYP	Q57v46	trypanosoma
187	40	43.0	596	2	Q5FUU2_GLUOX	Q5fuu2	gluconobact
188	40	43.0	600	2	Q6TFL4_HUMAN	Q6tfl4	homo sapien
189	40	43.0	600	2	Q56A24_RAT	Q56a24	rattus norv
190	40	43.0	600	2	Q812D9_RAT	Q812d9	rattus norv
191	40	43.0	600	2	Q8BRG6_MOUSE	Q8brg6	mus musculu
192	40	43.0	615	2	Q804Q2_GADMO	Q804q2	gadus morhu
193	40	43.0	616	2	Q5AR94_EMENI	Q5ar94	aspergillus
194	40	43.0	618	2	Q92200_EMENI	Q92200	emericella
195	40	43.0	619	2	Q4RV91_TETNG	Q4rv91	tetraodon n
196	40	43.0	620	2	Q9N9D4_9DIPT	Q9n9d4	megaselia a
197	40	43.0	624	2	Q9D5K3_MOUSE	Q9d5k3	mus musculu
198	40	43.0	627	2	Q4GZ34_9TRYP	Q4gz34	trypanosoma
199	40	43.0	695	1	SYTC_RAT	Q5xhy5	rattus norv
200	40	43.0	722	1	SYTC_MOUSE	Q9d0r2	mus musculu
201	40	43.0	722	2	Q3TL42_MOUSE	Q3tl42	m blastocys
202	40	43.0	722	2	Q3U630_MOUSE	Q3u630	mus musculu
203	40	43.0	735	2	Q7X1P3_9LACT	Q7x1p3	lactococcus
204	40	43.0	818	2	Q429H4_DESHA	Q429h4	desulfitoba
205	40	43.0	855	2	Q80TM0_MOUSE	Q80tm0	mus musculu
206	40	43.0	888	2	Q6LJF0_PHOPR	Q6ljf0	photobacter
207	40	43.0	934	2	Q7SDE7_NEUCR	Q7sde7	neurospora
208	40	43.0	943	2	Q7QE10_ANOGA	Q7qe10	anopheles g
209	40	43.0	971	2	Q5ISN1_MACFA	Q5isn1	macaca fasc
210	40	43.0	1011	2	Q2TYA3_ASPOR	Q2tya3	aspergillus
211	40	43.0	1052	2	Q5TUB0_ANOGA	Q5tub0	anopheles g
212	40	43.0	1056	2	Q4PI36_USTMA	Q4pi36	ustilago ma
213	40	43.0	1197	2	Q2NKI6_HUMAN	Q2nki6	homo sapien
214	40	43.0	1215	2	Q54AY2_DICDI	Q54ay2	dictyosteli
215	40	43.0	1222	2	Q513V5_ENTHI	Q513v5	entamoeba h
216	40	43.0	1438	2	Q2RAX4_ORYSA	Q2rax4	oryza sativ
217	40	43.0	1476	1	ATP7A_CRIGR	P49015	cricetulus
218	40	43.0	1482	2	Q4F8H5_BRARE	Q4f8h5	brachydanio
219	40	43.0	1491	1	ATP7A_MOUSE	Q64430	mus musculu
220	40	43.0	1492	1	ATP7A_RAT	P70705	rattus norv
221	40	43.0	1500	1	ATP7A_HUMAN	Q04656	homo sapien
222	40	43.0	1500	2	Q5JQN4_HUMAN	Q5jqn4	homo sapien
223	40	43.0	1590	2	Q6BCX2_MOUSE	Q6bcx2	mus musculu
224	40	43.0	1591	1	UN13B_HUMAN	O14795	homo sapien
225	40	43.0	1591	1	UN13B_MOUSE	Q9z1n9	mus musculu
226	40	43.0	1591	2	Q5VYM8_HUMAN	Q5vym8	homo sapien
227	40	43.0	1592	2	Q5RAK9_PONPY	Q5rak9	pongo pygma
228	40	43.0	1610	2	Q2NKJ5_HUMAN	Q2nkj5	homo sapien
229	40	43.0	1620	2	Q4LE73_HUMAN	Q4le73	homo sapien
230	40	43.0	1622	1	UN13B_RAT	Q62769	rattus norv
231	40	43.0	1622	2	Q5VYM9_HUMAN	Q5vym9	homo sapien
232	40	43.0	1632	2	Q4DWH5_TRYCR	Q4dwh5	trypanosoma
233	40	43.0	1944	2	Q4TBR0_TETNG	Q4tbr0	tetraodon n
234	40	43.0	1945	2	Q7RZX2_NEUCR	Q7rzx2	neurospora
235	40	43.0	2458	2	Q4Q772_LEIMA	Q4q772	leishmania
236	40	43.0	3047	2	Q4SZ59_TETNG	Q4sz59	tetraodon n
237	40	43.0	3463	2	Q7R1E2_GIALA	Q7r1e2	giardia lam
238	40	43.0	4202	2	Q8I2S8_PLAF7	Q8i2s8	plasmodium
239	39.5	42.5	401	2	Q40KW3_DESAC	Q40kw3	desulfuromo
240	39.5	42.5	794	1	NU107_SCHPO	Q10331	schizosacch
241	39.5	42.5	1137	2	O82196_ARATH	O82196	arabidopsis
242	39	41.9	71	2	Q84585_PBCV1	Q84585	paramecium
243	39	41.9	85	2	O44779_CAEEL	O44779	caenorhabdi
244	39	41.9	89	2	Q61XE2_CAEBR	Q61xe2	caenorhabdi
245	39	41.9	112	2	Q9F1P2_BURCE	Q9f1p2	burkholderi
246	39	41.9	118	2	Q50ZT6_ENTHI	Q50zt6	entamoeba h
247	39	41.9	122	2	Q4T3X8_TETNG	Q4t3x8	tetraodon n
248	39	41.9	129	2	Q4JA85_SULAC	Q4ja85	sulfolobus
249	39	41.9	132	2	Q9GV20_CIOSA	Q9gv20	ciona savig
250	39	41.9	145	2	Q7MRQ4_WOLSU	Q7mrq4	wolinella s

251	39	41.9	147	2	Q4XW43_PLACH	Q4xw43 plasmodium
252	39	41.9	151	2	Q4LZ05_9BURK	Q4lz05 burkholderi
253	39	41.9	152	2	Q8SXQ3_DROME	Q8sxq3 drosophila
254	39	41.9	152	2	O96067_DROME	O96067 drosophila
255	39	41.9	157	2	Q4UE00_THEAN	Q4ue00 theileria a
256	39	41.9	158	2	Q48BS2_PSE14	Q48bs2 pseudomonas
257	39	41.9	165	2	Q97SM3_STRPN	Q97sm3 streptococc
258	39	41.9	185	2	Q41MS4_METBU	Q41ms4 methanococc
259	39	41.9	193	2	Q56AQ2_9VIRU	Q56aq2 bacillus th
260	39	41.9	197	2	Q65JT8_BACLD	Q65jt8 bacillus li
261	39	41.9	198	2	Q8DT46_STRMU	Q8dt46 streptococc
262	39	41.9	199	2	Q4VXJ0_HUMAN	Q4vxj0 homo sapien
263	39	41.9	200	2	Q7PRQ6_ANOGA	Q7prq6 anopheles g
264	39	41.9	200	2	Q8II35_PLAF7	Q8ii35 plasmodium
265	39	41.9	203	2	Q5L2Y1_GEOKA	Q5l2y1 geobacillus
266	39	41.9	214	2	Q9PKG5_CHLMU	Q9pkg5 chlamydia m
267	39	41.9	220	2	Q5QT25_ORYSA	Q5qt25 oryza sativ
268	39	41.9	221	2	Q2ZB00_9GAMM	Q2zb00 shewanella
269	39	41.9	241	2	Q2KJG0_BOVIN	Q2kjg0 bos taurus
270	39	41.9	241	2	Q63K88_BURPS	Q63k88 burkholderi
271	39	41.9	252	2	Q3NDF0_9PROT	Q3ndf0 nitrosomona
272	39	41.9	255	2	Q3JL85_BURP1	Q3jl85 burkholderi
273	39	41.9	255	2	Q62CU2_BURMA	Q62cu2 burkholderi
274	39	41.9	277	1	XAPA_ECOLI	P45563 escherichia
275	39	41.9	279	2	Q731F9_BACC1	Q731f9 bacillus ce
276	39	41.9	285	2	Q6XR96_9BACT	Q6xr96 uncultured
277	39	41.9	314	1	Y207_ENCCU	Q8swh5 encephalito
278	39	41.9	316	2	Q6MJG1_BDEBA	Q6mjg1 bdellovibri
279	39	41.9	319	1	PHEG_COROI	P83592 corallina o
280	39	41.9	319	2	Q7XZS8_COROI	Q7xzs8 corallina o
281	39	41.9	324	2	Q49872_MYCLE	Q49872 mycobacteri
282	39	41.9	327	2	Q50XN8_ENTHI	Q50xn8 entamoeba h
283	39	41.9	328	2	Q9V4H8_DROME	Q9v4h8 drosophila
284	39	41.9	331	1	LDHC_PIG	Q9tsx5 sus scrofa
285	39	41.9	331	1	PLIB_AGKBL	O93233 agkistrodon
286	39	41.9	351	2	Q3ALZ0_SYNSC	Q3alz0 synechococc
287	39	41.9	363	2	Q7NQT2_CHRVO	Q7nqt2 chromobacte
288	39	41.9	366	2	Q2UF22_ASPOR	Q2uf22 aspergillus
289	39	41.9	381	2	Q388E9_9TRYP	Q388e9 trypanosoma
290	39	41.9	381	2	Q8WRU3_9TRYP	Q8wru3 trypanosoma
291	39	41.9	381	2	Q505M0_XENLA	Q505m0 xenopus lae
292	39	41.9	395	2	Q7PKD4_ANOGA	Q7pkd4 anopheles g
293	39	41.9	416	2	Q3CB69_9CLOT	Q3cb69 alkaliphilu
294	39	41.9	422	2	Q5LH60_BACFN	Q51h60 bacteroides
295	39	41.9	424	2	Q64Y19_BACFR	Q64y19 bacteroides
296	39	41.9	427	2	Q3IDF2_PSEHT	Q3idf2 pseudoalter
297	39	41.9	428	2	Q577Z9_BRUAB	Q577z9 brucella ab
298	39	41.9	428	2	Q8FW63_BRUSU	Q8fw63 brucella su
299	39	41.9	428	2	Q8YC63_BRUME	Q8yc63 brucella me
300	39	41.9	428	2	Q2YKL9_BRUA2	Q2ykl9 brucella ab
301	39	41.9	440	2	Q4XPC4_PLACH	Q4xpc4 plasmodium
302	39	41.9	450	1	PDE7B_HUMAN	Q9np56 homo sapien
303	39	41.9	450	2	Q5VWY9_HUMAN	Q5vwy9 homo sapien
304	39	41.9	450	2	Q6LFV8_PHOPR	Q6lfv8 photobacter
305	39	41.9	453	2	Q39L29_BURS3	Q39l29 burkholderi
306	39	41.9	455	2	Q4BFJ3_BURVI	Q4bfj3 burkholderi
307	39	41.9	456	2	Q3F9A4_9BURK	Q3f9a4 burkholderi
308	39	41.9	457	2	Q456C2_9BURK	Q456c2 burkholderi
309	39	41.9	458	2	Q515E5_ENTHI	Q515e5 entamoeba h
310	39	41.9	471	2	Q4IML0_GIBZE	Q4iml0 gibberella
311	39	41.9	471	2	Q35LK8_9BRAD	Q35lk8 bradyrhizob
312	39	41.9	476	2	Q8S7F0_ORYSA	Q8s7f0 oryza sativ
313	39	41.9	487	2	Q41NY4_METBU	Q41ny4 methanococc
314	39	41.9	493	2	O96286_PLAF7	O96286 plasmodium
315	39	41.9	505	2	Q9LFV2_ARATH	Q9lfv2 arabidopsis
316	39	41.9	508	2	Q4V398_ARATH	Q4v398 arabidopsis
317	39	41.9	508	2	Q5VNG4_ORYSA	Q5vng4 oryza sativ
318	39	41.9	509	2	Q6VG50_SIVCZ	Q6vg50 chimpanzee
319	39	41.9	516	2	Q8W385_ORYSA	Q8w385 oryza sativ
320	39	41.9	522	2	Q33GR3_METHU	Q33gr3 methanospir
321	39	41.9	526	2	Q8QL72_9NUCL	Q8ql72 mamestra co
322	39	41.9	538	2	Q378P9_RHOPA	Q378p9 rhodopseudo
323	39	41.9	538	2	Q6N0K3_RHOPA	Q6n0k3 rhodopseudo
324	39	41.9	542	2	Q2RS01_RHORU	Q2rs01 rhodospiril
325	39	41.9	568	2	Q41RK6_FERAC	Q41rk6 ferroplasma
326	39	41.9	576	1	PT1_BUCBP	Q89b04 buchnera ap
327	39	41.9	585	2	Q9U2Y8_CAEEL	Q9u2y8 caenorhabdi
328	39	41.9	586	2	Q4LE81_HUMAN	Q4le81 homo sapien
329	39	41.9	607	2	Q55WQ5_CRYNE	Q55wq5 cryptococcu
330	39	41.9	607	2	Q5KJJ1_CRYNE	Q5kjj1 cryptococcu
331	39	41.9	607	2	Q71A50_9NUCL	Q71a50 mamestra co
332	39	41.9	635	2	Q2WLL8_CLOBE	Q2wll8 clostridium
333	39	41.9	637	2	Q5WAV1_BACSK	Q5wav1 bacillus cl
334	39	41.9	659	2	Q6FRU1_CANGA	Q6fru1 candida gla
335	39	41.9	659	2	Q8DR86_STRR6	Q8dr86 streptococc
336	39	41.9	669	2	Q5V4P7_HALMA	Q5v4p7 haloarcula
337	39	41.9	699	2	Q4YX57_PLABE	Q4yx57 plasmodium
338	39	41.9	710	2	Q54J66_DICDI	Q54j66 dictyosteli
339	39	41.9	713	2	Q3VGJ7_9SPHN	Q3vgj7 sphingopyxi
340	39	41.9	714	2	Q86K58_DICDI	Q86k58 dictyosteli
341	39	41.9	774	2	Q7RR25_PLAYO	Q7rr25 plasmodium
342	39	41.9	784	2	Q4IN01_GIBZE	Q4in01 gibberella
343	39	41.9	809	2	Q9R9U6_PSEPU	Q9r9u6 pseudomonas
344	39	41.9	814	2	Q4RFH4_TETNG	Q4rfh4 tetraodon n
345	39	41.9	828	2	Q31E73_THICR	Q31e73 thiomicrosp
346	39	41.9	871	2	Q2LTU4_9DELT	Q2ltu4 syntrophus
347	39	41.9	923	2	Q47F71_DECAR	Q47f71 dechloromon
348	39	41.9	926	2	Q655X4_ORYSA	Q655x4 oryza sativ
349	39	41.9	929	2	O32491_BACNO	O32491 bacteroides
350	39	41.9	933	2	Q2N518_9DELT	Q2n518 desulfococc
351	39	41.9	968	2	Q32KG8_MOUSE	Q32kg8 mus musculu
352	39	41.9	999	2	Q941L1_BRANA	Q941l1 brassica na
353	39	41.9	1001	1	AHM5_ARATH	Q9s7j8 arabidopsis
354	39	41.9	1001	2	Q94KD6_ARATH	Q94kd6 arabidopsis
355	39	41.9	1012	2	Q6H6Z1_ORYSA	Q6h6z1 oryza sativ
356	39	41.9	1038	2	Q75E85_ASHGO	Q75e85 ashbya goss
357	39	41.9	1064	2	Q8XLD9_CLOPE	Q8xld9 clostridium
358	39	41.9	1077	2	Q7RDA2_PLAYO	Q7rda2 plasmodium
359	39	41.9	1124	2	Q9R0T2_RAT	Q9r0t2 rattus norv
360	39	41.9	1161	2	Q5DTZ0_MOUSE	Q5dtz0 mus musculu
361	39	41.9	1177	2	Q55JP8_CRYNE	Q55jp8 cryptococcu
362	39	41.9	1177	2	Q5K9V4_CRYNE	Q5k9v4 cryptococcu
363	39	41.9	1185	2	Q4QBV4_LEIMA	Q4qbv4 leishmania
364	39	41.9	1236	2	Q2ZBR1_9GAMM	Q2zbr1 shewanella
365	39	41.9	1236	2	Q363R0_9GAMM	Q363r0 shewanella
366	39	41.9	1299	2	Q57YF2_9TRYP	Q57yf2 trypanosoma
367	39	41.9	1334	2	Q5FFB0_EHRRG	Q5ffb0 ehrlichia r
368	39	41.9	1368	2	Q48TU5_STRPM	Q48tu5 streptococc
369	39	41.9	1368	2	Q48Z31_STRP1	Q48z31 streptococc
370	39	41.9	1368	2	Q99ZW2_STRP1	Q99zw2 streptococc
371	39	41.9	1413	2	Q4UJ10_THEAN	Q4uj10 theileria a
372	39	41.9	1415	2	Q2SJW5_9GAMM	Q2sjw5 hahella che
373	39	41.9	1432	2	Q4U3G5_CANFA	Q4u3g5 canis famil
374	39	41.9	1451	1	ATP7B_RAT	Q64535 rattus norv
375	39	41.9	1452	2	Q9QUG4_RAT	Q9qug4 rattus norv
376	39	41.9	1462	1	ATP7B_MOUSE	Q64446 mus musculu
377	39	41.9	1465	1	ATP7B_HUMAN	P35670 homo sapien
378	39	41.9	1505	1	ATP7B_SHEEP	Q9xt50 ovis aries
379	39	41.9	1626	2	Q4S7J8_TETNG	Q4s7j8 tetraodon n
380	39	41.9	1743	2	Q9XWX5_CAEEL	Q9xwx5 caenorhabdi
381	39	41.9	1868	2	Q4RYG5_TETNG	Q4ryg5 tetraodon n
382	39	41.9	2202	2	Q4QEP5_LEIMA	Q4qep5 leishmania
383	39	41.9	2291	2	Q9W1A9_DROME	Q9w1a9 drosophila
384	39	41.9	2943	2	Q8IK94_PLAF7	Q8ik94 plasmodium
385	39	41.9	5095	2	Q4Q3Q7_LEIMA	Q4q3q7 leishmania
386	38.5	41.4	169	2	Q6C1V7_YARLI	Q6c1v7 yarrowia li
387	38.5	41.4	300	2	Q76EH3_GYMSI	Q76eh3 gymnodinium
388	38.5	41.4	300	2	Q76EI5_9DINO	Q76ei5 symbiodiniu
389	38.5	41.4	355	2	Q5HHG4_STAAC	Q5hhg4 staphylococ
390	38.5	41.4	355	2	Q6GB05_STAAS	Q6gb05 staphylococ
391	38.5	41.4	355	2	Q6GIG7_STAAR	Q6gig7 staphylococ
392	38.5	41.4	355	2	Q8NXG7_STAAW	Q8nxg7 staphylococ
393	38.5	41.4	391	2	Q3FUB3_9BURK	Q3fub3 rhodoferax
394	38.5	41.4	438	2	Q9VNP8_DROME	Q9vnp8 drosophila
395	38.5	41.4	514	2	Q6BZG1_DEBHA	Q6bzg1 debaryomyce
396	38.5	41.4	583	2	Q8ENC6_OCEIH	Q8enc6 oceanobacil

397	38.5	41.4	690	2	Q8IM21_PLAF7	Q8im21	plasmodium
398	38.5	41.4	873	2	Q60MQ0_CAEBR	Q60mq0	caenorhabdi
399	38.5	41.4	2823	2	Q7RGM8_PLAYO	Q7rgm8	plasmodium
400	38	40.9	75	2	Q9NZG9_HUMAN	Q9nzg9	homo sapien
401	38	40.9	76	2	Q5TPS0_ANOGA	Q5tps0	anopheles g
402	38	40.9	81	2	Q4NCA8_9MICC	Q4nca8	arthrobacte
403	38	40.9	96	2	Q6YWJ1_ORYSA	Q6ywj1	oryza sativ
404	38	40.9	100	2	Q9ZME4_HELPJ	Q9zme4	helicobacte
405	38	40.9	101	2	Q5TYP9_BRARE	Q5typ9	brachydanio
406	38	40.9	104	1	DIRC1_HUMAN	Q969h9	homo sapien
407	38	40.9	122	2	Q4WVQ2_ASPFU	Q4wvq2	aspergillus
408	38	40.9	122	2	Q515Y4_ENTHI	Q515y4	entamoeba h
409	38	40.9	140	2	Q6ZUV6_HUMAN	Q6zuv6	homo sapien
410	38	40.9	144	2	Q5V686_HALMA	Q5v686	haloarcula
411	38	40.9	165	2	Q86U80_HUMAN	Q86u80	homo sapien
412	38	40.9	166	2	Q6LHC9_PHOPR	Q6lhc9	photobacter
413	38	40.9	176	2	Q6CD85_YARLI	Q6cd85	yarrowia li
414	38	40.9	181	2	Q4X980_PLACH	Q4x980	plasmodium
415	38	40.9	181	2	Q3X9Y2_METFL	Q3x9y2	methylobaci
416	38	40.9	183	2	Q9D2S7_MOUSE	Q9d2s7	mus musculu
417	38	40.9	186	2	Q5ZSE7_LEGPH	Q5zse7	legionella
418	38	40.9	195	2	Q4WY06_ASPFU	Q4wy06	aspergillus
419	38	40.9	201	2	Q8C5I2_MOUSE	Q8c5i2	mus musculu
420	38	40.9	202	2	Q8LMX9_ORYSA	Q8lmx9	oryza sativ
421	38	40.9	205	2	Q4XCI5_PLACH	Q4xci5	plasmodium
422	38	40.9	213	2	Q45UF1_9REOV	Q45uf1	adult diarr
423	38	40.9	214	2	Q7S2G9_NEUCR	Q7s2g9	neurospora
424	38	40.9	215	2	Q54730_SYNP7	Q54730	synechococc
425	38	40.9	216	2	Q5N261_SYNP6	Q5n261	synechococc
426	38	40.9	217	2	Q9LIJ7_ARATH	Q9lij7	arabidopsis
427	38	40.9	219	2	Q8PSS8_METMA	Q8pss8	methanosarc
428	38	40.9	219	2	Q8Q0G6_METMA	Q8q0g6	methanosarc
429	38	40.9	224	2	Q5W400_9HIV1	Q5w400	human immun
430	38	40.9	225	2	Q7VPY1_CHLPN	Q7vpy1	chlamydia p
431	38	40.9	225	2	Q9Z7X2_CHLPN	Q9z7x2	chlamydia p
432	38	40.9	228	2	Q31S52_SYNP7	Q31s52	synechococc
433	38	40.9	236	2	Q57V30_9TRYP	Q57v30	trypanosoma
434	38	40.9	236	2	Q2L6M2_DUGJA	Q216m2	dugesia jap
435	38	40.9	266	2	Q41LZ3_METBU	Q41lz3	methanococc
436	38	40.9	272	2	Q36CW7_9GAMM	Q36cw7	shewanella
437	38	40.9	276	2	Q92N72_RHIME	Q92n72	rhizobium m
438	38	40.9	277	2	Q8FFC6_ECOL6	Q8ffc6	escherichia
439	38	40.9	280	2	Q2NH92_9EURY	Q2nh92	methanospha
440	38	40.9	287	2	Q97XZ6_SULSO	Q97xz6	sulfolobus
441	38	40.9	288	2	Q5HU35_CAMJR	Q5hu35	campylobact
442	38	40.9	288	2	Q9PNM5_CAMJE	Q9pnm5	campylobact
443	38	40.9	297	2	Q5NGL9_FRATT	Q5ngl9	francisella
444	38	40.9	303	2	Q9PVG2_XENLA	Q9pvg2	xenopus lae
445	38	40.9	309	2	Q7ZAV1_9HIV1	Q7zav1	human immun
446	38	40.9	319	2	Q5Y172_XENTR	Q5y172	xenopus tro
447	38	40.9	324	2	Q4R6T4_MACFA	Q4r6t4	macaca fasc
448	38	40.9	331	1	LDHC_VULVU	Q29563	vulpes vulp
449	38	40.9	337	2	Q5ULS2_9CAUD	Q5uls2	lactobacill
450	38	40.9	339	1	RAD51_CANFA	Q8mki8	canis famil
451	38	40.9	339	1	RAD51_CRIGR	P70099	cricetulus
452	38	40.9	339	1	RAD51_HUMAN	Q06609	homo sapien
453	38	40.9	339	1	RAD51_MOUSE	Q08297	mus musculu
454	38	40.9	339	2	Q5U0A5_HUMAN	Q5u0a5	homo sapien
455	38	40.9	339	2	Q6FHX9_HUMAN	Q6fhx9	homo sapien
456	38	40.9	339	2	Q2KJ94_BOVIN	Q2kj94	bos taurus
457	38	40.9	339	2	Q3UAY5_MOUSE	Q3uay5	m bone marr
458	38	40.9	340	2	Q6ZNA8_HUMAN	Q6zna8	homo sapien
459	38	40.9	345	1	YGN8_YEAST	P53122	saccharomyc
460	38	40.9	351	2	Q5AF67_CANAL	Q5af67	candida alb
461	38	40.9	354	2	Q4WM90_ASPFU	Q4wm90	aspergillus
462	38	40.9	361	2	Q97RN5_STRPN	Q97rn5	streptococc
463	38	40.9	364	2	Q5DEP0_SCHJA	Q5dep0	schistosoma
464	38	40.9	366	2	Q48A60_COLP3	Q48a60	colwellia p
465	38	40.9	369	2	Q74NA2_NANEQ	Q74na2	nanoarchaeu
466	38	40.9	370	2	Q4DH98_TRYCR	Q4dh98	trypanosoma
467	38	40.9	381	2	Q3P6A8_9GAMM	Q3p6a8	shewanella
468	38	40.9	385	2	Q93787_CAEEL	Q93787	caenorhabdi
469	38	40.9	386	2	Q2LWH3_9DELT	Q2lwh3	syntrophus
470	38	40.9	392	2	Q7ZVV4_BRARE	Q7zvv4	brachydanio
471	38	40.9	393	2	Q3B8M6_XENLA	Q3b8m6	xenopus lae
472	38	40.9	393	2	Q5XGG8_XENTR	Q5xgg8	xenopus tro
473	38	40.9	395	1	TF2H2_HUMAN	Q13888	homo sapien
474	38	40.9	395	2	Q6P1K8_HUMAN	Q6p1k8	homo sapien
475	38	40.9	395	2	Q2TBV5_BOVIN	Q2tbv5	bos taurus
476	38	40.9	395	2	Q4T3D5_TETNG	Q4t3d5	tetraodon n
477	38	40.9	395	2	Q6GR42_XENLA	Q6gr42	xenopus lae
478	38	40.9	396	1	TF2H2_MOUSE	Q9jib4	mus musculu
479	38	40.9	396	2	Q7TPV0_MOUSE	Q7tpv0	mus musculu
480	38	40.9	398	2	Q91YN8_MOUSE	Q91yn8	mus musculu
481	38	40.9	406	2	Q4CYA6_TRYCR	Q4cya6	trypanosoma
482	38	40.9	407	2	Q6BHM6_DEBHA	Q6bhm6	debaryomyce
483	38	40.9	414	1	PP2C3_SCHPO	Q09173	schizosacch
484	38	40.9	414	2	Q3C9H8_9CLOT	Q3c9h8	alkaliphilu
485	38	40.9	421	2	Q6GMC6_XENLA	Q6gmc6	xenopus lae
486	38	40.9	424	2	Q96T72_HUMAN	Q96t72	homo sapien
487	38	40.9	425	2	Q4V7N9_XENLA	Q4v7n9	xenopus lae
488	38	40.9	426	1	PDE7A_RAT	O08593	rattus norv
489	38	40.9	428	2	Q53WL0_ORYSA	Q53wl0	oryza sativ
490	38	40.9	429	2	Q5QMR2_ORYSA	Q5qmr2	oryza sativ
491	38	40.9	429	2	Q3IY56_RHOS4	Q3iy56	rhodobacter
492	38	40.9	429	2	Q8GAH1_ARTNI	Q8gah1	arthrobacte
493	38	40.9	430	2	O31226_ARTNI	O31226	arthrobacte
494	38	40.9	432	2	Q6LZB4_METMP	Q6lzb4	methanococc
495	38	40.9	433	2	Q2U045_ASPOR	Q2u045	aspergillus
496	38	40.9	436	1	MBX1_SCHPO	O42954	schizosacch
497	38	40.9	441	2	Q4Y727_PLACH	Q4y727	plasmodium
498	38	40.9	443	2	Q2UGN2_ASPOR	Q2ugn2	aspergillus
499	38	40.9	446	2	Q9C7Z9_ARATH	Q9c7z9	arabidopsis
500	38	40.9	448	1	YAP1_CHICK	P46936	gallus gall
501	38	40.9	451	2	Q4V4Z3_DROME	Q4v4z3	drosophila
502	38	40.9	455	2	Q4PDU6_USTMA	Q4pdu6	ustilago ma
503	38	40.9	455	2	Q7XUV8_ORYSA	Q7xuv8	oryza sativ
504	38	40.9	456	1	PDE7A_MOUSE	P70453	mus musculu
505	38	40.9	456	2	Q5R5B5_PONPY	Q5r5b5	pongo pygma
506	38	40.9	456	2	Q3TFY5_MOUSE	Q3tfy5	mus musculu
507	38	40.9	472	2	Q7R601_GIALA	Q7r601	giardia lam
508	38	40.9	472	2	Q3EH67_ACTSC	Q3eh67	actinobacil
509	38	40.9	472	2	Q92PH9_RHIME	Q92ph9	rhizobium m
510	38	40.9	482	1	PDE7A_HUMAN	Q13946	homo sapien
511	38	40.9	482	2	Q3U3Y7_MOUSE	Q3u3y7	mus musculu
512	38	40.9	482	2	Q6P5G2_MOUSE	Q6p5g2	mus musculu
513	38	40.9	489	2	Q8QNN7_9PHYC	Q8qnn7	ectocarpus
514	38	40.9	503	2	O23215_ARATH	O23215	arabidopsis
515	38	40.9	504	2	Q7MXT9_PORGI	Q7mxt9	porphyromon
516	38	40.9	510	2	Q5DCH4_SCHJA	Q5dch4	schistosoma
517	38	40.9	512	2	Q4V4V2_DROME	Q4v4v2	drosophila
518	38	40.9	513	2	Q2JZ79_RHIET	Q2jz79	rhizobium e
519	38	40.9	529	2	Q9PVG3_XENLA	Q9pvg3	xenopus lae
520	38	40.9	532	2	Q69VQ6_ORYSA	Q69vq6	oryza sativ
521	38	40.9	535	2	Q54EK8_DICDI	Q54ek8	dictyosteli
522	38	40.9	535	2	Q7RH26_PLAYO	Q7rh26	plasmodium
523	38	40.9	538	2	Q8IQS7_DROME	Q8iqs7	drosophila
524	38	40.9	542	2	Q4T2L3_TETNG	Q4t2l3	tetraodon n
525	38	40.9	548	2	Q3XZP3_ENTFC	Q3xzp3	enterococcu
526	38	40.9	551	2	Q9SVE6_ARATH	Q9sve6	arabidopsis
527	38	40.9	551	2	Q83DR2_COXBU	Q83dr2	coxiella bu
528	38	40.9	558	2	Q9M084_ARATH	Q9m084	arabidopsis
529	38	40.9	560	1	TATR_NPVCF	P41716	choristoneu
530	38	40.9	560	2	Q77DF7_NPVCF	Q77df7	choristoneu
531	38	40.9	562	2	Q50XK3_ENTHI	Q50xk3	entamoeba h
532	38	40.9	562	2	Q84SR2_ORYSA	Q84sr2	oryza sativ
533	38	40.9	562	2	Q3EVA8_BACTI	Q3eva8	bacillus th
534	38	40.9	565	2	Q498D7_RAT	Q498d7	rattus norv
535	38	40.9	572	2	Q4R9C1_MACFA	Q4r9c1	macaca fasc
536	38	40.9	574	1	MBRL_MOUSE	Q8civ2	mus musculu
537	38	40.9	595	2	Q55BH0_DICDI	Q55bh0	dictyosteli
538	38	40.9	605	2	Q6INS2_XENLA	Q6ins2	xenopus lae
539	38	40.9	607	1	PANX2_MOUSE	Q6imp4	mus musculu
540	38	40.9	620	1	MBRL_HUMAN	Q4zin3	homo sapien
541	38	40.9	620	2	Q8TLE0_METAC	Q8tle0	methanosarc
542	38	40.9	623	2	Q6T448_LEIMA	Q6t448	leishmania

543	38	40.9	626	2	Q6L542_ORYSA	Q6l542	oryza sativ
544	38	40.9	631	2	Q66J88_XENLA	Q66j88	xenopus lae
545	38	40.9	633	1	PANX2_HUMAN	Q96rd6	homo sapien
546	38	40.9	641	2	Q8MJD4_RABIT	Q8mjd4	oryctolagus
547	38	40.9	645	2	Q4I3R8_GIBZE	Q4i3r8	gibberella
548	38	40.9	650	2	Q8H7Z4_ORYSA	Q8h7z4	oryza sativ
549	38	40.9	653	1	KCNA4_HUMAN	P22459	homo sapien
550	38	40.9	653	2	Q5REB6_PONPY	Q5reb6	pongo pygma
551	38	40.9	654	1	KCNA4_MOUSE	Q61423	mus musculu
552	38	40.9	654	1	KCNA4_MUSPF	Q28527	mustela put
553	38	40.9	654	2	Q8CBF8_MOUSE	Q8cbf8	m 16 days n
554	38	40.9	655	1	KCNA4_RAT	P15385	rattus norv
555	38	40.9	660	1	KCNA4_BOVIN	Q05037	bos taurus
556	38	40.9	661	2	Q9GLF1_BOVIN	Q9glf1	bos taurus
557	38	40.9	662	2	Q5ADT2_CANAL	Q5adt2	candida alb
558	38	40.9	664	1	PANX2_RAT	P60571	rattus norv
559	38	40.9	667	2	Q4JGM2_MOUSE	Q4jgm2	mus musculu
560	38	40.9	684	2	Q4WQY0_ASPFU	Q4wqy0	aspergillus
561	38	40.9	684	2	Q7QXI7_GIALA	Q7qxi7	giardia lam
562	38	40.9	690	2	Q5RG85_BRARE	Q5rg85	brachydanio
563	38	40.9	710	2	Q91FQ5_IRV6	Q91fq5	chilo iride
564	38	40.9	715	2	Q6CGA7_YARLI	Q6cga7	yarrowia li
565	38	40.9	723	2	Q496Z9_RAT	Q496z9	rattus norv
566	38	40.9	723	2	Q5ZLC2_CHICK	Q5zlc2	gallus gall
567	38	40.9	726	2	Q6CEG1_YARLI	Q6ceg1	yarrowia li
568	38	40.9	730	2	Q51EV6_ENTHI	Q51ev6	entamoeba h
569	38	40.9	748	1	TREB_EMENI	O42777	emericella
570	38	40.9	748	2	Q5B1E5_EMENI	Q5b1e5	aspergillus
571	38	40.9	757	1	DNM1_YEAST	P54861	saccharomyc
572	38	40.9	769	2	Q2WKR7_CLOBE	Q2wkr7	clostridium
573	38	40.9	772	1	RAD15_SCHPO	P26659	schizosacch
574	38	40.9	775	2	Q6NZF7_MOUSE	Q6nzf7	mus musculu
575	38	40.9	776	2	Q5AFV3_CANAL	Q5afv3	candida alb
576	38	40.9	790	2	Q8BLY2_MOUSE	Q8bly2	mus musculu
577	38	40.9	790	2	Q8CHT2_MOUSE	Q8cht2	mus musculu
578	38	40.9	797	2	Q5AQJ4_EMENI	Q5aqj4	aspergillus
579	38	40.9	807	2	Q8K3R3_MOUSE	Q8k3r3	mus musculu
580	38	40.9	811	2	Q9FH14_ARATH	Q9fh14	arabidopsis
581	38	40.9	814	2	Q3N3X2_9DELT	Q3n3x2	syntrophoba
582	38	40.9	819	2	Q3M6E0_ANAVT	Q3m6e0	anabaena va
583	38	40.9	827	2	Q2QSS4_ORYSA	Q2qss4	oryza sativ
584	38	40.9	831	2	Q8CDM4_MOUSE	Q8cdm4	mus musculu
585	38	40.9	841	2	Q6MDJ4_PARUW	Q6mdj4	parachlamyd
586	38	40.9	844	2	O14147_SCHPO	O14147	schizosacch
587	38	40.9	845	2	Q6EPV3_ORYSA	Q6epv3	oryza sativ
588	38	40.9	855	2	Q50SE9_ENTHI	Q50se9	entamoeba h
589	38	40.9	882	2	Q9VZQ9_DROME	Q9vzq9	drosophila
590	38	40.9	891	2	Q8IIR1_PLAF7	Q8iir1	plasmodium
591	38	40.9	913	2	P90742_CAEEL	P90742	caenorhabdi
592	38	40.9	926	2	Q7XVB0_ORYSA	Q7xvb0	oryza sativ
593	38	40.9	927	2	Q8IRD5_DROME	Q8ird5	drosophila
594	38	40.9	946	2	Q4X0P4_ASPFU	Q4x0p4	aspergillus
595	38	40.9	950	2	Q8K4M9_RAT	Q8k4m9	rattus norv
596	38	40.9	961	2	Q3UWQ7_MOUSE	Q3uwq7	mus musculu
597	38	40.9	969	2	Q7RMK2_PLAYO	Q7rmk2	plasmodium
598	38	40.9	976	2	Q54H51_DICDI	Q54h51	dictyosteli
599	38	40.9	980	2	Q2YC78_NITMU	Q2yc78	nitrosospir
600	38	40.9	984	2	Q55HV7_CRYNE	Q55hv7	cryptococcu
601	38	40.9	986	2	Q5K7E1_CRYNE	Q5k7e1	cryptococcu
602	38	40.9	992	2	Q7XRJ9_ORYSA	Q7xrj9	oryza sativ
603	38	40.9	995	2	Q4P9K4_USTMA	Q4p9k4	ustilago ma
604	38	40.9	997	1	CEBPZ_MOUSE	P53569	mus musculu
605	38	40.9	998	1	CEBPZ_HUMAN	Q03701	homo sapien
606	38	40.9	998	2	Q6NRA7_XENLA	Q6nra7	xenopus lae
607	38	40.9	1040	2	Q3TXW5_MOUSE	Q3txw5	mus musculu
608	38	40.9	1052	2	Q3TYA8_MOUSE	Q3tya8	mus musculu
609	38	40.9	1054	2	Q8NE75_HUMAN	Q8ne75	homo sapien
610	38	40.9	1068	1	PK3CA_BOVIN	P32871	bos taurus
611	38	40.9	1068	1	PK3CA_HUMAN	P42336	homo sapien
612	38	40.9	1069	2	Q4LE51_HUMAN	Q4le51	homo sapien
613	38	40.9	1073	2	Q4Q0M9_LEIMA	Q4q0m9	leishmania
614	38	40.9	1082	2	Q4PEH9_USTMA	Q4peh9	ustilago ma
615	38	40.9	1110	2	Q4IA83_GIBZE	Q4ia83	gibberella
616	38	40.9	1120	2	Q55QV1_CRYNE	Q55qv1	cryptococcu
617	38	40.9	1126	2	Q5KFB5_CRYNE	Q5kfb5	cryptococcu
618	38	40.9	1136	2	Q6I5B8_ORYSA	Q6i5b8	oryza sativ
619	38	40.9	1176	2	Q9RC30_BACTK	Q9rc30	bacillus th
620	38	40.9	1276	2	Q03016_YEAST	Q03016	saccharomyc
621	38	40.9	1291	2	Q94I49_ORYSA	Q94i49	oryza sativ
622	38	40.9	1292	2	Q8S5Q8_ORYSA	Q8s5q8	oryza sativ
623	38	40.9	1364	2	O59757_SCHPO	O59757	schizosacch
624	38	40.9	1375	2	Q2U1V1_ASPOR	Q2u1v1	aspergillus
625	38	40.9	1388	2	Q5IS90_9PRIM	Q5is90	saimiri bol
626	38	40.9	1411	2	Q6FSJ5_CANGA	Q6fsj5	candida gla
627	38	40.9	1468	2	Q3D6N9_STRAG	Q3d6n9	streptococc
628	38	40.9	1579	2	Q9ARZ4_ORYSA	Q9arz4	oryza sativ
629	38	40.9	1607	2	Q7XS00_ORYSA	Q7xs00	oryza sativ
630	38	40.9	1727	2	Q4SDE7_TETNG	Q4sde7	tetraodon n
631	38	40.9	1752	2	Q4Z6E8_PLABE	Q4z6e8	plasmodium
632	38	40.9	1781	2	Q6BK91_DEBHA	Q6bk91	debaryomyce
633	38	40.9	1847	2	Q7XSE2_ORYSA	Q7xse2	oryza sativ
634	38	40.9	2134	2	Q8CZT9_YERPE	Q8czt9	yersinia pe
635	38	40.9	2201	2	Q8ZHV3_YERPE	Q8zhv3	yersinia pe
636	38	40.9	2367	1	POL1_RRVC	Q6w8w4	r rna1 poly
637	38	40.9	3213	2	Q4HZN3_GIBZE	Q4hzn3	gibberella
638	38	40.9	3311	2	Q74QP0_YERPE	Q74qp0	yersinia pe
639	38	40.9	3577	2	Q7YV66_9TRYP	Q7yv66	trypanosoma
640	38	40.9	3886	2	Q666G1_YERPS	Q666g1	yersinia ps
641	38	40.9	4664	2	Q4QFY9_LEIMA	Q4qfy9	leishmania
642	37.5	40.3	211	2	Q3SD36_PARTE	Q3sd36	paramecium
643	37.5	40.3	219	2	Q6BFI4_PARTE	Q6bfi4	paramecium
644	37.5	40.3	327	2	Q47DV7_DECAR	Q47dv7	dechloromon
645	37.5	40.3	344	2	Q7RL10_PLAYO	Q7rl10	plasmodium
646	37.5	40.3	372	2	Q9HQQ1_HALSA	Q9hqq1	halobacteri
647	37.5	40.3	392	1	PANX3_HUMAN	Q96qz0	homo sapien
648	37.5	40.3	392	1	PANX3_MOUSE	Q8ceg0	mus musculu
649	37.5	40.3	392	1	PANX3_RAT	P60572	rattus norv
650	37.5	40.3	392	2	Q6IMP0_MOUSE	Q6imp0	mus musculu
651	37.5	40.3	804	2	Q7NAD0_PHOLL	Q7nad0	photorhabdu
652	37.5	40.3	838	2	Q9C8I5_ARATH	Q9c8i5	arabidopsis
653	37.5	40.3	900	2	Q7RMZ9_PLAYO	Q7rmz9	plasmodium
654	37.5	40.3	913	2	Q43IE5_9CHLB	Q43ie5	chlorobium
655	37.5	40.3	1021	2	Q8IDW2_PLAF7	Q8idw2	plasmodium
656	37.5	40.3	1195	2	Q6BKG7_DEBHA	Q6bkg7	debaryomyce
657	37.5	40.3	1811	2	Q3HG26_TRIER	Q3hg26	trichodesmi
658	37.5	40.3	3317	2	Q7QJK9_ANOGA	Q7qjk9	anopheles g
659	37	39.8	49	2	Q7RBP3_PLAYO	Q7rbp3	plasmodium
660	37	39.8	58	2	Q85WY7_PINKO	Q85wy7	pinus korai
661	37	39.8	68	2	Q30DP9_SHEEP	Q30dp9	ovis aries
662	37	39.8	84	2	Q9AYP3_ORYSA	Q9ayp3	oryza sativ
663	37	39.8	90	2	Q30R73_THIDN	Q30r73	thiomicrosp
664	37	39.8	95	2	Q655C6_ORYSA	Q655c6	oryza sativ
665	37	39.8	101	2	Q4MZF2_THEPA	Q4mzf2	theileria p
666	37	39.8	109	2	Q3CGV5_THEET	Q3cgv5	thermoanaer
667	37	39.8	110	2	Q4BVD3_CROWT	Q4bvd3	crocosphaer
668	37	39.8	115	2	Q5PR01_RAT	Q5pr01	rattus norv
669	37	39.8	124	2	O52117_BRUAB	O52117	brucella ab
670	37	39.8	131	2	Q61QC1_CAEBR	Q61qc1	caenorhabdi
671	37	39.8	132	2	Q974W6_SULTO	Q974w6	sulfolobus
672	37	39.8	138	2	Q4BUW9_CROWT	Q4buw9	crocosphaer
673	37	39.8	140	2	Q3MMX3_SIVCZ	Q3mmx3	chimpanzee
674	37	39.8	145	2	Q4IBB8_GIBZE	Q4ibb8	gibberella
675	37	39.8	146	2	Q3MPM4_CANAL	Q3mpm4	candida alb
676	37	39.8	146	2	Q59S55_CANAL	Q59s55	candida alb
677	37	39.8	151	2	Q8J4W6_9HIV1	Q8j4w6	human immun
678	37	39.8	155	2	Q6RTW8_9HIV1	Q6rtw8	human immun
679	37	39.8	172	2	Q95VY8_DROME	Q95vy8	drosophila
680	37	39.8	175	2	Q94JH8_ORYSA	Q94jh8	oryza sativ
681	37	39.8	176	2	O61722_DROME	O61722	drosophila
682	37	39.8	180	2	Q95KR9_SUNMU	Q95kr9	suncus muri
683	37	39.8	185	2	Q4CMJ8_TRYCR	Q4cmj8	trypanosoma
684	37	39.8	189	2	Q80S24_BFV	Q80s24	barmah fore
685	37	39.8	193	1	UGPI5_ARATH	Q9c7f7	arabidopsis
686	37	39.8	194	2	Q8L9Q7_ARATH	Q8l9q7	arabidopsis
687	37	39.8	194	2	Q9KT22_VIBCH	Q9kt22	vibrio chol
688	37	39.8	197	2	Q8PZK6_METMA	Q8pzk6	methanosarc

689	37	39.8	198	2	Q4XQJ4_PLACH	Q4xqj4	plasmodium
690	37	39.8	198	2	Q3IBN3_9BACT	Q3ibn3	uncultured
691	37	39.8	199	2	Q7RC35_PLAYO	Q7rc35	plasmodium
692	37	39.8	203	2	Q8TK31_METAC	Q8tk31	methanosarc
693	37	39.8	205	2	Q6M114_METMP	Q6m114	methanococc
694	37	39.8	206	2	Q67YC9_ARATH	Q67yc9	arabidopsis
695	37	39.8	206	2	Q8LB66_ARATH	Q8lb66	arabidopsis
696	37	39.8	211	2	Q2PAV8_9HIV1	Q2pav8	human immun
697	37	39.8	212	2	Q5TEN0_HUMAN	Q5ten0	homo sapien
698	37	39.8	223	2	Q9D9V5_MOUSE	Q9d9v5	mus musculu
699	37	39.8	227	2	Q5A1E6_CANAL	Q5a1e6	candida alb
700	37	39.8	229	2	Q9LK42_ARATH	Q9lk42	arabidopsis
701	37	39.8	231	2	Q3CU45_ALTAT	Q3cu45	pseudoalter
702	37	39.8	237	2	Q3GKB8_CHLVI	Q3gkb8	prosthecoch
703	37	39.8	238	2	Q688X6_ORYSA	Q688x6	oryza sativ
704	37	39.8	241	2	Q7QYV5_GIALA	Q7qyv5	giardia lam
705	37	39.8	241	2	Q4AP79_9CHLB	Q4ap79	chlorobium
706	37	39.8	247	1	SCPA_LACJO	Q74jm3	lactobacill
707	37	39.8	249	2	Q97FS0_CLOAB	Q97fs0	clostridium
708	37	39.8	255	2	Q5TMW4_ANOGA	Q5tmw4	anopheles g
709	37	39.8	255	2	Q40HB1_9RHOB	Q40hb1	jannaschia
710	37	39.8	259	2	Q9TXQ8_CAEEL	Q9txq8	caenorhabdi
711	37	39.8	261	2	Q3MEC3_ANAVT	Q3mec3	anabaena va
712	37	39.8	265	2	O85953_SPHAR	O85953	sphingomona
713	37	39.8	267	2	Q8BPC4_MOUSE	Q8bpc4	mus musculu
714	37	39.8	271	2	Q9UYN6_PYRAB	Q9uyn6	pyrococcus
715	37	39.8	273	2	Q62T44_BACLD	Q62t44	bacillus li
716	37	39.8	276	2	Q73Q97_TREDE	Q73q97	treponema d
717	37	39.8	279	2	Q4PDY1_USTMA	Q4pdy1	ustilago ma
718	37	39.8	285	2	Q3Z3E5_SHISS	Q3z3e5	shigella so
719	37	39.8	287	2	Q360T8_9GAMM	Q360t8	shewanella
720	37	39.8	288	2	Q3H8Z6_TRIER	Q3h8z6	trichodesmi
721	37	39.8	292	2	Q9FH59_ARATH	Q9fh59	arabidopsis
722	37	39.8	293	2	Q5L517_CHLAB	Q5l517	chlamydophi
723	37	39.8	296	2	Q7RG83_PLAYO	Q7rg83	plasmodium
724	37	39.8	296	2	Q5WHZ2_BACSK	Q5whz2	bacillus cl
725	37	39.8	302	2	Q9CT68_MOUSE	Q9ct68	mus musculu
726	37	39.8	303	1	RBM13_BRARE	Q6nyd4	brachydanio
727	37	39.8	303	2	Q65HP1_BACLD	Q65hp1	bacillus li
728	37	39.8	305	2	Q3H6R2_9ACTO	Q3h6r2	nocardioide
729	37	39.8	307	2	Q6GNB0_XENLA	Q6gnb0	xenopus lae
730	37	39.8	307	2	Q90ZT5_XENLA	Q90zt5	xenopus lae
731	37	39.8	311	2	Q5TSR8_ANOGA	Q5tsr8	anopheles g
732	37	39.8	312	2	Q54BF6_DICDI	Q54bf6	dictyosteli
733	37	39.8	313	1	SPY2_CHICK	Q9ptl2	gallus gall
734	37	39.8	314	2	Q5HZA2_RAT	Q5hza2	rattus norv
735	37	39.8	314	2	Q5PRF7_XENTR	Q5prf7	xenopus tro
736	37	39.8	314	2	Q5Y173_XENTR	Q5y173	xenopus tro
737	37	39.8	314	2	Q90ZT6_XENLA	Q90zt6	xenopus lae
738	37	39.8	315	1	SPY2_HUMAN	O43597	homo sapien
739	37	39.8	315	1	SPY2_MOUSE	Q9qxv8	mus musculu
740	37	39.8	315	2	Q5T6Z7_HUMAN	Q5t6z7	homo sapien
741	37	39.8	315	2	Q5R959_PONPY	Q5r959	pongo pygma
742	37	39.8	315	2	Q866R9_CERAE	Q866r9	cercopithec
743	37	39.8	315	2	Q8KAC7_CHLTE	Q8kac7	chlorobium
744	37	39.8	316	2	Q8TZ21_METKA	Q8tz21	methanopyru
745	37	39.8	316	2	Q6Z0A5_ORYSA	Q6z0a5	oryza sativ
746	37	39.8	324	2	Q831C4_ENTFA	Q831c4	enterococcu
747	37	39.8	327	2	Q4CVF7_TRYCR	Q4cvf7	trypanosoma
748	37	39.8	330	2	Q4Y677_PLACH	Q4y677	plasmodium
749	37	39.8	331	2	Q4CU91_TRYCR	Q4cu91	trypanosoma
750	37	39.8	331	2	Q9NDF7_TRIVA	Q9ndf7	trichomonas
751	37	39.8	331	2	Q9NDF9_TRIVA	Q9ndf9	trichomonas
752	37	39.8	331	2	Q9NDG0_TRIVA	Q9ndg0	trichomonas
753	37	39.8	331	2	Q9NDF6_TRIVA	Q9ndf6	trichomonas
754	37	39.8	331	2	Q9NDF8_TRIVA	Q9ndf8	trichomonas
755	37	39.8	332	2	Q7QAA2_ANOGA	Q7qaa2	anopheles g
756	37	39.8	332	2	Q9BIH7_ANOGA	Q9bih7	anopheles g
757	37	39.8	333	2	Q8IHT3_PLAF7	Q8iht3	plasmodium
758	37	39.8	334	2	Q81CY1_BACCR	Q81cy1	bacillus ce
759	37	39.8	336	2	Q8A2D9_BACTN	Q8a2d9	bacteroides
760	37	39.8	339	1	RAD51_RABIT	O77507	oryctolagus
761	37	39.8	341	1	APHA_MYCRA	Q48935	mycoplana r
762	37	39.8	343	2	Q5LIA5_BACFN	Q5lia5	bacteroides
763	37	39.8	343	2	Q64ZB8_BACFR	Q64zb8	bacteroides
764	37	39.8	347	2	Q8ESK7_OCEIH	Q8esk7	oceanobacil
765	37	39.8	353	2	Q7Z783_HUMAN	Q7z783	homo sapien
766	37	39.8	361	2	Q44R57_CHLLI	Q44r57	chlorobium
767	37	39.8	362	2	Q96S93_HUMAN	Q96s93	homo sapien
768	37	39.8	363	2	Q3SLR2_THIDA	Q3slr2	thiobacillu
769	37	39.8	364	2	Q4Y0G6_PLACH	Q4y0g6	plasmodium
770	37	39.8	365	1	SERC_LACLA	Q9chw5	lactococcus
771	37	39.8	366	2	Q3EWE5_BACTI	Q3ewe5	bacillus th
772	37	39.8	369	2	Q57EJ0_BRUAB	Q57ej0	brucella ab
773	37	39.8	369	2	Q8G211_BRUSU	Q8g211	brucella su
774	37	39.8	369	2	Q2YMQ8_BRUA2	Q2ymq8	brucella ab
775	37	39.8	373	2	Q7QI90_ANOGA	Q7qi90	anopheles g
776	37	39.8	377	2	Q8YFW9_BRUME	Q8yfw9	brucella me
777	37	39.8	378	2	Q7Q9L8_ANOGA	Q7q918	anopheles g
778	37	39.8	381	2	Q6QH99_9BACE	Q6qh99	bacteroides
779	37	39.8	381	2	Q4KGV6_PSEF5	Q4kgv6	pseudomonas
780	37	39.8	382	2	Q6FUL7_CANGA	Q6ful7	candida gla
781	37	39.8	385	2	Q5LRT4_SILPO	Q5lrt4	silicibacte
782	37	39.8	386	2	O17559_CAEEL	O17559	caenorhabdi
783	37	39.8	390	2	Q6L5Q8_STRMT	Q6l5q8	streptococc
784	37	39.8	393	2	Q9BWS9_HUMAN	Q9bws9	homo sapien
785	37	39.8	393	2	Q9BY52_HUMAN	Q9by52	homo sapien
786	37	39.8	393	2	Q96SK0_HUMAN	Q96sk0	homo sapien
787	37	39.8	393	2	Q5RFF6_PONPY	Q5rff6	pongo pygma
788	37	39.8	393	2	Q4K2S4_STRPN	Q4k2s4	streptococc
789	37	39.8	403	2	Q7PPS5_ANOGA	Q7pps5	anopheles g
790	37	39.8	407	2	Q2S4F7_9SPHI	Q2s4f7	salinibacte
791	37	39.8	409	2	Q4YWE9_PLABE	Q4ywe9	plasmodium
792	37	39.8	409	2	Q60RL3_CAEBR	Q60rl3	caenorhabdi
793	37	39.8	412	2	Q8MXG8_CAEEL	Q8mxg8	caenorhabdi
794	37	39.8	413	2	Q53CX2_9GAMA	Q53cx2	macaca fusc
795	37	39.8	414	2	Q8IEF6_PLAF7	Q8ief6	plasmodium
796	37	39.8	414	2	Q9GNU8_PLAFA	Q9gnu8	plasmodium
797	37	39.8	415	2	Q5R0W1_IDILO	Q5r0w1	idiomarina
798	37	39.8	420	1	YAGA_SCHPO	Q09873	schizosacch
799	37	39.8	428	2	Q7QNP7_GIALA	Q7qnp7	giardia lam
800	37	39.8	429	2	Q88HM5_PSEPK	Q88hm5	pseudomonas
801	37	39.8	433	2	Q96LW3_HUMAN	Q96lw3	homo sapien
802	37	39.8	434	2	Q7M7M5_WOLSU	Q7m7m5	wolinella s
803	37	39.8	435	2	Q41LD5_METBU	Q41ld5	methanococc
804	37	39.8	436	2	Q8MXG9_CAEEL	Q8mxg9	caenorhabdi
805	37	39.8	439	2	Q54YJ2_DICDI	Q54yj2	dictyosteli
806	37	39.8	441	2	Q6B0A1_HUMAN	Q6b0a1	homo sapien
807	37	39.8	441	2	Q8C1B9_MOUSE	Q8c1b9	mus musculu
808	37	39.8	445	2	Q9KAM7_BACHD	Q9kam7	bacillus ha
809	37	39.8	447	1	MPIP3_MOUSE	P48967	mus musculu
810	37	39.8	447	2	Q3THG4_MOUSE	Q3thg4	mus musculu
811	37	39.8	447	2	Q3UR74_MOUSE	Q3ur74	mus musculu
812	37	39.8	452	2	Q8NFL8_HUMAN	Q8nfl8	homo sapien
813	37	39.8	455	2	Q4H3A9_CIOIN	Q4h3a9	ciona intes
814	37	39.8	457	2	Q821P8_CHLCV	Q821p8	chlamydophi
815	37	39.8	458	2	Q5L4Z6_CHLAB	Q5l4z6	chlamydophi
816	37	39.8	460	2	Q8W495_ARATH	Q8w495	arabidopsis
817	37	39.8	460	2	Q3EFM0_ACTSC	Q3efm0	actinobacil
818	37	39.8	461	2	Q49B95_9DIPT	Q49b95	sitodiplosi
819	37	39.8	463	1	GSA_CHLRE	Q39566	chlamydomon
820	37	39.8	463	2	Q6C9M8_YARLI	Q6c9m8	yarrowia li
821	37	39.8	465	2	O81046_ARATH	O81046	arabidopsis
822	37	39.8	466	2	Q6IS76_HUMAN	Q6is76	homo sapien
823	37	39.8	466	2	Q9AU15_MEDTR	Q9au15	medicago tr
824	37	39.8	466	2	Q8S7V6_ORYSA	Q8s7v6	oryza sativ
825	37	39.8	467	2	Q84UE1_MEDTR	Q84ue1	medicago tr
826	37	39.8	472	2	Q5EFD8_TRIVA	Q5efd8	trichomonas
827	37	39.8	474	2	Q8CI50_MOUSE	Q8ci50	mus musculu
828	37	39.8	476	2	Q7QDV1_ANOGA	Q7qdv1	anopheles g
829	37	39.8	481	2	Q6E279_ARATH	Q6e279	arabidopsis
830	37	39.8	481	2	Q84WS1_ARATH	Q84ws1	arabidopsis
831	37	39.8	483	2	Q8R203_MOUSE	Q8r203	mus musculu
832	37	39.8	487	2	Q7RDX2_PLAYO	Q7rdx2	plasmodium
833	37	39.8	498	2	Q8H7L9_ORYSA	Q8h7l9	oryza sativ
834	37	39.8	499	2	Q6NQ51_ARATH	Q6nq51	arabidopsis

835	37	39.8	501	2	Q9XH61_9ASTR	Q9xh61	matricaria
836	37	39.8	505	2	O59785_SCHPO	O59785	schizosacch
837	37	39.8	506	2	Q6MMM6_BDEBA	Q6mmm6	bdellovibri
838	37	39.8	507	2	Q9LMF6_ARATH	Q9lmf6	arabidopsis
839	37	39.8	508	2	Q6E278_ARATH	Q6e278	arabidopsis
840	37	39.8	509	2	Q9XI85_ARATH	Q9xi85	arabidopsis
841	37	39.8	510	1	GAG_SIVMS	P31634	simian immu
842	37	39.8	510	2	Q6Z341_ORYSA	Q6z341	oryza sativ
843	37	39.8	512	2	Q2LYY6_DROPS	Q2lyy6	drosophila
844	37	39.8	513	2	Q6ZM76_BRARE	Q6zm76	brachydanio
845	37	39.8	514	2	Q3NXB7_9GAMM	Q3nxb7	shewanella
846	37	39.8	514	2	Q7WUM2_ACTMI	Q7wum2	actinoplane
847	37	39.8	518	2	Q3W6U6_9ACTO	Q3w6u6	frankia sp.
848	37	39.8	526	2	O02190_CIOIN	O02190	ciona intes
849	37	39.8	526	2	Q4H359_CIOIN	Q4h359	ciona intes
850	37	39.8	528	2	Q4YTZ2_PLABE	Q4ytz2	plasmodium
851	37	39.8	529	1	NMT_AJECA	P34763	ajellomyces
852	37	39.8	530	2	Q3HHB9_TRIER	Q3hhb9	trichodesmi
853	37	39.8	530	2	Q4CJI8_CLOTM	Q4cji8	clostridium
854	37	39.8	532	2	Q8GVL6_ORYSA	Q8gvl6	oryza sativ
855	37	39.8	540	2	Q8K2A4_MOUSE	Q8k2a4	mus musculu
856	37	39.8	540	2	Q9JIB9_MOUSE	Q9jib9	mus musculu
857	37	39.8	542	2	Q8EW43_MYCPE	Q8ew43	mycoplasma
858	37	39.8	546	2	Q5XKG7_HUMAN	Q5xkg7	homo sapien
859	37	39.8	546	2	Q726H6_DESVH	Q726h6	desulfovibr
860	37	39.8	547	2	Q3Y3B8_ENTFC	Q3y3b8	enterococcu
861	37	39.8	553	2	Q5XI17_RAT	Q5xi17	rattus norv
862	37	39.8	559	2	Q46HZ9_PROMT	Q46hz9	prochloroco
863	37	39.8	560	2	Q2RRA3_RHORU	Q2rra3	rhodospiril
864	37	39.8	561	2	Q86CZ6_CAEEL	Q86cz6	caenorhabdi
865	37	39.8	562	2	Q37KN2_RHOPA	Q37kn2	rhodopseudo
866	37	39.8	569	2	Q5AJA6_CANAL	Q5aja6	candida alb
867	37	39.8	574	2	Q8IWH5_HUMAN	Q8iwh5	homo sapien
868	37	39.8	583	2	Q8NFL4_HUMAN	Q8nfl4	homo sapien
869	37	39.8	587	2	Q6MF24_PARUW	Q6mf24	parachlamyd
870	37	39.8	592	2	O02191_CIOIN	O02191	ciona intes
871	37	39.8	592	2	Q7UV94_RHOBA	Q7uv94	rhodopirell
872	37	39.8	593	2	Q63FZ0_BACCZ	Q63fz0	bacillus ce
873	37	39.8	593	2	Q81V45_BACAN	Q81v45	bacillus an
874	37	39.8	593	2	Q73DI8_BACC1	Q73di8	bacillus ce
875	37	39.8	598	2	Q3ARI6_CHLCH	Q3ari6	chlorobium
876	37	39.8	600	2	Q605T7_METCA	Q605t7	methylococc
877	37	39.8	605	2	Q8BDR3_PAPVR	Q8bdr3	reindeer pa
878	37	39.8	606	1	ALBUA_XENLA	P08759	xenopus lae
879	37	39.8	620	2	Q38UP3_LACSS	Q38up3	lactobacill
880	37	39.8	630	2	Q46BN2_METBA	Q46bn2	methanosarc
881	37	39.8	633	2	Q32P14_MOUSE	Q32p14	mus musculu
882	37	39.8	641	2	Q68E90_AERPU	Q68e90	aeromonas p
883	37	39.8	647	1	XBP1_YEAST	P40489	saccharomyc
884	37	39.8	648	2	Q2SC60_9GAMM	Q2sc60	hahella che
885	37	39.8	651	2	Q5TYS1_BRARE	Q5tys1	brachydanio
886	37	39.8	651	2	Q9W7F8_BRARE	Q9w7f8	brachydanio
887	37	39.8	652	2	Q21306_CAEEL	Q21306	caenorhabdi
888	37	39.8	653	2	Q2WS12_CLOBE	Q2ws12	clostridium
889	37	39.8	658	2	Q55G45_DICDI	Q55g45	dictyosteli
890	37	39.8	663	2	Q8D403_VIBVU	Q8d403	vibrio vuln
891	37	39.8	678	2	Q7QUM5_GIALA	Q7qum5	giardia lam
892	37	39.8	678	2	Q39S32_GEOMG	Q39s32	geobacter m
893	37	39.8	693	2	Q4R6C7_MACFA	Q4r6c7	macaca fasc
894	37	39.8	694	2	Q5P9E1_ANAMM	Q5p9e1	anaplasma m
895	37	39.8	695	2	Q8R428_CAVPO	Q8r428	cavia porce
896	37	39.8	707	2	Q96MP4_HUMAN	Q96mp4	homo sapien
897	37	39.8	718	2	Q6C6P5_YARLI	Q6c6p5	yarrowia li
898	37	39.8	728	2	Q3UKB0_MOUSE	Q3ukb0	m 13 days p
899	37	39.8	731	2	Q4T149_TETNG	Q4t149	tetraodon n
900	37	39.8	733	2	Q9BZQ1_HUMAN	Q9bzq1	homo sapien
901	37	39.8	733	2	Q8NC68_HUMAN	Q8nc68	homo sapien
902	37	39.8	733	2	Q5R5T0_PONPY	Q5r5t0	pongo pygma
903	37	39.8	749	2	Q6FZI5_BARQU	Q6fzi5	bartonella
904	37	39.8	759	2	Q4P4W5_USTMA	Q4p4w5	ustilago ma
905	37	39.8	760	2	Q4MV80_BACCE	Q4mv80	bacillus ce
906	37	39.8	767	2	Q6MYA3_ASPFU	Q6mya3	aspergillus
907	37	39.8	770	2	Q4WS59_ASPFU	Q4ws59	aspergillus
908	37	39.8	774	2	Q7RTG3_PLAYO	Q7rtg3	plasmodium
909	37	39.8	777	2	Q3WQG8_9RHIZ	Q3wqg8	mesorhizobi
910	37	39.8	783	2	Q967G0_CRYPV	Q967g0	cryptospori
911	37	39.8	786	2	Q44RB6_CHLLI	Q44rb6	chlorobium
912	37	39.8	796	2	Q869U8_DICDI	Q869u8	dictyosteli
913	37	39.8	799	2	Q9V964_DROME	Q9v964	drosophila
914	37	39.8	811	2	Q551L2_DICDI	Q55112	dictyosteli
915	37	39.8	814	2	Q4HND2_CAMUP	Q4hnd2	campylobact
916	37	39.8	815	2	Q3G4L7_9DELT	Q3g417	pelobacter
917	37	39.8	816	2	Q4E834_9RICK	Q4e834	wolbachia e
918	37	39.8	816	2	Q5GTP5_WOLTR	Q5gtp5	wolbachia s
919	37	39.8	816	2	Q73G34_WOLPM	Q73g34	wolbachia p
920	37	39.8	818	2	Q622U6_CAEBR	Q622u6	caenorhabdi
921	37	39.8	826	2	Q86S89_9CILI	Q86s89	polyplastro
922	37	39.8	866	2	Q6FY30_CANGA	Q6fy30	candida gla
923	37	39.8	870	2	Q6UAN0_TETNG	Q6uan0	tetraodon n
924	37	39.8	876	2	Q3QIT4_9GAMM	Q3qit4	shewanella
925	37	39.8	876	2	Q6NEQ4_CORDI	Q6neq4	corynebacte
926	37	39.8	898	2	Q8H902_ORYSA	Q8h902	oryza sativ
927	37	39.8	898	2	Q6NZG4_MOUSE	Q6nzg4	mus musculu
928	37	39.8	930	2	Q6CHP7_YARLI	Q6chp7	yarrowia li
929	37	39.8	931	2	Q5I9W1_CAEEL	Q5i9w1	caenorhabdi
930	37	39.8	936	2	Q5CNV6_CRYHO	Q5cnv6	cryptospori
931	37	39.8	936	2	Q5CVN3_CRYPV	Q5cvn3	cryptospori
932	37	39.8	945	2	Q2SRS9_MYCCA	Q2srs9	mycoplasma
933	37	39.8	948	2	Q61XA1_CAEBR	Q61xa1	caenorhabdi
934	37	39.8	954	2	Q2UCE2_ASPOR	Q2uce2	aspergillus
935	37	39.8	989	1	FRQ_NEUCR	P19970	neurospora
936	37	39.8	993	2	Q81IG5_BACCR	Q81ig5	bacillus ce
937	37	39.8	996	2	Q3MY03_9DELT	Q3my03	syntrophoba
938	37	39.8	998	2	Q5A8A5_CANAL	Q5a8a5	candida alb
939	37	39.8	1016	2	Q67U26_ORYSA	Q67u26	oryza sativ
940	37	39.8	1032	2	Q7RRI1_PLAYO	Q7rri1	plasmodium
941	37	39.8	1047	2	O23269_ARATH	O23269	arabidopsis
942	37	39.8	1058	2	Q9RGV8_SALTI	Q9rgv8	salmonella
943	37	39.8	1062	2	Q8RY24_ARATH	Q8ry24	arabidopsis
944	37	39.8	1064	2	Q9MAU0_ARATH	Q9mau0	arabidopsis
945	37	39.8	1065	2	Q3JLL6_BURP1	Q3jll6	burkholderi
946	37	39.8	1065	2	Q2T6D1_BURTH	Q2t6d1	burkholderi
947	37	39.8	1067	2	Q4L744_STAHJ	Q41744	staphylococ
948	37	39.8	1070	2	Q6BVK2_DEBHA	Q6bvk2	debaryomyce
949	37	39.8	1071	2	Q62CH9_BURMA	Q62ch9	burkholderi
950	37	39.8	1072	2	Q2UU52_ASPOR	Q2uu52	aspergillus
951	37	39.8	1105	2	Q7MFH6_VIBVY	Q7mfh6	vibrio vuln
952	37	39.8	1114	2	Q5K7U0_CRYNE	Q5k7u0	cryptococcu
953	37	39.8	1114	2	Q55IA4_CRYNE	Q55ia4	cryptococcu
954	37	39.8	1118	2	Q4P7X3_USTMA	Q4p7x3	ustilago ma
955	37	39.8	1125	2	Q63KK6_BURPS	Q63kk6	burkholderi
956	37	39.8	1126	2	Q5TMM2_ANOGA	Q5tmm2	anopheles g
957	37	39.8	1145	2	Q7PZ65_ANOGA	Q7pz65	anopheles g
958	37	39.8	1164	2	Q4S6H5_TETNG	Q4s6h5	tetraodon n
959	37	39.8	1170	1	ITA2_BOVIN	P53710	bos taurus
960	37	39.8	1198	2	Q480N8_COLP3	Q480n8	colwellia p
961	37	39.8	1209	2	Q3EYR3_BACTI	Q3eyr3	bacillus th
962	37	39.8	1214	2	Q4N5A7_THEPA	Q4n5a7	theileria p
963	37	39.8	1224	2	Q3APY1_CHLCH	Q3apy1	chlorobium
964	37	39.8	1230	2	Q7R656_GIALA	Q7r656	giardia lam
965	37	39.8	1256	2	Q4S276_TETNG	Q4s276	tetraodon n
966	37	39.8	1265	2	Q7G647_ORYSA	Q7g647	oryza sativ
967	37	39.8	1265	2	Q8W5E1_ORYSA	Q8w5e1	oryza sativ
968	37	39.8	1305	2	Q3XLU2_9PROT	Q3xlu2	magnetococc
969	37	39.8	1323	2	Q7XXG9_ORYSA	Q7xxg9	oryza sativ
970	37	39.8	1421	2	Q4WID6_ASPFU	Q4wid6	aspergillus
971	37	39.8	1473	2	Q54TV0_DICDI	Q54tv0	dictyosteli
972	37	39.8	1478	2	Q6CUQ0_KLULA	Q6cuq0	kluyveromyc
973	37	39.8	1492	2	Q4SJX4_TETNG	Q4sjx4	tetraodon n
974	37	39.8	1526	2	Q6CAZ5_YARLI	Q6caz5	yarrowia li
975	37	39.8	1562	2	Q54LE5_DICDI	Q54le5	dictyosteli
976	37	39.8	1568	2	Q7Z8R6_9SACH	Q7z8r6	pichia inos
977	37	39.8	1586	2	Q3UHG2_MOUSE	Q3uhg2	mus musculu
978	37	39.8	1592	2	Q4PGM7_USTMA	Q4pgm7	ustilago ma
979	37	39.8	1596	2	Q57XS0_9TRYP	Q57xs0	trypanosoma
980	37	39.8	1605	2	Q7XNT6_ORYSA	Q7xnt6	oryza sativ

981	37	39.8	1649	2	Q60K37_CAEBR	Q60k37	caenorhabdi
982	37	39.8	1649	2	Q4S0X4_TETNG	Q4s0x4	tetraodon n
983	37	39.8	1703	1	UN13A_HUMAN	Q9upw8	homo sapien
984	37	39.8	1709	2	Q4SDC9_TETNG	Q4sdc9	tetraodon n
985	37	39.8	1712	2	Q4KUS2_MOUSE	Q4kus2	mus musculu
986	37	39.8	1714	2	Q4UJ04_THEAN	Q4uj04	theileria a
987	37	39.8	1722	2	Q8S636_ORYSA	Q8s636	oryza sativ
988	37	39.8	1735	1	UN13A_RAT	Q62768	rattus norv
989	37	39.8	1736	2	Q86AT9_DICDI	Q86at9	dictyosteli
990	37	39.8	1736	2	Q95PH7_DICDI	Q95ph7	dictyosteli
991	37	39.8	1864	2	Q6LFE6_PLAF7	Q6lfe6	plasmodium
992	37	39.8	1902	2	Q4RV37_TETNG	Q4rv37	tetraodon n
993	37	39.8	1931	2	Q8W2U3_ORYSA	Q8w2u3	oryza sativ
994	37	39.8	1933	2	Q7EY18_ORYSA	Q7ey18	oryza sativ
995	37	39.8	1946	2	Q4N6K9_THEPA	Q4n6k9	theileria p
996	37	39.8	1964	2	Q8I1X6_PLAF7	Q8i1x6	plasmodium
997	37	39.8	2002	2	Q5CW10_CRYPV	Q5cw10	cryptospori
998	37	39.8	2060	2	Q9P980_PICAN	Q9p980	pichia angu
999	37	39.8	2254	2	Q80N16_9PICO	Q80n16	ljungan vir
1000	37	39.8	2380	2	Q86C65_DICDI	Q86c65	dictyosteli
1001	37	39.8	2750	2	Q54V59_DICDI	Q54v59	dictyosteli
1002	37	39.8	3374	2	Q8JJZ3_9FLAV	Q8jjz3	montana myo
1003	37	39.8	4837	2	Q54MQ5_DICDI	Q54mq5	dictyosteli
1004	37	39.8	10061	2	Q8I3Z1_PLAF7	Q8i3z1	plasmodium
1005	37	39.8	12268	2	Q8MQ08_CAEEL	Q8mq08	caenorhabdi
1006	37	39.8	13100	2	Q09165_CAEEL	Q09165	caenorhabdi
1007	36.5	39.2	78	2	Q92GA1_RICCN	Q92ga1	rickettsia
1008	36.5	39.2	101	2	Q8PTP0_METMA	Q8ptp0	methanosarc
1009	36.5	39.2	238	2	Q18773_CAEEL	Q18773	caenorhabdi
1010	36.5	39.2	258	2	Q3HHM6_TRIER	Q3hhm6	trichodesmi
1011	36.5	39.2	274	2	Q6CZS8_ERWCT	Q6czs8	erwinia car
1012	36.5	39.2	296	2	Q4R7D4_MACFA	Q4r7d4	macaca fasc
1013	36.5	39.2	307	2	Q7RB95_PLAYO	Q7rb95	plasmodium
1014	36.5	39.2	308	2	Q9VNL8_DROME	Q9vnl8	drosophila
1015	36.5	39.2	377	2	Q64I72_HUMAN	Q64i72	homo sapien
1016	36.5	39.2	397	2	Q3UTN0_MOUSE	Q3utn0	mus musculu
1017	36.5	39.2	433	2	Q4U8N5_THEAN	Q4u8n5	theileria a
1018	36.5	39.2	499	2	Q6TUH4_RAT	Q6tuh4	rattus norv
1019	36.5	39.2	608	2	Q86AG5_DICDI	Q86ag5	dictyosteli
1020	36.5	39.2	655	2	Q551A2_DICDI	Q551a2	dictyosteli
1021	36.5	39.2	657	1	THOC1_HUMAN	Q96fv9	homo sapien
1022	36.5	39.2	657	1	THOC1_MOUSE	Q8r3n6	mus musculu
1023	36.5	39.2	729	2	Q4R966_MACFA	Q4r966	macaca fasc
1024	36.5	39.2	803	1	GYRB_SALTI	P0a2i4	salmonella
1025	36.5	39.2	803	1	GYRB_SALTY	P0a2i3	salmonella
1026	36.5	39.2	804	2	Q57I03_SALCH	Q57i03	salmonella
1027	36.5	39.2	804	2	Q5PKU9_SALPA	Q5pku9	salmonella
1028	36.5	39.2	805	2	Q6CYR7_ERWCT	Q6cyr7	erwinia car
1029	36.5	39.2	813	2	Q3U142_MOUSE	Q3u142	mus musculu
1030	36.5	39.2	813	2	Q640M9_MOUSE	Q640m9	mus musculu
1031	36.5	39.2	813	2	Q9JHD1_MOUSE	Q9jhd1	mus musculu
1032	36.5	39.2	832	1	PCAF_HUMAN	Q92831	homo sapien
1033	36.5	39.2	1056	2	Q5L7U8_BACFN	Q5l7u8	bacteroides
1034	36.5	39.2	1056	2	Q64N19_BACFR	Q64n19	bacteroides
1035	36.5	39.2	1526	2	Q8IK87_PLAF7	Q8ik87	plasmodium
1036	36.5	39.2	1756	1	YCF1_PINTH	P41647	pinus thunb
1037	36.5	39.2	2269	2	Q54NC6_DICDI	Q54nc6	dictyosteli
1038	36.5	39.2	3085	2	Q4SYV0_TETNG	Q4syv0	tetraodon n
1039	36.5	39.2	4196	1	DYHC_SCHPO	O13290	schizosacch
1040	36	38.7	15	1	ALLS_MANSE	P42559	manduca sex
1041	36	38.7	47	2	Q5V6I6_HALMA	Q5v6i6	haloarcula
1042	36	38.7	49	2	Q86YZ5_HUMAN	Q86yz5	homo sapien
1043	36	38.7	53	2	Q6KEQ0_SPOFR	Q6keq0	spodoptera
1044	36	38.7	61	2	Q95P88_MESMA	Q95p88	mesobuthus
1045	36	38.7	61	2	Q967L8_MESMA	Q967l8	mesobuthus
1046	36	38.7	63	2	Q6JSD9_HUMAN	Q6jsd9	homo sapien
1047	36	38.7	68	2	Q9JW83_NEIMA	Q9jw83	neisseria m
1048	36	38.7	70	2	P79261_MACMU	P79261	macaca mula
1049	36	38.7	72	2	Q8TP30_METAC	Q8tp30	methanosarc
1050	36	38.7	94	2	Q56WL3_ARATH	Q56wl3	arabidopsis
1051	36	38.7	103	2	Q8VWY0_CUCSA	Q8vwy0	cucumis sat
1052	36	38.7	105	2	Q5WMV0_ORYSA	Q5wmv0	oryza sativ
1053	36	38.7	108	1	Y3403_METJA	Q60302	methanococc
1054	36	38.7	111	2	Q8ZUX1_PYRAE	Q8zux1	pyrobaculum
1055	36	38.7	120	2	Q3G5B8_9DELT	Q3g5b8	pelobacter
1056	36	38.7	121	2	Q95NV8_DROME	Q95nv8	drosophila
1057	36	38.7	122	2	Q9VKK5_DROME	Q9vkk5	drosophila
1058	36	38.7	122	2	Q8QZZ4_MOUSE	Q8qzz4	mus musculu
1059	36	38.7	123	2	Q4Z715_PLABE	Q4z715	plasmodium
1060	36	38.7	124	2	Q4PLI0_SAMCR	Q4pli0	samia cynth
1061	36	38.7	125	1	ALLS_SPOFR	Q868f8	spodoptera
1062	36	38.7	125	2	Q26115_PSEUI	Q26115	pseudaletia
1063	36	38.7	133	2	Q41PS3_METBU	Q41ps3	methanococc
1064	36	38.7	135	2	Q3AR22_CHLCH	Q3ar22	chlorobium
1065	36	38.7	138	2	Q3FKE2_9BURK	Q3fke2	rhodoferax
1066	36	38.7	150	2	Q8Q5A8_SIVCZ	Q8q5a8	chimpanzee
1067	36	38.7	151	2	Q6ZSE1_HUMAN	Q6zse1	homo sapien
1068	36	38.7	153	2	Q3PRI0_NITHA	Q3pri0	nitrobacter
1069	36	38.7	156	2	Q8EP94_OCEIH	Q8ep94	oceanobacil
1070	36	38.7	157	2	Q4XII0_PLACH	Q4xii0	plasmodium
1071	36	38.7	162	2	Q8RDM2_FUSNN	Q8rdm2	fusobacteri
1072	36	38.7	165	2	Q3AMJ6_SYNSC	Q3amj6	synechococc
1073	36	38.7	166	2	Q9X2X7_BACAN	Q9x2x7	bacillus an
1074	36	38.7	167	2	P89672_9CALI	P89672	san miguel
1075	36	38.7	168	2	Q8YSE6_ANASP	Q8yse6	anabaena sp
1076	36	38.7	171	2	Q5PR44_BRARE	Q5pr44	brachydanio
1077	36	38.7	174	2	Q8LE65_ARATH	Q8le65	arabidopsis
1078	36	38.7	176	2	Q9LZ14_ARATH	Q9lz14	arabidopsis
1079	36	38.7	177	2	Q46C96_METBA	Q46c96	methanosarc
1080	36	38.7	181	2	O68236_BORBU	O68236	borrelia bu
1081	36	38.7	183	2	Q8SVT1_ENCCU	Q8svt1	encephalito
1082	36	38.7	183	2	Q4DX76_TRYCR	Q4dx76	trypanosoma
1083	36	38.7	184	2	Q2NGF8_9EURY	Q2ngf8	methanospha
1084	36	38.7	184	2	Q47J06_DECAR	Q47j06	dechloromon
1085	36	38.7	185	2	Q6M181_METMP	Q6m181	methanococc
1086	36	38.7	186	2	Q8QNF4_9PHYC	Q8qnf4	ectocarpus
1087	36	38.7	187	2	O69144_CLOPA	O69144	clostridium
1088	36	38.7	189	2	Q8TP31_METAC	Q8tp31	methanosarc
1089	36	38.7	194	2	Q5VTP5_BRARE	Q5vtp5	brachydanio
1090	36	38.7	196	1	ENGB_STAAR	Q6gg32	staphylococ
1091	36	38.7	203	1	CTF2_PANTR	Q6r2r2	pan troglod
1092	36	38.7	203	2	Q3X3Z5_9ACTN	Q3x3z5	rubrobacter
1093	36	38.7	204	2	Q5RGN5_BRARE	Q5rgn5	brachydanio
1094	36	38.7	207	2	Q4HF63_CAMCO	Q4hf63	campylobact
1095	36	38.7	208	2	Q6LYC5_METMP	Q6lyc5	methanococc
1096	36	38.7	212	2	Q5WXI2_LEGPL	Q5wxi2	legionella
1097	36	38.7	212	2	Q5X658_LEGPA	Q5x658	legionella
1098	36	38.7	212	2	Q5ZWH4_LEGPH	Q5zwh4	legionella
1099	36	38.7	212	2	Q6MEJ5_PARUW	Q6mej5	parachlamyd
1100	36	38.7	213	2	Q57MX7_SALCH	Q57mx7	salmonella
1101	36	38.7	218	1	Y363_RICPR	Q9zdg6	rickettsia
1102	36	38.7	218	2	Q7LJG9_FUSMI	Q7ljg9	fusarium me
1103	36	38.7	218	2	Q8NIF1_FUSAU	Q8nif1	fusarium au
1104	36	38.7	218	2	Q8NJA4_FUSAU	Q8nja4	fusarium au
1105	36	38.7	218	2	Q4XK65_PLACH	Q4xk65	plasmodium
1106	36	38.7	219	2	Q4SJS4_TETNG	Q4sjs4	tetraodon n
1107	36	38.7	221	2	Q7R4V7_GIALA	Q7r4v7	giardia lam
1108	36	38.7	222	2	Q4Q9I2_LEIMA	Q4q9i2	leishmania
1109	36	38.7	224	2	Q5T4P8_HUMAN	Q5t4p8	homo sapien
1110	36	38.7	226	2	Q5T4P9_HUMAN	Q5t4p9	homo sapien
1111	36	38.7	227	2	O80561_ARATH	O80561	arabidopsis
1112	36	38.7	227	2	Q8ESP1_OCEIH	Q8espl	oceanobacil
1113	36	38.7	229	2	Q4RRI4_TETNG	Q4rri4	tetraodon n
1114	36	38.7	230	2	Q4SW99_TETNG	Q4sw99	tetraodon n
1115	36	38.7	232	2	Q7Z2T5_HUMAN	Q7z2t5	homo sapien
1116	36	38.7	233	2	Q8XMB3_CLOPE	Q8xmb3	clostridium
1117	36	38.7	234	2	Q6HZG7_BACAN	Q6hzg7	bacillus an
1118	36	38.7	235	2	Q4Q9H9_LEIMA	Q4q9h9	leishmania
1119	36	38.7	235	2	Q4MP09_BACCE	Q4mp09	bacillus ce
1120	36	38.7	235	2	Q8KYS9_BACAN	Q8kys9	bacillus an
1121	36	38.7	235	2	Q6F006_BACAN	Q6f006	bacillus an
1122	36	38.7	236	2	Q9M4D3_MAIZE	Q9m4d3	zea mays (m
1123	36	38.7	237	2	Q9UL48_HUMAN	Q9ul48	homo sapien
1124	36	38.7	239	2	Q7U978_SYNPX	Q7u978	synechococc
1125	36	38.7	245	1	DERL1_DROME	Q9vq57	drosophila
1126	36	38.7	245	1	Y9K1_ENCCU	Q8stk1	encephalito

1127	36	38.7	246	2	Q4ELB7_LISMO	Q4elb7 listeria mo
1128	36	38.7	246	2	Q4ESX7_LISMO	Q4esx7 listeria mo
1129	36	38.7	246	2	Q71XK4_LISMF	Q71xk4 listeria mo
1130	36	38.7	246	2	Q8Y5A6_LISMO	Q8y5a6 listeria mo
1131	36	38.7	247	2	Q3VQK2_9CHLB	Q3vqk2 pelodictyon
1132	36	38.7	248	2	Q81R91_BACAN	Q81r91 bacillus an
1133	36	38.7	253	2	Q4MRT9_BACCE	Q4mrt9 bacillus ce
1134	36	38.7	255	2	Q8EKE4_SHEON	Q8eke4 shewanella
1135	36	38.7	258	1	Y706_ENCCU	Q8sv55 encephalito
1136	36	38.7	258	2	Q64EC4_9ARCH	Q64ec4 uncultured
1137	36	38.7	262	2	Q6WZA5_STRVI	Q6wza5 streptomyce
1138	36	38.7	267	2	Q2WZY7_9GAMM	Q2wzy7 shewanella
1139	36	38.7	267	2	Q36M88_MARHY	Q36m88 marinobacte
1140	36	38.7	267	2	Q63C13_BACCZ	Q63c13 bacillus ce
1141	36	38.7	268	2	Q9Y7L2_SCHPO	Q9y7l2 schizosacch
1142	36	38.7	271	1	CBIO_SALTI	Q8z5n5 salmonella
1143	36	38.7	271	1	CBIO_SALTY	Q05596 salmonella
1144	36	38.7	271	2	Q2VZ82_MAGSA	Q2vz82 magnetospir
1145	36	38.7	271	2	Q3EGZ8_ACTSC	Q3egz8 actinobacil
1146	36	38.7	271	2	Q5PDU4_SALPA	Q5pdu4 salmonella
1147	36	38.7	272	2	Q8EJU1_SHEON	Q8eju1 shewanella
1148	36	38.7	273	1	GAH6_HUMAN	Q8n8a4 homo sapien
1149	36	38.7	277	2	Q2ZVH7_SHEPU	Q2zvh7 shewanella
1150	36	38.7	279	2	Q3EYH7_BACTI	Q3eyh7 bacillus th
1151	36	38.7	281	1	TNF10_HUMAN	P50591 homo sapien
1152	36	38.7	281	2	Q6IBA9_HUMAN	Q6iba9 homo sapien
1153	36	38.7	282	1	LRPR_STREQ	Q54087 streptococc
1154	36	38.7	282	1	QUEF_PHOLL	Q7n8q7 photorhabdu
1155	36	38.7	282	2	Q8K5R9_STRP3	Q8k5r9 streptococc
1156	36	38.7	282	2	Q8NZA7_STRP8	Q8nza7 streptococc
1157	36	38.7	289	2	Q4VSR6_PIG	Q4vsr6 sus scrofa
1158	36	38.7	296	2	Q48R79_STRPM	Q48r79 streptococc
1159	36	38.7	296	2	Q877Z1_STRP3	Q877z1 streptococc
1160	36	38.7	296	2	Q5X9T7_STRP6	Q5x9t7 streptococc
1161	36	38.7	297	1	YACD_BACSU	P37566 bacillus su
1162	36	38.7	298	2	Q9M4G3_MAIZE	Q9m4g3 zea mays (m
1163	36	38.7	300	2	Q5U675_HUMAN	Q5u675 homo sapien
1164	36	38.7	300	2	Q5FL97_LACAC	Q5fl97 lactobacill
1165	36	38.7	302	1	ICOSL_HUMAN	O75144 homo sapien
1166	36	38.7	303	2	Q47X67_COLP3	Q47x67 colwellia p
1167	36	38.7	304	2	Q8KW55_9RHOB	Q8kw55 ruegeria sp
1168	36	38.7	304	2	Q2JIH5_9CYAN	Q2jih5 cyanobacter
1169	36	38.7	305	2	Q3H6N4_9ACTO	Q3h6n4 nocardioide
1170	36	38.7	305	2	Q3RWQ7_RALME	Q3rwq7 ralstonia m
1171	36	38.7	309	2	Q7MP36_VIBVY	Q7mp36 vibrio vuln
1172	36	38.7	309	2	Q899L3_CLOTE	Q899l3 clostridium
1173	36	38.7	314	2	Q9BRF8_HUMAN	Q9brf8 homo sapien
1174	36	38.7	314	2	Q9H9M9_HUMAN	Q9h9m9 homo sapien
1175	36	38.7	314	2	Q9NUT6_HUMAN	Q9nut6 homo sapien
1176	36	38.7	314	2	Q5RCR9_PONPY	Q5rcr9 pongo pygma
1177	36	38.7	314	2	Q6LGX6_PHOPR	Q6lgx6 photobacter
1178	36	38.7	315	2	Q5R6B0_PONPY	Q5r6b0 pongo pygma
1179	36	38.7	317	1	RPOA_MESFL	Q6f1w7 mesoplasma
1180	36	38.7	319	2	Q5TU72_ANOGA	Q5tu72 anopheles g
1181	36	38.7	319	2	Q39W53_GEOMG	Q39w53 geobacter m
1182	36	38.7	321	2	Q70KC5_EUCGU	Q70kc5 eucalyptus
1183	36	38.7	324	2	Q40MB1_DESAC	Q40mb1 desulfuromo
1184	36	38.7	326	2	Q3XB08_METFL	Q3xb08 methylobaci
1185	36	38.7	327	2	Q4PZF0_NEIGO	Q4pzf0 neisseria g
1186	36	38.7	327	2	Q5F966_NEIG1	Q5f966 neisseria g
1187	36	38.7	327	2	Q9JU60_NEIMA	Q9ju60 neisseria m
1188	36	38.7	327	2	Q9JZ63_NEIMB	Q9jz63 neisseria m
1189	36	38.7	330	2	Q3UDU4_MOUSE	Q3udu4 mus musculu
1190	36	38.7	331	2	Q68X12_RICTY	Q68x12 rickettsia
1191	36	38.7	332	1	LDHA_RAT	P04642 rattus norv
1192	36	38.7	332	2	Q7QPE7_GIALA	Q7qpe7 giardia lam
1193	36	38.7	334	2	Q6BHW7_DEBHA	Q6bhw7 debaryomyce
1194	36	38.7	335	2	Q8EPK6_OCEIH	Q8epk6 oceanobacil
1195	36	38.7	337	2	Q3CJ21_THEET	Q3cj21 thermoanaer
1196	36	38.7	338	2	Q9P5Y4_NEUCR	Q9p5y4 neurospora
1197	36	38.7	341	2	Q5R918_PONPY	Q5r918 pongo pygma
1198	36	38.7	343	2	Q6BQF7_DEBHA	Q6bqf7 debaryomyce
1199	36	38.7	349	2	Q8I4G2_CAEEL	Q8i4g2 caenorhabdi
1200	36	38.7	352	2	Q3KQ80_XENLA	Q3kq80 xenopus lae
1201	36	38.7	353	2	Q7VLV5_HAEDU	Q7vlv5 haemophilus
1202	36	38.7	354	2	Q8CAZ8_MOUSE	Q8caz8 mus musculu
1203	36	38.7	356	2	Q4UM00_RICFE	Q4um00 rickettsia
1204	36	38.7	356	2	Q6G5K5_BARHE	Q6g5k5 bartonella
1205	36	38.7	358	2	Q4Q0M2_LEIMA	Q4q0m2 leishmania
1206	36	38.7	359	1	PEX12_CRILO	Q9et67 cricetulus
1207	36	38.7	359	1	PEX12_HUMAN	O00623 homo sapien
1208	36	38.7	359	1	PEX12_MOUSE	Q8vc48 mus musculu
1209	36	38.7	359	2	Q3CQD5_ALTAT	Q3cqd5 pseudoalter
1210	36	38.7	359	2	Q3TLN1_MOUSE	Q3tln1 mus musculu
1211	36	38.7	359	2	Q5SWQ8_MOUSE	Q5swq8 m peroxisom
1212	36	38.7	361	2	Q7RU38_NEUCR	Q7ru38 neurospora
1213	36	38.7	361	2	Q54RJ5_DICDI	Q54rj5 dictyosteli
1214	36	38.7	363	2	Q93778_CAEEL	Q93778 caenorhabdi
1215	36	38.7	363	2	Q479L9_DECAR	Q47919 dechloromon
1216	36	38.7	364	2	Q43E91_9CHLB	Q43e91 chlorobium
1217	36	38.7	368	2	Q60MW8_CAEBR	Q60mw8 caenorhabdi
1218	36	38.7	370	2	Q6NGX8_CORDI	Q6ngx8 corynebacte
1219	36	38.7	373	2	Q4R318_MACFA	Q4r318 macaca fasc
1220	36	38.7	376	2	Q7PXM2_ANOGA	Q7pxm2 anopheles g
1221	36	38.7	378	2	Q3C074_XANC5	Q3c074 xanthomonas
1222	36	38.7	383	2	Q3H4I5_9ACTO	Q3h4i5 nocardioide
1223	36	38.7	383	2	Q7MPQ7_VIBVY	Q7mpq7 vibrio vuln
1224	36	38.7	384	2	Q7RGG2_PLAYO	Q7rgg2 plasmodium
1225	36	38.7	385	2	Q2UTE6_ASPOR	Q2ute6 aspergillus
1226	36	38.7	387	1	TOM40_YEAST	P23644 saccharomyc
1227	36	38.7	387	2	Q6B1Q9_YEAST	Q6b1q9 saccharomyc
1228	36	38.7	388	1	5HT4R_CAVPO	O70528 cavia porce
1229	36	38.7	389	1	RAD9A_MOUSE	Q9z0f6 mus musculu
1230	36	38.7	390	2	Q4K2Q5_STRPN	Q4k2q5 streptococc
1231	36	38.7	390	2	Q5LHH7_BACFN	Q5lhh7 bacteroides
1232	36	38.7	390	2	Q64YF1_BACFR	Q64yf1 bacteroides
1233	36	38.7	391	1	OMP41_PORGI	Q9s3r9 porphyromon
1234	36	38.7	391	2	Q60FT2_PORGI	Q60ft2 porphyromon
1235	36	38.7	393	2	Q5CBI2_9THEM	Q5cbi2 thermotoga
1236	36	38.7	396	2	Q30SJ8_THIDN	Q30sj8 thiomicrosp
1237	36	38.7	399	2	Q6BRL7_DEBHA	Q6brl7 debaryomyce
1238	36	38.7	401	2	O93408_XENLA	O93408 xenopus lae
1239	36	38.7	401	2	Q9YHW3_XENLA	Q9yhw3 xenopus lae
1240	36	38.7	403	1	YD87_SCHPO	Q10412 schizosacch
1241	36	38.7	408	2	Q4IC12_GIBZE	Q4ic12 gibberella
1242	36	38.7	408	2	Q336K5_HUMAN	Q336k5 homo sapien
1243	36	38.7	408	2	Q5BJM5_RAT	Q5bjm5 rattus norv
1244	36	38.7	408	2	Q9CXH2_MOUSE	Q9cxh2 mus musculu
1245	36	38.7	408	2	Q9JIY0_MOUSE	Q9jiy0 m tnf intra
1246	36	38.7	409	2	Q53GL0_HUMAN	Q53gl0 homo sapien
1247	36	38.7	409	2	Q9NRV3_HUMAN	Q9nrv3 homo sapien
1248	36	38.7	410	2	Q6Q2D6_BOMMO	Q6q2d6 bombyx mori
1249	36	38.7	411	2	Q6FJJ4_CANGA	Q6fjj4 candida gla
1250	36	38.7	413	2	Q2NID2_9EURY	Q2nid2 methanospha
1251	36	38.7	416	2	Q8SY00_DROME	Q8sy00 drosophila
1252	36	38.7	416	2	Q4V8D6_RAT	Q4v8d6 rattus norv
1253	36	38.7	419	2	Q5V694_HALMA	Q5v694 haloarcula
1254	36	38.7	419	2	Q9H2Y3_HUMAN	Q9h2y3 homo sapien
1255	36	38.7	419	2	Q9HAW0_HUMAN	Q9haw0 homo sapien
1256	36	38.7	419	2	Q9NUY6_HUMAN	Q9nuy6 homo sapien
1257	36	38.7	420	2	Q3UAW9_MOUSE	Q3uaw9 mus musculu
1258	36	38.7	420	2	Q9CZF0_MOUSE	Q9czf0 m 10, 11 da
1259	36	38.7	425	2	Q49AK1_HUMAN	Q49ak1 homo sapien
1260	36	38.7	425	2	Q4Q0L6_LEIMA	Q4q0l6 leishmania
1261	36	38.7	425	2	Q3QVK8_9RHOB	Q3qvk8 silicibacte
1262	36	38.7	430	2	Q4E138_TRYCR	Q4e138 trypanosoma
1263	36	38.7	431	2	Q56XT4_ARATH	Q56xt4 arabidopsis
1264	36	38.7	431	2	Q5LID0_BACFN	Q5lid0 bacteroides
1265	36	38.7	431	2	Q64ZF0_BACFR	Q64zf0 bacteroides
1266	36	38.7	431	2	Q87FT3_VIBPA	Q87ft3 vibrio para
1267	36	38.7	435	2	Q8IZ51_HUMAN	Q8iz51 homo sapien
1268	36	38.7	440	1	HIPA_ECOLI	P23874 escherichia
1269	36	38.7	440	2	P77507_ECOLI	P77507 escherichia
1270	36	38.7	442	2	Q2M0P7_DROPS	Q2m0p7 drosophila
1271	36	38.7	443	2	Q2PYG1_9BACT	Q2pyg1 uncultured
1272	36	38.7	447	2	Q4HII9_CAMCO	Q4hii9 campylobact

1273	36	38.7	448	2	Q2UQN3_ASPOR	Q2uqn3 aspergillus
1274	36	38.7	448	2	Q5XGM0_XENLA	Q5xgm0 xenopus lae
1275	36	38.7	449	2	O22820_ARATH	O22820 arabidopsis
1276	36	38.7	449	2	Q3EBH1_ARATH	Q3ebh1 arabidopsis
1277	36	38.7	452	2	Q4JLP9_LACRE	Q4jlp9 lactobacill
1278	36	38.7	455	2	Q7T3E7_BRARE	Q7t3e7 brachydanio
1279	36	38.7	458	2	Q4Z5A0_PLABE	Q4z5a0 plasmodium
1280	36	38.7	458	2	Q31IC7_THICR	Q31ic7 thiomicrosp
1281	36	38.7	460	2	Q3JCC9_NITOC	Q3jcc9 nitrosococc
1282	36	38.7	461	2	Q86KZ2_DICDI	Q86kz2 dictyosteli
1283	36	38.7	463	2	Q4UER5_THEAN	Q4uer5 theileria a
1284	36	38.7	465	2	Q37KR2_RHOPA	Q37kr2 rhodopseudo
1285	36	38.7	466	2	Q84UE2_MEDTR	Q84ue2 medicago tr
1286	36	38.7	470	2	Q9LUI1_ARATH	Q9lui1 arabidopsis
1287	36	38.7	470	2	Q68EK2_BRARE	Q68ek2 brachydanio
1288	36	38.7	478	2	Q9ESE0_RAT	Q9ese0 rattus norv
1289	36	38.7	481	2	Q3AQQ1_CHLCH	Q3aqq1 chlorobium
1290	36	38.7	483	1	UXAB_YERPE	Q8zic5 yersinia pe
1291	36	38.7	483	2	Q665N9_YERPS	Q665n9 yersinia ps
1292	36	38.7	486	2	Q6BRY8_DEBHA	Q6bry8 debaryomyce
1293	36	38.7	489	2	Q49YV7_STAS1	Q49yv7 staphylococ
1294	36	38.7	493	2	Q6CGB7_YARLI	Q6cgb7 yarrowia li
1295	36	38.7	500	2	Q52V15_9VIRU	Q52v15 mint virus
1296	36	38.7	501	2	Q8I5I6_PLAF7	Q8i5i6 plasmodium
1297	36	38.7	506	1	GAG_SIVM1	P05894 simian immu
1298	36	38.7	506	2	Q8H0D7_9GENT	Q8h0d7 ophiorrhiza
1299	36	38.7	509	2	Q8T3H5_DROME	Q8t3h5 drosophila
1300	36	38.7	509	2	Q9VVQ9_DROME	Q9vvq9 drosophila
1301	36	38.7	510	2	Q5EB91_RAT	Q5eb91 rattus norv
1302	36	38.7	513	2	Q3QEJ2_9GAMM	Q3qej2 shewanella
1303	36	38.7	514	2	Q5WQ06_9ENTR	Q5wq06 buchnera ap
1304	36	38.7	521	2	Q7RZ86_NEUCR	Q7rz86 neurospora
1305	36	38.7	531	2	Q4Q076_LEIMA	Q4q076 leishmania
1306	36	38.7	537	2	Q4YZ44_PLABE	Q4yz44 plasmodium
1307	36	38.7	541	2	Q661T7_BORGA	Q661t7 borrelia ga
1308	36	38.7	542	2	Q5ISA5_9PRIM	Q5isa5 saimiri bol
1309	36	38.7	543	1	YDE3_SCHPO	Q10437 schizosacch
1310	36	38.7	544	2	Q6ZNA6_HUMAN	Q6zna6 homo sapien
1311	36	38.7	545	2	Q5Z0Y3_NOCFA	Q5z0y3 nocardia fa
1312	36	38.7	550	2	Q8NJX0_YARLI	Q8njx0 yarrowia li
1313	36	38.7	550	2	Q9VAJ7_DROME	Q9vaj7 drosophila
1314	36	38.7	551	2	Q2S432_9SPHI	Q2s432 salinibacte
1315	36	38.7	552	2	Q51H50_ENTHI	Q51h50 entamoeba h
1316	36	38.7	555	2	Q8IIC9_PLAF7	Q8iic9 plasmodium
1317	36	38.7	555	2	Q6SZP8_PHYIN	Q6szp8 phytophthor
1318	36	38.7	555	2	Q46W20_RALEJ	Q46w20 ralstonia e
1319	36	38.7	556	2	Q91GC6_NPVEP	Q91gc6 epiphyas po
1320	36	38.7	558	1	GLTL1_MOUSE	Q9jj61 m putative
1321	36	38.7	558	1	SYQ_BRAJA	Q89kr6 bradyrhizob
1322	36	38.7	558	2	Q60GT0_MOUSE	Q60gt0 m udp-n-ace
1323	36	38.7	560	2	Q36UV7_RHOPA	Q36uv7 rhodopseudo
1324	36	38.7	560	2	Q6N5R6_RHOPA	Q6n5r6 rhodopseudo
1325	36	38.7	561	2	Q2IW97_RHOPA	Q2iw97 rhodopseudo
1326	36	38.7	562	1	SYQ_NEIMA	P57000 neisseria m
1327	36	38.7	562	1	SYQ_NEIMB	P56927 neisseria m
1328	36	38.7	563	2	Q35J92_9BRAD	Q35j92 bradyrhizob
1329	36	38.7	564	2	Q5E0C5_VIBF1	Q5e0c5 vibrio fisc
1330	36	38.7	564	2	Q7TP14_RAT	Q7tp14 rattus norv
1331	36	38.7	570	2	Q5CL15_CRYHO	Q5cl15 cryptospori
1332	36	38.7	570	2	Q5CPZ1_CRYPV	Q5cpz1 cryptospori
1333	36	38.7	573	2	Q5F7G0_NEIG1	Q5f7g0 neisseria g
1334	36	38.7	576	2	Q4C0A5_CROWT	Q4c0a5 crocosphaer
1335	36	38.7	579	1	Y751_OCEIH	Q8es91 oceanobacil
1336	36	38.7	579	2	Q9HRH7_HALSA	Q9hrh7 halobacteri
1337	36	38.7	579	2	Q4XVH9_PLACH	Q4xvh9 plasmodium
1338	36	38.7	580	2	Q4CBY3_CLOTM	Q4cby3 clostridium
1339	36	38.7	581	2	O74485_SCHPO	O74485 schizosacch
1340	36	38.7	584	2	Q583W8_9TRYP	Q583w8 trypanosoma
1341	36	38.7	586	2	Q8ELJ0_OCEIH	Q8elj0 oceanobacil
1342	36	38.7	586	2	Q4SDQ7_TETNG	Q4sdq7 tetraodon n
1343	36	38.7	594	1	DCE1_FELCA	P14748 felis silve
1344	36	38.7	594	1	DCE1_HUMAN	Q99259 homo sapien
1345	36	38.7	594	1	DCE1_PANTR	Q5is68 pan troglod
1346	36	38.7	594	1	DCE1_PIG	P48319 sus scrofa
1347	36	38.7	594	2	Q53TQ7_HUMAN	Q53tq7 homo sapien
1348	36	38.7	594	2	Q8IVA8_HUMAN	Q8iva8 homo sapien
1349	36	38.7	597	2	O16382_CAEEL	O16382 caenorhabdi
1350	36	38.7	597	2	Q6DEY9_XENTR	Q6dey9 xenopus tro
1351	36	38.7	598	2	Q6DCZ1_XENLA	Q6dcz1 xenopus lae
1352	36	38.7	602	2	Q6CLX0_KLULA	Q6clx0 kluyveromyc
1353	36	38.7	602	2	Q9N403_CAEEL	Q9n403 caenorhabdi
1354	36	38.7	605	2	Q5BE88_EMENI	Q5be88 aspergillus
1355	36	38.7	608	2	Q43QF1_SOLUS	Q43qf1 solibacter
1356	36	38.7	614	1	FBF1_CAEEL	Q9n5m6 caenorhabdi
1357	36	38.7	618	2	Q3PUK4_NITHA	Q3puk4 nitrobacter
1358	36	38.7	622	1	MUTL_CLOAB	Q97i20 clostridium
1359	36	38.7	624	1	GLSA2_BRAJA	Q89kv2 bradyrhizob
1360	36	38.7	627	2	Q3IQV3_NATPD	Q3iqv3 natronomona
1361	36	38.7	630	2	Q6BK57_DEBHA	Q6bk57 debaryomyce
1362	36	38.7	630	2	Q6KIK0_MYCMO	Q6kik0 mycoplasma
1363	36	38.7	633	1	GIDA2_FUSNN	Q8ri88 fusobacteri
1364	36	38.7	633	2	Q5E0B6_VIBF1	Q5e0b6 vibrio fisc
1365	36	38.7	638	2	Q2YBS6_NITMU	Q2ybs6 nitrosospir
1366	36	38.7	640	1	SRP72_YEAST	P38688 saccharomyc
1367	36	38.7	640	2	Q7RW79_NEUCR	Q7rw79 neurospora
1368	36	38.7	640	2	Q8SRH2_ENCCU	Q8srh2 encephalito
1369	36	38.7	643	2	Q8CTZ1_STAES	Q8ctz1 staphylococ
1370	36	38.7	643	2	Q9ERV6_MOUSE	Q9erv6 mus musculu
1371	36	38.7	644	2	Q9CGW3_LACLA	Q9cgw3 lactococcus
1372	36	38.7	646	2	Q2UQW8_ASPOR	Q2uqw8 aspergillus
1373	36	38.7	647	2	Q3Q7Y8_9GAMM	Q3q7y8 shewanella
1374	36	38.7	649	2	Q4HA25_9DEIO	Q4ha25 deinococcus
1375	36	38.7	652	2	Q6AI46_HUMAN	Q6ai46 homo sapien
1376	36	38.7	653	2	Q2WYY6_9GAMM	Q2wyy6 shewanella
1377	36	38.7	653	2	Q2ZR96_SHEPU	Q2zr96 shewanella
1378	36	38.7	654	2	Q9RYI7_DEIRA	Q9ryi7 deinococcus
1379	36	38.7	655	2	Q69ZR3_MOUSE	Q69zr3 mus musculu
1380	36	38.7	655	2	Q9WVF5_MOUSE	Q9wvf5 m epidermal
1381	36	38.7	656	2	Q5FC33_CAEEL	Q5fc33 caenorhabdi
1382	36	38.7	657	2	Q8C191_MOUSE	Q8c191 mus musculu
1383	36	38.7	662	2	Q90W36_COLLI	Q90w36 columba liv
1384	36	38.7	662	2	Q9YGX8_CHICK	Q9ygx8 gallus gall
1385	36	38.7	670	2	Q9LW73_ARATH	Q9lw73 arabidopsis
1386	36	38.7	670	2	Q896X0_CLOTE	Q896x0 clostridium
1387	36	38.7	671	2	Q6GW04_DICDI	Q6gw04 dictyosteli
1388	36	38.7	671	2	Q5RBH7_PONPY	Q5rbh7 pongo pygma
1389	36	38.7	672	2	Q37UW0_SPHAR	Q37uw0 novosphingo
1390	36	38.7	676	1	RPOC1_HUPLU	Q5scx9 huperzia lu
1391	36	38.7	682	2	Q3B0R1_SYNS9	Q3b0r1 synechococc
1392	36	38.7	684	2	Q86D21_CAEEL	Q86d21 caenorhabdi
1393	36	38.7	692	2	Q46CE3_METBA	Q46ce3 methanosarc
1394	36	38.7	694	2	Q7SEV8_NEUCR	Q7sev8 neurospora
1395	36	38.7	695	2	Q9UT10_SCHPO	Q9ut10 schizosacch
1396	36	38.7	695	2	Q350W7_9GAMM	Q350w7 alkalilimni
1397	36	38.7	703	2	Q6DI76_MOUSE	Q6di76 mus musculu
1398	36	38.7	704	2	Q61ZE4_CAEBR	Q61ze4 caenorhabdi
1399	36	38.7	705	2	Q4W276_9CALI	Q4w276 rabbit vesi
1400	36	38.7	714	2	Q7UPF6_RHOBA	Q7upf6 rhodopirell
1401	36	38.7	715	2	Q44AX7_SOLUS	Q44ax7 solibacter
1402	36	38.7	719	2	Q4IMH1_GIBZE	Q4imh1 gibberella
1403	36	38.7	725	1	SYTC_CAEEL	P52709 caenorhabdi
1404	36	38.7	729	2	Q94400_CAEEL	Q94400 caenorhabdi
1405	36	38.7	733	2	Q2M032_DROPS	Q2m032 drosophila
1406	36	38.7	735	2	Q6H5M0_ORYSA	Q6h5m0 oryza sativ
1407	36	38.7	741	1	RN5A_HUMAN	Q05823 homo sapien
1408	36	38.7	741	2	Q5W0L2_HUMAN	Q5w0l2 homo sapien
1409	36	38.7	741	2	Q5RAY3_PONPY	Q5ray3 pongo pygma
1410	36	38.7	752	2	Q9FKZ9_ARATH	Q9fkz9 arabidopsis
1411	36	38.7	770	2	Q96H55_HUMAN	Q96h55 homo sapien
1412	36	38.7	770	2	Q64QD3_BACFR	Q64qd3 bacteroides
1413	36	38.7	783	2	Q86ZJ7_PODAN	Q86zj7 podospora a
1414	36	38.7	783	2	Q9WJ22_9VIRU	Q9wj22 ophiostoma
1415	36	38.7	784	2	Q5NCP0_MOUSE	Q5ncp0 mus musculu
1416	36	38.7	787	2	Q4YXU8_PLABE	Q4yxu8 plasmodium
1417	36	38.7	788	2	Q7S4U7_NEUCR	Q7s4u7 neurospora
1418	36	38.7	792	2	Q74XG5_YERPE	Q74xg5 yersinia pe

1419	36	38.7	792	2	Q66FH7_YERPS	Q66fh7 yersinia ps
1420	36	38.7	792	2	Q8ZJ27_YERPE	Q8zj27 yersinia pe
1421	36	38.7	797	2	Q8IKP0_PLAF7	Q8ikp0 plasmodium
1422	36	38.7	799	2	Q2R0R4_ORYSA	Q2r0r4 oryza sativ
1423	36	38.7	805	2	Q2QX81_ORYSA	Q2qx81 oryza sativ
1424	36	38.7	809	2	Q2WPT0_CLOBE	Q2wpt0 clostridium
1425	36	38.7	813	2	Q2NIR1_9MOLU	Q2nir1 aster yello
1426	36	38.7	814	2	Q302R1_STRSU	Q302r1 streptococc
1427	36	38.7	816	2	Q48MX5_PSE14	Q48mx5 pseudomonas
1428	36	38.7	817	2	Q21854_CAEEL	Q21854 caenorhabdi
1429	36	38.7	818	2	Q5WA51_CHICK	Q5wa51 gallus gall
1430	36	38.7	818	2	Q5ZIH8_CHICK	Q5zih8 gallus gall
1431	36	38.7	819	2	Q2ZIH4_CALSA	Q2zih4 caldicellul
1432	36	38.7	819	2	Q3PTX1_NITHA	Q3ptx1 nitrobacter
1433	36	38.7	819	2	Q6YR62_ONYPE	Q6yr62 onion yello
1434	36	38.7	823	2	Q3MV46_9DELT	Q3mv46 syntrophoba
1435	36	38.7	825	2	Q7SHP1_NEUCR	Q7shp1 neurospora
1436	36	38.7	833	2	Q93HU8_ENTFA	Q93hu8 enterococcu
1437	36	38.7	836	2	Q6BL30_DEBHA	Q6bl30 debaryomyce
1438	36	38.7	846	2	Q6BUQ8_DEBHA	Q6buq8 debaryomyce
1439	36	38.7	852	1	SSY1_YEAST	Q03770 saccharomyc
1440	36	38.7	856	2	Q9CZ62_MOUSE	Q9cz62 m 10, 11 da
1441	36	38.7	860	2	Q4DXJ4_TRYCR	Q4dxj4 trypanosoma
1442	36	38.7	860	2	Q8DIX1_SYNEL	Q8dix1 synechococc
1443	36	38.7	861	2	Q53SM6_HUMAN	Q53sm6 homo sapien
1444	36	38.7	861	2	Q55CT4_DICDI	Q55ct4 dictyosteli
1445	36	38.7	865	1	GLND_BORBR	Q7wj96 bordetella
1446	36	38.7	865	1	GLND_BORPA	Q7wa62 bordetella
1447	36	38.7	865	1	GLND_BORPE	Q7vyd2 bordetella
1448	36	38.7	870	1	EPAS1_HUMAN	Q99814 homo sapien
1449	36	38.7	870	2	Q9XTA4_BOVIN	Q9xta4 bos taurus
1450	36	38.7	871	2	Q5H726_FUGRU	Q5h726 fugu rubrip
1451	36	38.7	884	2	Q50UK8_ENTHI	Q50uk8 entamoeba h
1452	36	38.7	886	2	Q8IEN6_PLAF7	Q8ien6 plasmodium
1453	36	38.7	888	2	Q31G41_THICR	Q31g41 thiomicrosp
1454	36	38.7	889	2	Q4P917_USTMA	Q4p917 ustilago ma
1455	36	38.7	891	2	Q75DC4_ASHGO	Q75dc4 ashbya goss
1456	36	38.7	892	2	Q8NQ92_CORGL	Q8nq92 corynebacte
1457	36	38.7	894	2	Q6MV75_NEUCR	Q6mv75 neurospora
1458	36	38.7	904	2	Q9W6G1_PROAT	Q9w6g1 protopterus
1459	36	38.7	911	2	Q7Z1H8_APLCA	Q7z1h8 aplysia cal
1460	36	38.7	912	2	Q9SUE7_ARATH	Q9sue7 arabidopsis
1461	36	38.7	916	2	Q5F807_NEIG1	Q5f807 neisseria g
1462	36	38.7	920	2	Q7S094_NEUCR	Q7s094 neurospora
1463	36	38.7	926	2	Q4UEX6_THEAN	Q4uex6 theileria a
1464	36	38.7	928	1	ATC1_YARLI	O43108 yarrowia li
1465	36	38.7	941	2	Q3RJY1_RALME	Q3rjy1 ralstonia m
1466	36	38.7	967	2	Q9X085_THEMA	Q9x085 thermotoga
1467	36	38.7	978	2	Q874G6_KLULA	Q874g6 kluyveromyc
1468	36	38.7	980	2	Q5VPE8_ORYSA	Q5vpe8 oryza sativ
1469	36	38.7	983	2	Q874C2_TRAVE	Q874c2 trametes ve
1470	36	38.7	1004	2	Q6H5Y7_ORYSA	Q6h5y7 oryza sativ
1471	36	38.7	1012	2	O96757_DROME	O96757 drosophila
1472	36	38.7	1012	2	Q9VFH9_DROME	Q9vfh9 drosophila
1473	36	38.7	1014	2	Q4WQD5_ASPFU	Q4wqd5 aspergillus
1474	36	38.7	1016	2	Q6TFU0_ERWAM	Q6tfu0 erwinia amy
1475	36	38.7	1016	2	Q8GFR7_CITFR	Q8gfr7 citrobacter
1476	36	38.7	1017	2	Q9LKV5_ARATH	Q9lkv5 arabidopsis
1477	36	38.7	1027	2	Q6CL64_KLULA	Q6cl64 kluyveromyc
1478	36	38.7	1051	2	Q6FR16_CANGA	Q6fr16 candida gla
1479	36	38.7	1053	2	Q7Q3D3_ANOGA	Q7q3d3 anopheles g
1480	36	38.7	1055	2	Q55HI4_CRYNE	Q55hi4 cryptococcu
1481	36	38.7	1055	2	Q5K722_CRYNE	Q5k722 cryptococcu
1482	36	38.7	1060	2	Q6CPI0_KLULA	Q6cpi0 kluyveromyc
1483	36	38.7	1067	2	Q874G3_SACEX	Q874g3 saccharomyc
1484	36	38.7	1070	2	Q874G2_SACEX	Q874g2 saccharomyc
1485	36	38.7	1072	2	Q4EG09_LISMO	Q4eg09 listeria mo
1486	36	38.7	1072	2	Q4EPE7_LISMO	Q4epe7 listeria mo
1487	36	38.7	1072	2	Q71Z25_LISMF	Q71z25 listeria mo
1488	36	38.7	1072	2	Q8Y6P0_LISMO	Q8y6p0 listeria mo
1489	36	38.7	1072	2	Q92B65_LISIN	Q92b65 listeria in
1490	36	38.7	1078	2	Q5CI20_CRYHO	Q5ci20 cryptospori
1491	36	38.7	1085	2	Q2R1Z6_ORYSA	Q2r1z6 oryza sativ
1492	36	38.7	1087	2	Q303Z6_ARATH	Q303z6 arabidopsis
1493	36	38.7	1090	2	Q2RR87_RHORU	Q2rr87 rhodospiril
1494	36	38.7	1093	2	Q54GV1_DICDI	Q54gv1 dictyosteli
1495	36	38.7	1098	2	Q6FKL7_CANGA	Q6fkl7 candida gla
1496	36	38.7	1099	2	Q54KF6_DICDI	Q54kf6 dictyosteli
1497	36	38.7	1112	1	SENP6_HUMAN	Q9gzr1 homo sapien
1498	36	38.7	1127	2	Q3E8X8_ARATH	Q3e8x8 arabidopsis
1499	36	38.7	1141	2	Q4I3Q3_GIBZE	Q4i3q3 gibberella
1500	36	38.7	1146	2	Q9VFI0_DROME	Q9vfi0 drosophila

ALIGNMENTS

RESULT 1
Q53R12_HUMAN
ID Q53R12_HUMAN PRELIMINARY; PRT; 229 AA.
AC Q53R12;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein FLJ22800.
GN Name=FLJ22800;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Nguyen C., Harris A., Meyer R.;
RT "The sequence of Homo sapiens BAC clone RP11-563C6.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.H.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Wilson R.K.;
RL Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
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CC ---
DR EMBL; AC097662; AAY24253.1; -; Genomic_DNA.
DR Ensembl; ENSG00000168955; Homo sapiens.
DR GO; GO:0016021; C:integral to membrane; IEA.
KW Hypothetical protein.
SQ SEQUENCE 229 AA; 25075 MW; 1718E0594997A1A1 CRC64;

Query Match 100.0%; Score 93; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 9.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSLVEEDQFSQNPISCFE 18
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Db 32 VSLVEEDQFSQNPISCFE 49

RESULT 2
Q5U609_HUMAN
ID Q5U609_HUMAN PRELIMINARY; PRT; 229 AA.
AC Q5U609;
DT 07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 07-DEC-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE TM4SF20 protein.
GN Name=TM4SF20;

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OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Colon;
RG   NIH MGC Project;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; BC035754; AAH35754.1; -; mRNA.
DR   Ensembl; ENSG00000168955; Homo sapiens.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR008661; L6_membrane.
DR   Pfam; PF05805; L6_membrane; 1.
SQ   SEQUENCE   229 AA;  25137 MW;  B750504AFD7C247D CRC64;

  Query Match            100.0%;  Score 93;  DB 2;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 9.7e-08;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VSLVEEDQFSQNPISCFE 18
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Db         32 VSLVEEDQFSQNPISCFE 49


RESULT 3
Q6UWS1_HUMAN
ID   Q6UWS1_HUMAN   PRELIMINARY;   PRT;   229 AA.
AC   Q6UWS1;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   TCCE518.
GN   ORFNames=UNQ518;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA   Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA   Wood W.I., Godowski P.J., Gray A.M.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
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CC   ---------------------------------------------------------------------
DR   EMBL; AY358671; AAQ89034.1; -; mRNA.
DR   Ensembl; ENSG00000168955; Homo sapiens.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR008661; L6_membrane.
DR   Pfam; PF05805; L6_membrane; 1.
SQ   SEQUENCE   229 AA;  25109 MW;  1718ED342C58C903 CRC64;

  Query Match            100.0%;  Score 93;  DB 2;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 9.7e-08;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VSLVEEDQFSQNPISCFE 18
              ||||||||||||||||||
Db         32 VSLVEEDQFSQNPISCFE 49


RESULT 4
Q9H5X9_HUMAN
ID   Q9H5X9_HUMAN   PRELIMINARY;   PRT;   229 AA.
AC   Q9H5X9;
DT   01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2001, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Hypothetical protein FLJ22800.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Ileal mucosa;
RA   Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
RA   Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
RA   Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,
RA   Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
RA   Isogai T., Sugano S.;
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AK026453; BAB15488.1; -; mRNA.
DR   Ensembl; ENSG00000168955; Homo sapiens.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR008661; L6_membrane.
DR   Pfam; PF05805; L6_membrane; 1.
SQ   SEQUENCE   229 AA;  25103 MW;  B7505D2798B34CDF CRC64;

  Query Match            100.0%;  Score 93;  DB 2;  Length 229;
  Best Local Similarity  100.0%;  Pred. No. 9.7e-08;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VSLVEEDQFSQNPISCFE 18
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Db         32 VSLVEEDQFSQNPISCFE 49
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RESULT 5
Q3T0Z4_BOVIN
ID   Q3T0Z4_BOVIN   PRELIMINARY;   PRT;   230 AA.
AC   Q3T0Z4;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-MAR-2006, entry version 4.
DE   Hypothetical protein.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Crossbred x Angus; TISSUE=Ileum;
RA   Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,
RA   Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C.,
RA   Wagner L., Bala M., Barbazuk S., Barber S., Babakaiff R., Beland J.,
RA   Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,
RA   Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D.,
RA   Siddiqui A., Holt R., Jones S.J., Marra M.A.;
RL   Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC102196; AAI02197.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR008661; L6_membrane.
DR   Pfam; PF05805; L6_membrane; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   230 AA;  25214 MW;  FF48895B0B2F6932 CRC64;

  Query Match             76.3%;  Score 71;  DB 2;  Length 230;
  Best Local Similarity   66.7%;  Pred. No. 0.00079;
  Matches   12;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VSLVEEDQFSQNPISCFE 18
              :: |:|||| :|||||||
Db         32 LNFVDEDQFFENPISCFE 49


RESULT 6
Q9CQY8_MOUSE
ID   Q9CQY8_MOUSE   PRELIMINARY;   PRT;   226 AA.
AC   Q9CQY8;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 20.
DE   11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length
DE   enriched library, clone:5033426G15 product:similar to CDNA: FLJ22800
DE   FIS, CLONE KAIA2630 (10 day old male pancreas cDNA, RIKEN full-length
DE   enriched library, clone:1810018L02 product:similar to CDNA: FLJ22800
DE   FIS, CLONE KAIA2630).
GN   Name=Tm4sf20;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
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RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
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RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
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RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
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RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
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RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
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RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AK017195; BAB30629.1; -; mRNA.
DR   EMBL; AK007532; BAB25093.1; -; mRNA.
DR   Ensembl; ENSMUSG00000026149; Mus musculus.
DR   MGI; MGI:1913511; Tm4sf20.
DR   GO; GO:0005615; C:extracellular space; RCA.
DR   GO; GO:0016021; C:integral to membrane; RCA.
DR   InterPro; IPR008661; L6_membrane.
DR   Pfam; PF05805; L6_membrane; 1.
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  Best Local Similarity  72.2%;  Pred. No. 0.0012;
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Qy          1 VSLVEEDQFSQNPISCFE 18
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Db         32 ISLVEADSTSQNPISCYE 49


RESULT 7
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ID   Q9D3Q0_MOUSE   PRELIMINARY;   PRT;   226 AA.
AC   Q9D3Q0;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 21.
DE   11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length
DE   enriched library, clone:5033430P14 product:similar to CDNA: FLJ22800
DE   FIS, CLONE KAIA2630.
GN   Name=Tm4sf20; Synonyms=1810018L02Rik;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
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RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
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RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
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RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
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RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
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RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
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RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
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RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
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RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
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RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
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RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AK017209; BAB30635.1; -; mRNA.
DR   Ensembl; ENSMUSG00000026149; Mus musculus.
DR   MGI; MGI:1913511; 1810018L02Rik.
DR   MGI; MGI:1913511; Tm4sf20.
DR   GO; GO:0005615; C:extracellular space; RCA.
DR   GO; GO:0016021; C:integral to membrane; RCA.
DR   InterPro; IPR008661; L6_membrane.
DR   Pfam; PF05805; L6_membrane; 1.
SQ   SEQUENCE   226 AA;  24786 MW;  3FE6BA06703344B7 CRC64;

  Query Match             75.3%;  Score 70;  DB 2;  Length 226;
  Best Local Similarity   72.2%;  Pred. No. 0.0012;
  Matches   13;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 VSLVEEDQFSQNPISCFE 18
              :|||| |  |||||||:|
Db         32 ISLVEADSTSQNPISCYE 49


RESULT 8
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ID   Q9D3R0_MOUSE   PRELIMINARY;   PRT;   226 AA.
AC   Q9D3R0;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 21.
DE   11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length
DE   enriched library, clone:5033405M13 product:similar to CDNA: FLJ22800
```

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DE   FIS, CLONE KAIA2630.
GN   Name=Tm4sf20; Synonyms=1810018L02Rik;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
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RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AK017154; BAB30618.1; -; mRNA.
DR   Ensembl; ENSMUSG00000026149; Mus musculus.
DR   MGI; MGI:1913511; 1810018L02Rik.
DR   MGI; MGI:1913511; Tm4sf20.
DR   GO; GO:0005615; C:extracellular space; RCA.
DR   GO; GO:0016021; C:integral to membrane; RCA.
DR   InterPro; IPR008661; L6_membrane.
DR   Pfam; PF05805; L6_membrane; 1.
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  Matches   13;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 VSLVEEDQFSQNPISCFE 18
              :|||| |  |||||||:|
Db         32 ISLVEADSTSQNPISCYE 49


RESULT 9
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ID   Q3FNJ8_9BURK   PRELIMINARY;   PRT;   445 AA.
AC   Q3FNJ8;
DT   08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT   08-NOV-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   ATP-binding region, ATPase-like:Histidine kinase, HAMP
DE   region:Histidine kinase A, N-terminal precursor.
GN   ORFNames=RferDRAFT_1076;
OS   Rhodoferax ferrireducens DSM 15236.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Comamonadaceae; Rhodoferax.
OX   NCBI_TaxID=338969;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=DSM 15236;
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Richardson P.;
RT   "Sequencing of the draft genome and assembly of Rhodoferax
RT   ferrireducens DSM 15236.";
RL   Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=DSM 15236;
RG   US DOE Joint Genome Institute (JGI-ORNL);
RA   Larimer F., Land M.;
RT   "Annotation of the draft genome assembly of Rhodoferax ferrireducens
RT   DSM 15236.";
RL   Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AAJK01000020; EAO39657.1; -; Genomic_DNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0016301; F:kinase activity; IEA.
DR   GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR003594; ATP_bd_ATPase.
DR   InterPro; IPR003660; His_kin_HAMP.
DR   InterPro; IPR004358; His_kin_like_C.
DR   InterPro; IPR003661; His_kinA_N.
DR   InterPro; IPR005467; His_kinase.
DR   Pfam; PF00672; HAMP; 1.
DR   Pfam; PF02518; HATPase_c; 1.
DR   Pfam; PF00512; HisKA; 1.
DR   PRINTS; PR00344; BCTRLSENSOR.
DR   SMART; SM00304; HAMP; 1.
DR   SMART; SM00387; HATPase_c; 1.
DR   SMART; SM00388; HisKA; 1.
DR   PROSITE; PS50885; HAMP; 1.
DR   PROSITE; PS50109; HIS_KIN; 1.
KW   ATP-binding; Kinase; Signal.
FT   SIGNAL        1     28       Potential.
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  Best Local Similarity   69.2%;  Pred. No. 20;
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Qy          1 VSLVEEDQFSQNP 13
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Db         84 VTLITEDQVSQNP 96


RESULT 10
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AC   Q43H61;
DT   13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   13-SEP-2005, sequence version 1.
DT   07-FEB-2006, entry version 2.
DE   Alpha amylase, catalytic region.
GN   ORFNames=Cpha266DRAFT_1397;
OS   Chlorobium phaeobacteroides DSM 266.
OC   Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC   Chlorobium/Pelodictyon group; Chlorobium.
OX   NCBI_TaxID=290317;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=DSM 266;
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Richardson P.;
RT   "Sequencing of the draft genome and assembly of Chlorobium
RT   phaeobacteroides DSM 266.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=DSM 266;
RG   US DOE Joint Genome Institute (JGI-ORNL);
RA   Larimer F., Land M.;
RT   "Annotation of the draft genome assembly of Chlorobium
RT   phaeobacteroides DSM 266.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
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CC   ---------------------------------------------------------------------
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DR   EMBL; AAIB01000010; EAM34995.1; -; Genomic_DNA.
DR   GO; GO:0004556; F:alpha-amylase activity; IEA.
DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR   InterPro; IPR006589; Alp_amyl_cat_sub.
DR   Pfam; PF00128; Alpha-amylase; 1.
SQ   SEQUENCE   505 AA;  58217 MW;  65006F5E47969D6E CRC64;

  Query Match             51.6%;  Score 48;  DB 2;  Length 505;
  Best Local Similarity   60.0%;  Pred. No. 23;
  Matches    9;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 VEEDQFSQNPISCFE 18
              | :|: ||:| ||||
Db        171 VSKDEQSQDPESCFE 185


RESULT 11
Q9C252_NEUCR
ID   Q9C252_NEUCR   PRELIMINARY;   PRT;   126 AA.
AC   Q9C252;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 18.
DE   Probable small nuclear ribonucleoprotein chain D2.
GN   Name=B18D24.220;
OS   Neurospora crassa.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX   NCBI_TaxID=5141;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA   Nyakatura G., Mewes H.W., Mannhaupt G.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   German Neurospora genome project;
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AL513466; CAC28820.1; -; Genomic_DNA.
DR   HSSP; P62316; 1B34.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0005732; C:small nucleolar ribonucleoprotein complex; IEA.
DR   GO; GO:0006397; P:mRNA processing; IEA.
DR   InterPro; IPR006649; Euk_arc_LSM_core.
DR   InterPro; IPR001163; LSM_snRNP_core.
DR   Pfam; PF01423; LSM; 1.
DR   ProDom; PD020287; snRNP; 1.
DR   SMART; SM00651; Sm; 1.
KW   Ribonucleoprotein; Viral nucleoprotein.
SQ   SEQUENCE   126 AA;  14372 MW;  5DD84379C2316C86 CRC64;

  Query Match             50.5%;  Score 47;  DB 2;  Length 126;
  Best Local Similarity   50.0%;  Pred. No. 7.3;
  Matches    9;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VSLVEEDQFSQNPISCFE 18
              |||:|| :|| |:|  :
Db         24 VSLLEEHEFSAGPLSILQ 41


RESULT 12
Q7V7K2_PROMM
ID   Q7V7K2_PROMM   PRELIMINARY;   PRT;   601 AA.
AC   Q7V7K2;
DT   01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2003, sequence version 1.
DT   07-MAR-2006, entry version 12.
DE   Hypothetical protein precursor.
GN   OrderedLocusNames=PMT0742;
OS   Prochlorococcus marinus (strain MIT 9313).
OC   Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC   Prochlorococcus.
OX   NCBI_TaxID=74547;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA   Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA   Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA   Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA   Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA   Webb E.A., Zinser E.R., Chisholm S.W.;
RT   "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT   niche differentiation.";
RL   Nature 424:1042-1047(2003).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; BX572097; CAE20917.1; -; Genomic_DNA.
DR   GenomeReviews; BX548175_GR; PMT0742.
DR   BioCyc; PMAR74547:PMT0742-MONOMER; -.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   InterPro; IPR013027; FAD_pyr_redox.
DR   Pfam; PF07992; Pyr_redox_2; 1.
KW   Complete proteome; Hypothetical protein; Signal.
FT   SIGNAL        1     28       Potential.
SQ   SEQUENCE   601 AA;  66706 MW;  AF953044BEB36E3B CRC64;

  Query Match             49.5%;  Score 46;  DB 2;  Length 601;
  Best Local Similarity   47.1%;  Pred. No. 64;
  Matches    8;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VSLVEEDQFSQNPISCF 17
              :: ||:|   || :|||
Db         78 IAKVEQDGLDQNWVSCF 94


RESULT 13
Q3IFH2_PSEHT
ID   Q3IFH2_PSEHT   PRELIMINARY;   PRT;   299 AA.
AC   Q3IFH2;
DT   08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT   08-NOV-2005, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Hypothetical protein.
GN   OrderedLocusNames=PSHAa2660; ORFNames=PSHAa2660;
OS   Pseudoalteromonas haloplanktis (strain TAC 125).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC   Pseudoalteromonadaceae; Pseudoalteromonas.
OX   NCBI_TaxID=326442;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=16169927; DOI=10.1101/gr.4126905;
RA   Medigue C., Krin E., Pascal G., Barbe V., Bernsel A., Bertin P.N.,
RA   Cheung F., Cruveiller S., D'Amico S., Duilio A., Fang G., Feller G.,
RA   Ho C., Mangenot S., Marino G., Nilsson J., Parrilli E., Rocha E.P.C.,
RA   Rouy Z., Sekowska A., Tutino M.L., Vallenet D., von Heijne G.,
RA   Danchin A.;
RT   "Coping with cold: the genome of the versatile marine Antarctica
RT   bacterium Pseudoalteromonas haloplanktis TAC125.";
RL   Genome Res. 15:1325-1335(2005).
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CC   ---------------------------------------------------------------------
DR   EMBL; CR954246; CAI87708.1; -; Genomic_DNA.
DR   InterPro; IPR006314; Dyp_peroxidase.
DR   Pfam; PF04261; Dyp_perox; 1.
DR   TIGRFAMs; TIGR01413; Dyp_perox_fam; 1.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   299 AA;  33889 MW;  7EDBD1DC9E461D40 CRC64;
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  Query Match             48.9%;  Score 45.5;  DB 2;  Length 299;
  Best Local Similarity   52.6%;  Pred. No. 36;
  Matches   10;  Conservative    4;  Mismatches    2;  Indels    3;  Gaps    1;

Qy          1 VSLVEE---DQFSQNPISC 16
              || :||   ||||:: :||
Db         38 VSAIEEEFSDQFSESMLSC 56


RESULT 14
Q4N5J1_THEPA
ID   Q4N5J1_THEPA   PRELIMINARY;   PRT;   143 AA.
AC   Q4N5J1;
DT   02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT   02-AUG-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Hypothetical protein.
GN   ORFNames=TP02_0299;
OS   Theileria parva.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
OC   Theileria.
OX   NCBI_TaxID=5875;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Muguga;
RX   PubMed=15994558; DOI=10.1126/science.1110439;
RA   Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
RA   Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.,
RA   Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
RA   Jiang L., Lynn J., Weaver B., Shoaibi A., Domingo A.R., Wasawo D.,
RA   Crabtree J., Wortman J.R., Haas B., Angiuoli S.V., Creasy T.H., Lu C.,
RA   Suh B., Silva J.C., Utterback T.R., Feldblyum T.V., Pertea M.,
RA   Allen J., Nierman W.C., Taracha E.L., Salzberg S.L., White O.R.,
RA   Fitzhugh H.A., Morzaria S., Venter J.C., Fraser C.M., Nene V.;
RT   "Genome Sequence of Theileria parva, a Bovine Pathogen That Transforms
RT   Lymphocytes.";
RL   Science 309:134-137(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Muguga;
RA   Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
RA   Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA   Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,
RA   Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R.,
RA   Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
RA   Utterback T., Feldblyum T., Pertea M., Allen J., Taracha E.L.,
RA   Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
RA   Fraser C.M., Nene V.;
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
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CC   ---------------------------------------------------------------------
DR   EMBL; AAGK01000002; EAN32582.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   143 AA;  16977 MW;  500D0921D3856550 CRC64;

  Query Match             48.4%;  Score 45;  DB 2;  Length 143;
  Best Local Similarity   50.0%;  Pred. No. 19;
  Matches    8;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 LVEEDQFSQNPISCFE 18
              ||::||| :| |  :|
Db         39 LVDDDQFPRNDIDIYE 54


RESULT 15
Q7T301_BRARE
ID   Q7T301_BRARE   PRELIMINARY;   PRT;   238 AA.
AC   Q7T301;
DT   01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2003, sequence version 1.
DT   07-FEB-2006, entry version 14.
DE   Basic helix-loop-helix domain containing, class B, 5.
GN   Name=bhlhb5;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RG   NIH MGC Project;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
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CC   ---------------------------------------------------------------------
DR   EMBL; BC053312; AAH53312.1; -; mRNA.
DR   Ensembl; ENSDARG00000025861; Danio rerio.
DR   ZFIN; ZDB-GENE-040426-1411; bhlhb5.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0030528; F:transcription regulator activity; IEA.
DR   GO; GO:0045449; P:regulation of transcription; IEA.
DR   InterPro; IPR001092; HLH_basic.
DR   InterPro; IPR011598; HLH_DNA_bd.
DR   Pfam; PF00010; HLH; 1.
DR   SMART; SM00353; HLH; 1.
DR   PROSITE; PS50888; HLH; 1.
SQ   SEQUENCE   238 AA;  25499 MW;  4F3D0949829EBF99 CRC64;

  Query Match             48.4%;  Score 45;  DB 2;  Length 238;
  Best Local Similarity   88.9%;  Pred. No. 34;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 SQNPISCFE 18
              ||:||||||
Db         17 SQSPISCFE 25


Search completed: November 21, 2006, 20:09:29
Job time : 86.367 secs
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